

| Result No. | Score | Query Match | Length | DB ID  | Description                               |
|------------|-------|-------------|--------|--------|---|
| 1          | 14    | 100.0       | 14     | W35340 | Human acetylcholinesterase                |
| 2          | 14    | 100.0       | 39     | R77010 | Alternative human C-terminal fragment     |
| 3          | 14    | 100.0       | 45     | W48800 | Human AChE splice                         |
| 4          | 14    | 100.0       | 45     | W68144 | Amino acid sequenc                        |
| 5          | 14    | 100.0       | 45     | W74586 | Human foetal acetylcholinesterase         |
| 6          | 14    | 100.0       | 500    | R06990 | Human acetylcholinesterase                |
| 7          | 14    | 100.0       | 614    | R06989 | Torpedo californicus acetylcholinesterase |
| 8          | 14    | 100.0       | 575    | W39078 | Torpedo californicus peptide fragment O   |
| 9          | 9     | 64.3        | 575    | W39079 | Streptococcus pneumoniae secreted protein |
| 10         | 9     | 64.3        | 35.7   | W63398 | Product of ORF 1 f                        |
| 11         | 5     | 35.7        | 12     | W61227 | ICAM-1 inhibiting protein                 |
| 12         | 5     | 35.7        | 111    | W74955 | Human platelet glycoprotein               |
| 13         | 5     | 35.7        | 136    | W32750 | Human LACI K1 derivative                  |
| 14         | 5     | 35.7        | 256    | P70559 | LACI K1 derivative                        |
| 15         | 5     | 35.7        | 261    | R63805 | Hepatitis C virus                         |
| 16         | 5     | 35.7        | 319    | R63349 | Human acetylcholinesterase                |
| 17         | 4     | 28.6        | 4      | W35341 | Human acetylcholinesterase                |
| 18         | 4     | 28.6        | 4      | W35342 | Human acetylcholinesterase                |
| 19         | 4     | 28.6        | 4      | W35343 | ICAM-1 inhibiting protein                 |
| 20         | 4     | 28.6        | 8      | R25957 | Human platelet glycoprotein               |
| 21         | 4     | 28.6        | 10     | W76015 | Human LACI K1 derivative                  |
| 22         | 4     | 28.6        | 12     | R78593 | Hepatitis C virus                         |
| 23         | 4     | 28.6        | 12     | R78578 | Hepatitis C virus                         |
| 24         | 4     | 28.6        | 12     | R96443 | Clot-inducing peptide                     |
| 25         | 4     | 28.6        | 12     | R96444 | Prorenin derived peptide                  |
| 26         | 4     | 28.6        | 13     | R67073 | Retro-peptide                             |
| 27         | 4     | 28.6        | 14     | W21535 | New Snake venom lopus                     |
| 28         | 4     | 28.6        | 14     | W21536 | Snake venom lopus                         |
| 29         | 4     | 28.6        | 15     | R26578 | Snake venom lopus                         |
| 30         | 4     | 28.6        | 15     | W50991 | Snake venom lopus                         |
| 31         | 4     | 28.6        | 15     | W50990 | Snake venom lopus                         |
| 32         | 4     | 28.6        | 15     | W50992 | Snake venom lopus                         |
| 33         | 4     | 28.6        | 15     | W50993 | Snake venom lopus                         |

|  |                                |
|--|--------------------------------|
| Title:   | US-09-155-076-1                |
| Perfect score:                                     | 14                             |
| Sequence:  | 1 AEHRWSSYMHWK 14              |
| Scoring table:                                     | OLIGO Gap0 60.0 , Gapext 60.0  |
| Searched:  | 188963 seqs, 23686106 residues |
| Word size :  | 0                              |
| Total number of hits satisfying chosen parameters: | 188963                         |
| Minimum DB seq length: 0                           |                                |
| Maximum DB seq length: 1000000                     |                                |
| Post-processing: Listing first 45 summaries        |                                |
| Database :   | A_Geneseq_36:*                 |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID  | Description                               |
|------------|-------|-------------|--------|--------|---|
| 1          | 14    | 100.0       | 14     | W35340 | Human acetylcholinesterase                |
| 2          | 14    | 100.0       | 39     | R77010 | Alternative human C-terminal fragment     |
| 3          | 14    | 100.0       | 45     | W48800 | Human AChE splice                         |
| 4          | 14    | 100.0       | 45     | W68144 | Amino acid sequenc                        |
| 5          | 14    | 100.0       | 45     | W74586 | Human foetal acetylcholinesterase         |
| 6          | 14    | 100.0       | 500    | R06990 | Human acetylcholinesterase                |
| 7          | 14    | 100.0       | 614    | R06989 | Torpedo californicus acetylcholinesterase |
| 8          | 14    | 100.0       | 575    | W39078 | Torpedo californicus peptide fragment O   |
| 9          | 9     | 64.3        | 575    | W39079 | Streptococcus pneumoniae secreted protein |
| 10         | 9     | 64.3        | 35.7   | W63398 | Product of ORF 1 f                        |
| 11         | 5     | 35.7        | 12     | W61227 | ICAM-1 inhibiting protein                 |
| 12         | 5     | 35.7        | 111    | W74955 | Human platelet glycoprotein               |
| 13         | 5     | 35.7        | 136    | W32750 | Human LACI K1 derivative                  |
| 14         | 5     | 35.7        | 256    | P70559 | LACI K1 derivative                        |
| 15         | 5     | 35.7        | 261    | R63805 | Hepatitis C virus                         |
| 16         | 5     | 35.7        | 319    | R63349 | Human acetylcholinesterase                |
| 17         | 4     | 28.6        | 4      | W35341 | Human acetylcholinesterase                |
| 18         | 4     | 28.6        | 4      | W35342 | Human acetylcholinesterase                |
| 19         | 4     | 28.6        | 4      | W35343 | ICAM-1 inhibiting protein                 |
| 20         | 4     | 28.6        | 8      | R25957 | Human platelet glycoprotein               |
| 21         | 4     | 28.6        | 10     | W76015 | Human LACI K1 derivative                  |
| 22         | 4     | 28.6        | 12     | R78593 | Hepatitis C virus                         |
| 23         | 4     | 28.6        | 12     | R78578 | Hepatitis C virus                         |
| 24         | 4     | 28.6        | 12     | R96443 | Hepatitis C virus                         |
| 25         | 4     | 28.6        | 12     | R96444 | Clot-inducing peptide                     |
| 26         | 4     | 28.6        | 13     | R67073 | Prorenin derived peptide                  |
| 27         | 4     | 28.6        | 14     | W21535 | Retro-peptide                             |
| 28         | 4     | 28.6        | 14     | W21536 | New Snake venom lopus                     |
| 29         | 4     | 28.6        | 15     | R26578 | Snake venom lopus                         |
| 30         | 4     | 28.6        | 15     | W50991 | Snake venom lopus                         |
| 31         | 4     | 28.6        | 15     | W50990 | Snake venom lopus                         |
| 32         | 4     | 28.6        | 15     | W50992 | Snake venom lopus                         |
| 33         | 4     | 28.6        | 15     | W50993 | Snake venom lopus                         |

## ALIGNMENTS

| RESULT | 1   |
|--------|---|
| ID     | W35340  |
| AC     | W35340;   |
| DT     | 17-APR-1998 (first entry)   |
| DE     | Human acetylcholinesterase 14-mer peptide.  |
| KW     | Acetylcholinesterase; AChE; neuronal degeneration; Parkinson's disease; Alzheimer's disease; stroke; cancer; calcium channel modulator; antibody; inhibitor.  |
| OS     | Homo sapiens.   |
| PN     | W09735962-A1. - <i>mut amyloid</i>  |
| PD     | 02-OCT-1997;  |
| PF     | 21-MAR-1997;  |
| PR     | 22-MAR-1996; GB-006040.   |
| PI     | (ISIS) ISIS INNOVATION LTD.   |
| DR     | WP: 97-489626/45.   |
| PT     | Peptide(s) from acetylcholine esterase which open calcium channels - used for treating disorders of the central nervous system, cancer and stroke.  |
| PS     | Claim 1; Page 20; 27pp; English.  |
| CC     | This 14-mer Peptide corresponds to residues 535-548 of the Acetylcholinesterase mature protein. This peptide is known to act alone or in synergism with a fragment of beta-amyloid to contribute to neuronal degeneration. Compounds that inhibit the biological activity of the novel peptides, and antibodies, can be used to control cytoplasmic calcium ion currents <i>in vivo</i> , and are useful for treating disorders of the central nervous system (e.g. Parkinson's and Alzheimer's diseases), stroke and cancer. |
| SQ     | Sequence 14 AA;   |

| Query Match | Best Local Similarity | Matches | Indels | DB | Gaps |
|-------------|-----------------------|---------|--------|----|------|
| QY          | 1 AEHRWSSYMHWK 14     | 0       | 0      | 0; | 0;   |
| Db          | 1 AEHRWSSYMHWK 14     | 0       | 0      | 0; | 0;   |

| RESULT | 2  |
|--------|--|
| ID     | R77010   |
| AC     | R77010;  |
| DT     | 31-MAR-1996 (first entry)  |
| KW     | Acetylcholinesterase; acetyl cholinesterase; EC-3.1.1.7; Chromosome-7q22; acetyl choline-hydrolyzing enzyme. |
| OS     | Homo sapiens.  |
| BN     | W0953158-A1.   |
| PD     | 31-AUG-1995;   |
| PR     | 28-FEB-1995; 022866.   |
| PR     | 28-FEB-1994; 18-20255;   |
| PR     | 09-JAN-1995; US-370156.  |
| PA     | (KOHN) KOHN, K. I.   |

| RESULT | 1                                |
|--------|----------------------------------|
| ID     | R77010 standard; Protein; 39 AA. |
| AC     | R77010;                          |

(YISS ) YISSUM RES & DEV CO;  
 PA Shani M, Soreq H, Zakut H;  
 PI WPI; 95\_31109/40.  
 Alternative forms of human acetyl cholinesterase (ChE) gene -  
 expressed in transgenic animal assay system for evaluating anti-ChE  
 activity of organo-phosphate(s), etc. or as model of ChE imbalance  
 Disclosure; Fig.; 55PP; English.

PT Human acetylcholinesterase (EC-3.1.1.7) is accumulated at  
 CC neuromuscular junctions where it serves a vital function in  
 CC modulating cholinergic neurotransmission. This alternatively  
 spliced form of human AChE may be expressed in transgenic animals  
 CC which are used in an assay system for determining the anti-ChE  
 activity of organophosphates, carbamates, anti-ChE drugs, plant  
 CC glycoalkaloids and snake venoms.  
 SQ Sequence 39 AA;

Query Match 100.0%; Score 14; DB 1; Length 45;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-10;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYMYHWK 14  
 Db 17 AEFHRWSSYMYHWK 30

RESULT 4  
 W68144 standard; Protein: 45 AA.  
 ID W68144  
 AC W68144;  
 DE Human AChE splice variant E1-4, 6.  
 DT 05-OCT-1998 (first entry)  
 KW Nucleic acid sequence; acetylcholinesterase; human; myasthenia gravis;  
 KW Acetylcholinesterase; Alzheimer's disease; central nervous system;  
 KW neuromuscular junction; cholinergic signalling; brain.  
 KW Homo sapiens.  
 OS Homo sapiens.  
 PN W09826062-A2.  
 PD 18-JUN-1998  
 PF 12-DEC-1997; D23598.  
 PR 21-JUL-1997; D235334.  
 PR 12-DEC-1996; US-035366.  
 PR 13-FEB-1997; US-037777.  
 PR 02-MAY-1997; US-037777.  
 PA (KOHN) KORN K I.  
 PA (YISS ) YISSUM RES & DEV CO.  
 PI Eckstein F, Friedman A, Raufer D, Seidman S, Soreq H;  
 DR WPI; 98-3-8522/30.  
 PT Synthetic nucleic acid resistant antisense oligodeoxynucleotides -  
 directed against acetylcholinesterase, useful for treating  
 Parkinson's and Alzheimer's diseases and myasthenia gravis  
 Disclosure; Fig 12; 89PP; English.  
 PS This represents the amino acid sequence of a human acetylcholinesterase  
 (AChE) splice variant. The invention provides sequences shown in W41278  
 to W41285 that represent synthetic nucleic acids resistant antisense  
 oligodeoxynucleotides which are capable of selectively modulating human  
 acetylcholinesterase (AChE) production. These oligonucleotides are  
 targeted to a splice junction in a splice variant of AChE mRNA and are  
 capable of selectively modulating human AChE production in the central  
 nervous system and neuromuscular junction. The invention also provides a  
 method for determining the efficacy of these human AChE specific  
 antisense oligonucleotides. These antisense oligonucleotides can be used  
 to restore balanced cholinergic signalling in the brain. Particularly  
 related to learning and memory as well as stress disorders. Parkinson's  
 and Alzheimer's disease. They can also be used to reduce production and  
 therefore deposition of AChE in the neuromuscular junctions of patients  
 with e.g. myasthenia gravis. The oligonucleotides work effectively at low  
 doses while avoiding many of the side effects associated with Tacrine and  
 related cholinergic drugs for Alzheimer's disease and Pyridostigmine and  
 related drugs for myasthenia gravis.  
 SQ Sequence 45 AA;

Query Match 100.0%; Score 14; DB 1; Length 45;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-10;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYMYHWK 14  
 Db 17 AEFHRWSSYMYHWK 30

RESULT 5  
 W74386 standard; Protein: 45 AA.  
 ID W74386  
 AC W74386;  
 DT 21-DEC-1998 (first entry)  
 DE Amino acid sequence of the human AChE variant 1.  
 KW Nucleic acid resistance; inhibition; human; acetyl-cholinesterase; AChE;

(YISS ) YISSUM RES & DEV CO;  
 PA Shani M, Soreq H, Zakut H;  
 PI WPI; 95\_31109/40.  
 Alternative forms of human acetyl cholinesterase (ChE) gene -  
 expressed in transgenic animal assay system for evaluating anti-ChE  
 activity of organo-phosphate(s), etc. or as model of ChE imbalance  
 Disclosure; Fig.; 55PP; English.

PT Human acetylcholinesterase (EC-3.1.1.7) is accumulated at  
 CC neuromuscular junctions where it serves a vital function in  
 CC modulating cholinergic neurotransmission. This alternatively  
 spliced form of human AChE may be expressed in transgenic animals  
 CC which are used in an assay system for determining the anti-ChE  
 activity of organophosphates, carbamates, anti-ChE drugs, plant  
 CC glycoalkaloids and snake venoms.  
 SQ Sequence 39 AA;

Query Match 100.0%; Score 14; DB 1; Length 45;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-10;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYMYHWK 14  
 Db 17 AEFHRWSSYMYHWK 30

RESULT 4  
 W68144 standard; Protein: 45 AA.  
 ID W68144  
 AC W68144;  
 DE Human AChE splice variant E1-4, 6.  
 DT 05-OCT-1998 (first entry)  
 KW Nucleic acid sequence; acetylcholinesterase; human; myasthenia gravis;  
 KW Acetylcholinesterase; Alzheimer's disease; central nervous system;  
 KW neuromuscular junction; cholinergic signalling; brain.  
 KW Homo sapiens.  
 OS Homo sapiens.  
 PN W09826062-A2.  
 PD 18-JUN-1998  
 PF 12-DEC-1997; D23598.  
 PR 21-JUL-1997; D235334.  
 PR 12-DEC-1996; US-035366.  
 PR 13-FEB-1997; US-037777.  
 PR 02-MAY-1997; US-037777.  
 PA (KOHN) KORN K I.  
 PA (YISS ) YISSUM RES & DEV CO.  
 PI Eckstein F, Friedman A, Raufer D, Seidman S, Soreq H;  
 DR WPI; 98-3-8522/30.  
 PT Synthetic nucleic acid resistant antisense oligodeoxynucleotides -  
 directed against acetylcholinesterase, useful for treating  
 Parkinson's and Alzheimer's diseases and myasthenia gravis  
 Disclosure; Fig 12; 89PP; English.  
 PS This represents the amino acid sequence of a human acetylcholinesterase  
 (AChE) splice variant. The invention provides sequences shown in W41278  
 to W41285 that represent synthetic nucleic acids resistant antisense  
 oligodeoxynucleotides which are capable of selectively modulating human  
 acetylcholinesterase (AChE) production. These oligonucleotides are  
 targeted to a splice junction in a splice variant of AChE mRNA and are  
 capable of selectively modulating human AChE production in the central  
 nervous system and neuromuscular junction. The invention also provides a  
 method for determining the efficacy of these human AChE specific  
 antisense oligonucleotides. These antisense oligonucleotides can be used  
 to restore balanced cholinergic signalling in the brain. Particularly  
 related to learning and memory as well as stress disorders. Parkinson's  
 and Alzheimer's disease. They can also be used to reduce production and  
 therefore deposition of AChE in the neuromuscular junctions of patients  
 with e.g. myasthenia gravis. The oligonucleotides work effectively at low  
 doses while avoiding many of the side effects associated with Tacrine and  
 related cholinergic drugs for Alzheimer's disease and Pyridostigmine and  
 related drugs for myasthenia gravis.  
 SQ Sequence 45 AA;

Query Match 100.0%; Score 14; DB 1; Length 45;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-10;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYMYHWK 14  
 Db 17 AEFHRWSSYMYHWK 30

RESULT 5  
 W74386 standard; Protein: 45 AA.  
 ID W74386  
 AC W74386;  
 DT 21-DEC-1998 (first entry)  
 DE Amino acid sequence of the human AChE variant 1.  
 KW Nucleic acid resistance; inhibition; human; acetyl-cholinesterase; AChE;

*[Signature]*

KW Central nervous system; CNS.  
 OS Homo sapiens.  
 PN WO9839486-A1.  
 PD 11-SEP-1998.  
 PR 06-MAR-1998; D04503.  
 PR 06-MAR-1992; US-040203.

PA (YISS ) YISSUM RES & DEV CO.  
 PI Seidman S, Shoham E, Soreq H;  
 DR 98-506377/43.  
 PT Treatment of injury to central nervous system - by administration of:  
 inhibitor of acetyl-cholinesterase production  
 Disclosure; Page 61; 88pp; English.  
 This is the amino acid sequence of a human acetyl-cholinesterase (AChE) variant used in the method of the invention, where inhibitors of AChE are used to treat injury to the central nervous system (CNS). The AChE inhibitor can also be used to facilitate transplantation of neuronal cells to the CNS of a patient. The inhibitor can also be used to improve hippocampal neuron survival following injury to the CNS. The CNS injuries that can be treated with the method include epilepsy, stroke, Huntington's disease, head injury, spinal injury, pain, Parkinson's disease, myelin deficiencies, neuromuscular disorders, neurological pain, amyotrophic lateral sclerosis, Alzheimer's disease, and affective disorders of the brain. Sequence 45 AA;

Query Match 100.0%; Score 14; DB 1; Length 45;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-10; Indels 0; Gaps 0;

Qy 1 AEFRHSSSYMYHWK 14  
 Db 17 AEFRHSSSYMYHWK 30

RESULT 6

R06990 R06990 standard; protein; 500 AA.  
 ID R06990  
 AC R06990  
 DT 16-JAN-1991 (first entry)  
 DE Human foetal acetylcholinesterase (hAChE) primary transcript.  
 KW Organophosphorous poisoning; OP; cancer; leukaemia;  
 KW megakaryocytopoiesis; ovarian cancer.  
 OS Homo sapiens.  
 PN EP-388806-A.  
 ND 26-SEP-1990.  
 PR 20-MAR-1990; 105274.  
 PR 21-MAR-1989; IL-089703.  
 PA (YISS ) YISSUM RES & DEV CO.

PI Soreq H, Zakut H;  
 DR 98-291865/39.  
 PR Human acetyl-cholinesterase DNA and prodn. of recombinant hAChE - for treatment of organo-phosphorous poisoning, and diagnosis of haemocytopenic disorders and ovarian carcinomas.  
 Disclosure; Fig 1c; 41pp; English.  
 Gene product is useful as an active pharmaceutical component for the prophylaxis and treatment of organophosphorous poisoning, and post-surgical apnea due to succinylcholine administration. cDNA probe to the sequence may be used in diagnosis of various leukaemias, abnormal megakaryocytopoiesis and ovarian carcinomas. Sequence 500 AA;

Query Match 100.0%; Score 14; DB 1; Length 500;  
 Best Local Similarity 100.0%; Pred. No. 9.4e-10; Indels 0; Gaps 0;

Qy 1 AEFRHSSSYMYHWK 14  
 Db 472 AEFRHSSSYMYHWK 485

RESULT 7

R06989 R06989 standard; protein; 613 AA.  
 ID R06989  
 AC R06989  
 DT 16-JAN-1991 (first entry)  
 DE Human acetylcholinesterase (hAChE) primary transcript.  
 KW Organophosphorous poisoning; OP; cancer; leukaemia;  
 KW megakaryocytopoiesis; ovarian cancer.  
 OS Homo sapiens.  
 PN EP-388906-A.  
 DR 90-291865/39.

PT 26-SEP-1990; 105274.  
 PR 20-MAR-1990; 105274.  
 PA (YISS ) YISSUM RES & DEV CO.  
 PI Soreq H, Zakut H;  
 DR 90-291865/39.  
 PR Human acetyl-cholinesterase DNA and prodn. of recombinant hAChE - for treatment of organo-phosphorous poisoning, and diagnosis of haemocytopenic disorders and ovarian carcinomas.  
 Disclosure; Page 25; 47pp; English.  
 Gene Product is useful as an active pharmaceutical component for the prophylaxis and treatment of organophosphorous Poisoning, and post-surgical apnea due to succinylcholine administration. cDNA probe to the sequence may be used in diagnosis of various leukemias, abnormal megakaryocytopoiesis and ovarian carcinomas. Sequence 613 AA;

Query Match 100.0%; Score 14; DB 1; Length 613;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-09; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFRHSSSYMYHWK 14  
 Db 585 AEFRHSSSYMYHWK 598

RESULT 8

R80726 R80726 standard; protein; 614 AA.  
 ID R80726  
 AC R80726  
 DT 31-MAR-1996 (first entry)  
 DE Human acetylcholinesterase (AChE) protein.  
 KW Acetylcholinesterase; acetyl cholinesterase; EC-3.1.1.7;  
 KW chromosome-7q22; acetylcholine-hydrolyzing enzyme.  
 OS Homo sapiens.  
 PN WO93151-A1.  
 PD 31-AUG-1995; U02806.  
 PR 28-FEB-1995; U02806.  
 PR 09-JAN-1995; US-570155.  
 PA (KOHN /) KOHN K I.  
 PA (YISS ) YISSUM RES & DEV CO.  
 PI Shani M, Soreq H, Zakut H;  
 DR 95-3111499/40.  
 DR N/PDB; Q99002.

PT Alternative forms of human acetyl cholinesterase (ChE) gene - expressed in transgenic animal assay system for evaluating anti-ChE activity of organo-phosphate(s), etc. or as model of ChE imbalance Claim 3; Fig 1B; 55pp; English.  
 Gene product is accumulated at neuromuscular junctions where it serves a vital function in modulating cholinergic neurotransmission. Alternatively spliced forms of human AChE may be expressed in transgenic animals which are used in an assay system for determining the anti-ChE activity of organophosphates, carbamates, anti-ChE drugs, plant glycoalkaloids and snake venoms. Sequence 614 AA;

Query Match 100.0%; Score 14; DB 1; Length 614;

Best Local Similarity 100.0%; Pred. No. 1.1e-09;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEPRWSSYMWIK 14  
DB 586 AEPRWSSYMWIK 599

RESULT 9

W39078 standard; protein; 575 AA.  
AC W39078;  
DT 08-APR-1998 (first entry)  
DE Torpedo californica acetylcholinesterase AChE.  
KW Acetylcholinesterase; AChE; organophosphate; detoxification; oxime;  
KW ray; chemical agent; treatment; prevention; aging; mutant.  
OS Torpedo californica.  
FH Location/Qualifiers  
Region 67 .94 "region as indicated in specification"  
FT Modified\_site 59 .61 "note= "site as indicated in specification."  
FT Region 254 .265 "note= "site as indicated in specification"  
FT Region 402 .521 "note= "site as indicated in specification"  
FT Modified\_site 416 .418 "note= "site as indicated in specification"  
FT Modified\_site 457 .459 "note= "site as given in specification"  
FT Modified\_site 533 .535 "note= "site as given in specification"  
FT PD 09-DEC-1997; 348920.  
FT PN US5695750-A.  
PR 25-NOV-1994; US 348920.  
PA (USSA ) US SEC OF ARMY.  
PI Doctor BP, Maxwell D, Radic Z, Saxena A, Taylor P;  
DR WPI: 98-041233/04.  
PT Mutant Torpedo acetyl:cholinesterase - useful for detoxifying  
organo-phosphate compounds  
PS Claim 1: FIG 2; 12pp; English.  
CC This sequence represents a variant of the enzyme acetylcholinesterase  
CC (AChE) from Torpedo californica which is capable of detoxifying  
CC organophosphates. This E1990 mutant has greater resistance to aging  
CC than the wild-type AChE and can destroy organophosphates in an  
CC environmentally friendly manner. When combined with an oxime, this  
CC mutant's ability to detoxify several organophosphates is amplified  
CC and is predicted to have applications for the detoxification of chemical  
CC warfare agents such as sarin or as a means of treating or preventing the  
CC deleterious effects of organophosphate exposure in organisms.  
SQ Sequence 575 AA;

Query Match 64.3%; Score 9; DB 1; Length 575;  
Best Local Similarity 100.0%; Pred. No. 0.001; Mismatches 0; Indels 0; Gaps 0;

QY 2 EFHRWSSYM 10  
DB 548 EFHRWSSYM 556

RESULT 11

R63398 standard; Protein; 12 AA.  
ID R63398  
AC R63398;  
DT 09-AUG-1995 (first entry)  
DE Peptide fragment of VI region of hepatitis C virus.  
KW Hepatitis C virus; HCV; Primer; probe; detection; diagnosis;  
KW classification; immunisation; prophylaxis; serotyping.  
OS Hepatitis C virus.  
PN WO9125601-A.  
AC R63398;  
DT 10-NOV-1994.  
DE Peptide fragment of VI region of hepatitis C virus - and related  
KW vectors, polypeptide(s) and antibodies, useful for immunisation,  
KW treatment, diagnosis and typing of HCV isolates  
OS (INNO-) INNOGENETICS NV SA.  
PA Maerens G, Stuyver L;  
DR WPI: 94-358277/44.  
PT New polynucleotide sequences from hepatitis C virus - and related  
PT vectors, polypeptide(s) and antibodies, useful for immunisation,  
PT treatment, diagnosis and typing of HCV isolates  
PS Claim 15; Page 277; 404pp; English  
CC Compositions comprising at least 5, and pref. 8 or more contiguous  
CC nucleotides selected from an HCV type 3 genomic sequence, more  
CC particularly (i) the region spanning positions 417-957 of the  
Core/E1 region of HCV subtype 3a; (ii) the region spanning positions

Best Local Similarity 100.0%; Pred. No. 1.1e-09;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEPRWSSYMWIK 14  
DB 586 AEPRWSSYMWIK 599

RESULT 9

W39078 standard; protein; 575 AA.  
AC W39078;  
DT 08-APR-1998 (first entry)  
DE Torpedo californica acetylcholinesterase AChE mutant E1990.  
KW Acetylcholinesterase; AChE; organophosphate; detoxification; oxime;  
KW ray; chemical agent; treatment; prevention; aging; mutant.  
OS Torpedo californica.  
OS Synthetic.  
FH Location/Qualifiers

CC 4664-4730 of the NS3 region of HCV type 3; (iii) the region spanning CC positions 4832-5232 of the NS3/4 region of HCV type 3; (iv) the CC region spanning positions 8023-8235 of the NS5 region of the BR36 subgroup of HCV subtype 3a; or (v) an HCV subtype 3c genomic sequence; or, from a subtype 2d genomic sequence, a type 4 genomic sequence; or the coding region of subtype 5a, may be used as primers to amplify nucleic acid from isolates belonging to a specific genotype, or as a probe for specific detection/classification of such nucleic acid. Polypeptides encoded by the nucleotides in such compositions may be used for immunisation against HCV, for the detection of antibodies directed against HCV and for serotyping. This polypeptide corresponds to positions 192-203 of the V1 region of HCV. Sequence 12 AA;

| Query Match           | Score        | DB       | Length |
|-----------------------|--------------|----------|--------|
| Best Local Similarity | 35.7%        | 1        | 12;    |
| Matches               | 100.0%       | No. 2,3; |        |
| 5;                    | Conservative | 0;       |        |
| Db                    | Mismatches   | Indels   | Gaps   |
| SQ                    | 0;           | 0;       | 0;     |

RESULT 12

W61227 standard: Protein: 111 AA.  
AC W61227;  
DT 02-OCT-1998 (first entry)

DE Streptococcus pneumoniae Sp102 protein;  
KW Streptococcus pneumoniae; antigen; vaccine; infection; diagnosis;  
KW detection; pneumonia; otitis media; meningitis.  
OS Streptococcus pneumoniae.

PN W09818930-A2.  
PD 07-MAY-1998.  
PR 30-OCT-1996; US-029960.  
(HOMA-) HUMAN GENOME SCI. INC.  
PI Choi GH, Hromockyj A, Johnson LS, Kunsch CA;  
DR WPI: 98-272224/24.  
DR N-PSDB; V27413.

PT Nucleic acid encoding antigenic peptide(s) from Streptococcus pneumoniae - or their epitope-containing fragments, useful in protective or therapeutic vaccines, and for diagnosis  
PT Claim 11; Page 85; 118pp; English.  
PS The present sequence represents a protein from Streptococcus pneumoniae. The nucleic acid sequence encoding the Streptococcus pneumoniae protein can be useful in vaccines for inducing protective antibodies against Streptococcus pneumoniae, for treatment or prevention of infection e.g. pneumonia, otitis media or meningitis. Probes based on the nucleic acid are used to detect Streptococcus infection (by usual hybridisation or amplification methods), also for isolating Streptococcus genes or their allelic variants. The protein can be used similarly to detect specific antibodies in standard immunoassays, especially for diagnosing or monitoring infections. Antibodies which bind the protein are used to detect corresponding antigens, to purify the protein and for passive e.g. by injection, orally or through the skin, vaccines are administered, (especially 10-3000 mu g/ml per dose). Sequence 111 AA;

| Query Match           | Score        | DB      | Length |
|-----------------------|--------------|---------|--------|
| Best Local Similarity | 35.7%        | 1       | 111;   |
| Matches               | 100.0%       | No. 15; |        |
| 5;                    | Conservative | 0;      |        |
| Db                    | Mismatches   | Indels  | Gaps   |
| SQ                    | 0;           | 0;      | 0;     |

Qy 1 AEFRR 5  
Db 37 AEFR 41

RESULT 13

W74955

ID W74955; standard; Protein: 136 AA.

AC W74955;

DT 25-JAN-1999 (first entry)

DE Human secreted protein encoded by gene 77 clone HOEAS24.

KW Human; secreted protein; testis; tumour; fetal brain tissue;

KW fusion protein; cancer; central nervous system; seizure;

KW diagnosis; neurodegenerative disease.

OS Homo sapiens

Key Location/Qualifiers

FH Mic-difference 136

FT /label= unknown

PN W09839448-A2.

PD 11-SEP-1998;

PP 004493.

PR 06-MAR-1998; US-061060

PR 02-OCT-1997; US-061060

PR 07-MAR-1997; US-038621

PR 07-MAR-1997; US-040162

PR 07-MAR-1997; US-040163

PR 07-MAR-1997; US-040163

PR 07-MAR-1997; US-040333

PR 07-MAR-1997; US-040334

PR 07-MAR-1997; US-040336

PR 07-MAR-1997; US-04066

PR 11-APR-1997; US-043311

PR 11-APR-1997; US-043312

PR 11-APR-1997; US-043313

PR 11-APR-1997; US-043314

PR 11-APR-1997; US-043568

PR 11-APR-1997; US-043576

PR 11-APR-1997; US-043578

PR 11-APR-1997; US-043580

PR 11-APR-1997; US-043669

PR 11-APR-1997; US-043670

PR 11-APR-1997; US-043671

PR 11-APR-1997; US-043674

PR 11-APR-1997; US-043677

PR 23-MAY-1997; US-047492

PR 23-MAY-1997; US-047500

PR 23-MAY-1997; US-047501

PR 23-MAY-1997; US-047502

PR 23-MAY-1997; US-047503

PR 23-MAY-1997; US-047581

PR 23-MAY-1997; US-047582

PR 23-MAY-1997; US-047588

PR 23-MAY-1997; US-047589

PR 23-MAY-1997; US-047584

PR 23-MAY-1997; US-047585

PR 23-MAY-1997; US-047592

PR 23-MAY-1997; US-047593

PR 23-MAY-1997; US-047594

PR 23-MAY-1997; US-047595

PR 23-MAY-1997; US-047596

PR 23-MAY-1997; US-047597

PR 23-MAY-1997; US-047598

PR 23-MAY-1997; US-047600

PR 23-MAY-1997; US-047601

PR 23-MAY-1997; US-047612

PR 23-MAY-1997; US-047613

PR 23-MAY-1997; US-047614

PR 23-MAY-1997; US-047615

PR 23-MAY-1997; US-047617

PR 23-MAY-1997; US-047618

PR 23-MAY-1997; US-047632

PR 23-MAY-1997; US-047633

PR 06-JUN-1997; US-048964

PR 06-JUN-1997; US-048974,

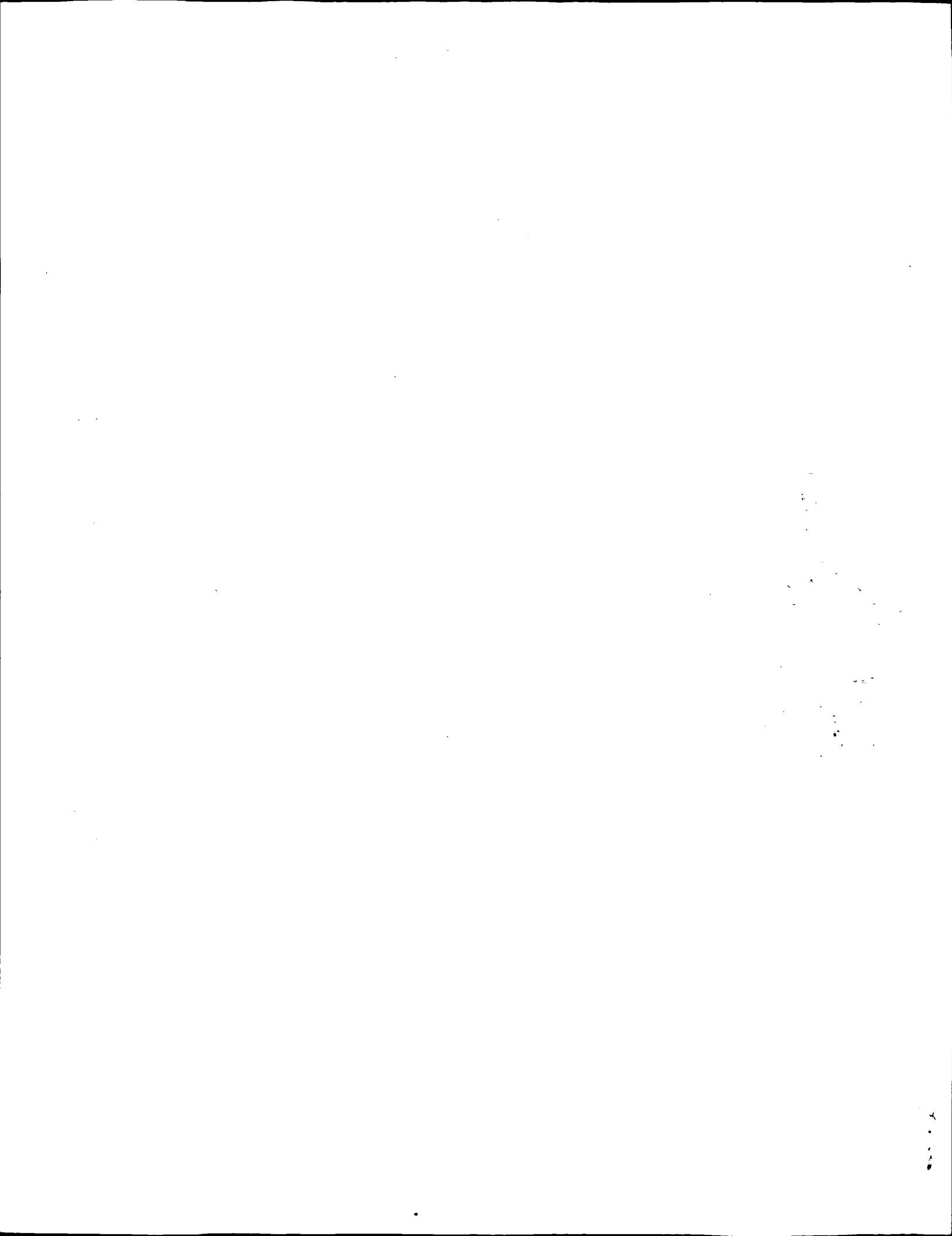
|                       |   |                       |           |             |            |
|-----------------------|---|-----------------------|-----------|-------------|------------|
| PR                    | 13-JUN-1997;  | US-049610.            | Qy        | 7           | SSMV 11    |
| PR                    | 08-JUL-1997;  | US-051926.            | Db        | 33          | SSMV 37    |
| PR                    | 16-JUL-1997;  | US-052874.            |           |             |            |
| PR                    | 18-AUG-1997;  | US-055724.            |           |             |            |
| PR                    | 22-AUG-1997;  | US-056630.            |           |             |            |
| PR                    | 22-AUG-1997;  | US-056631.            |           |             |            |
| PR                    | 22-AUG-1997;  | US-056632.            |           |             |            |
| PR                    | 22-AUG-1997;  | US-056636.            |           |             |            |
| PR                    | 22-AUG-1997;  | US-056637.            |           |             |            |
| PR                    | 22-AUG-1997;  | US-056662.            |           |             |            |
| PR                    | 22-AUG-1997;  | US-056664.            |           |             |            |
| PR                    | 22-AUG-1997;  | US-056845.            |           |             |            |
| PR                    | 22-AUG-1997;  | US-056862.            |           |             |            |
| PR                    | 22-AUG-1997;  | US-056864.            |           |             |            |
| PR                    | 22-AUG-1997;  | US-056872.            |           |             |            |
| PR                    | 22-AUG-1997;  | US-056874.            |           |             |            |
| PR                    | 22-AUG-1997;  | US-056875.            |           |             |            |
| PR                    | 22-AUG-1997;  | US-056876.            |           |             |            |
| PR                    | 22-AUG-1997;  | US-056877.            |           |             |            |
| PR                    | 22-AUG-1997;  | US-056878.            |           |             |            |
| PR                    | 22-AUG-1997;  | US-056879.            |           |             |            |
| PR                    | 22-AUG-1997;  | US-056880.            |           |             |            |
| PR                    | 22-AUG-1997;  | US-056881.            |           |             |            |
| PR                    | 22-AUG-1997;  | US-056882.            |           |             |            |
| PR                    | 22-AUG-1997;  | US-056884.            |           |             |            |
| PR                    | 22-AUG-1997;  | US-056886.            |           |             |            |
| PR                    | 22-AUG-1997;  | US-056887.            |           |             |            |
| PR                    | 22-AUG-1997;  | US-056888.            |           |             |            |
| PR                    | 22-AUG-1997;  | US-056889.            |           |             |            |
| PR                    | 22-AUG-1997;  | US-056892.            |           |             |            |
| PR                    | 22-AUG-1997;  | US-056894.            |           |             |            |
| PR                    | 22-AUG-1997;  | US-056894.            |           |             |            |
| PR                    | 22-AUG-1997;  | US-056895.            |           |             |            |
| PR                    | 22-AUG-1997;  | US-056898.            |           |             |            |
| PR                    | 22-AUG-1997;  | US-056908.            |           |             |            |
| PR                    | 22-AUG-1997;  | US-056909.            |           |             |            |
| PR                    | 22-AUG-1997;  | US-05610.             |           |             |            |
| PR                    | 22-AUG-1997;  | US-056911.            |           |             |            |
| PR                    | 05-SEP-1997;  | US-057650.            |           |             |            |
| PR                    | 05-SEP-1997;  | US-057669.            |           |             |            |
| PR                    | 05-SEP-1997;  | US-057761.            |           |             |            |
| PR                    | 12-SEP-1997;  | US-058785.            |           |             |            |
| PA                    | (HODA -)  | HUMAN GENOME SCI INC. |           |             |            |
| PI                    | Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA,           |                       |           |             |            |
| PI                    | Feng P, Ferrie AM, Fischer CL, Florence KA, Greene JM, Hu JS,             |                       |           |             |            |
| PI                    | Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA,             |                       |           |             |            |
| PI                    | Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;                      |                       |           |             |            |
| WPI:                  | 98-506364/43.   |                       |           |             |            |
| DR                    | N-PSDB; V59740.   |                       |           |             |            |
| PT                    | New isolated human genes and the secreted polypeptide(s) they encode      |                       |           |             |            |
| PT                    | - useful for diagnosis and treatment of e.g. cancers, neurological        |                       |           |             |            |
| PT                    | disorders, immune diseases, inflammation or blood disorders               |                       |           |             |            |
| PS                    | Claim 1; Page 672; 721pp; English.  |                       |           |             |            |
| CC                    | This sequence represents a secreted human protein encoded by the nucleic  |                       |           |             |            |
| CC                    | acid molecule designated Gene 77 from the human cDNA clone HOEAS24        |                       |           |             |            |
| CC                    | (deposited as clone ATCC 97000 and ATCC 209046).                          |                       |           |             |            |
| CC                    | The gene can be used to generate fusion proteins by linking to the gene   |                       |           |             |            |
| CC                    | to a human immunoglobulin Fc portion (e.g. V59502) for increasing the     |                       |           |             |            |
| CC                    | stability of the fused protein as compared to the human protein only.     |                       |           |             |            |
| CC                    | The invention relates to 186 novel genes and their fragments (nucleic     |                       |           |             |            |
| CC                    | acid sequences: V59511-V59812; amino acid sequences W74731-W75026), which |                       |           |             |            |
| CC                    | are useful for preventing, treating or ameliorating medical conditions    |                       |           |             |            |
| CC                    | e.g. by protein or gene therapy. Also, pathological conditions can be     |                       |           |             |            |
| CC                    | diagnosed by determining the amount of the new polypeptides in a sample   |                       |           |             |            |
| CC                    | or by determining the presence of mutations in the new polynucleotides.   |                       |           |             |            |
| CC                    | Specific uses are described for each of the 186 polynucleotides, based on |                       |           |             |            |
| CC                    | which tissues they are most highly expressed in (see V55511 for described |                       |           |             |            |
| Sequence              | 136 AA;   |                       |           |             |            |
| Query Match           | 35.7%   | Score 5;              | DB 1;     | Length 136; | 1 AEFFR 5  |
| Best Local Similarity | 100.0%  | Pred. No. 18;         |           |             |            |
| Matches 5;            | Conservative  | 0; Mismatches         | 0; Indels | 0; Gaps     | 0;         |
| Query Match           | 35.7%   | Score 5;              | DB 1;     | Length 261; | 1 AEFFR 88 |
| Best Local Similarity | 100.0%  | Pred. No. 32;         |           |             |            |
| Matches 5;            | Conservative  | 0; Mismatches         | 0; Indels | 0; Gaps     | 0;         |

Wed Sep 13 08:11:25 2000

us-09-155-076-1.rag

Page 7

Search completed: September 13, 2000, 02:25:00  
Job time: 173 sec



post-processing: Listing first 45 summaries

|            |                  |        |   |
|------------|------------------|--------|---|
| database : | SPTREMBL_12:*    | RESULT | 1 |
|            | 1: sp_archaea:*  | 062763 |   |
|            | 2: sp_bacteria:* |        |   |

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3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodont:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

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No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| result | No. | Query Match |       |        |       | Description |                     |        |       |
|--------|-----|-------------|-------|--------|-------|-------------|---------------------|--------|-------|
|        |     | Score       | Match | Length | DB ID | Score       | Match               | Length | DB ID |
| 1      | 1   | 14          | 100.0 | 611    | 6     | 062763      | 062763 felis silve  | 062763 |       |
| 2      | 2   | 10          | 71.4  | 633    | 13    | 042275      | 042275 electrophor  | 042275 |       |
| 3      | 3   | 9           | 64.3  | 95     | 13    | 09W678      | 09W678 torpedo cal  | 09W678 |       |
| 4      | 4   | 6           | 42.9  | 469    | 2     | P73738      | P73738 syncytiotro  | P73738 |       |
| 5      | 5   | 5           | 35.7  | 149    | 12    | Q81753      | Q81753 hepatitis c  | Q81753 |       |
| 6      | 6   | 5           | 35.7  | 193    | 12    | Q81558      | Q81558 hepatitis c  | Q81558 |       |
| 7      | 7   | 5           | 35.7  | 219    | 8     | Q9XQ7       | Q9XQ7 heterocapsa   | Q9XQ7  |       |
| 8      | 8   | 5           | 35.7  | 235    | 13    | Q9W708      | Q9W708 parallelthy  | Q9W708 |       |
| 9      | 9   | 5           | 35.7  | 244    | 12    | P88361      | P88361 human immun  | P88361 |       |
| 10     | 10  | 5           | 35.7  | 251    | 12    | P88358      | P88358 human immun  | P88358 |       |
| 11     | 11  | 5           | 35.7  | 251    | 12    | Q2117       | Q2117 caenorhabdi   | Q2117  |       |
| 12     | 12  | 5           | 35.7  | 255    | 5     | Q2117       | Q2117 mouse adeno   | Q2117  |       |
| 13     | 13  | 5           | 35.7  | 262    | 12    | O10441      | O10441 rizobium m   | O10441 |       |
| 14     | 14  | 5           | 35.7  | 263    | 6     | O97972      | O97972 orcytoblagus | O97972 |       |
|        |     |             |       | 285    | 2     | Q52970      | Q52970 rizobium m   | Q52970 |       |
|        |     |             |       | 285    | 2     | Q52970      | Q52970 epichloë ty  | Q52970 |       |
| 15     | 15  | 5           | 35.7  | 294    | 8     | Q9XMG3      | Q9XMG3 hepatitis c  | Q9XMG3 |       |
| 16     | 16  | 5           | 35.7  | 318    | 12    | Q68891      | Q68891 hepatitis c  | Q68891 |       |
| 17     | 17  | 5           | 35.7  | 319    | 12    | Q81557      | Q81557 hepatitis c  | Q81557 |       |
| 18     | 18  | 5           | 35.7  | 335    | 7     | O24964      | O24964 archaeoglob  | O24964 |       |
| 19     | 19  | 5           | 35.7  | 339    | 2     | O32123      | O32123 bacillus su  | O32123 |       |

OS Electrophorus electricus (Electric eel);  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;  
 OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Gymnotiformes;  
 OC Gymnotoidei; Electrophoridae; Electrophorus.  
 RN [1]  
 RP SEQUENCE FROM N.A.

RA TABATA S.; Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
 RL RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PCC6803;  
 RX MEDLINE; 97/061201.  
 RA KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,  
 RA MIYAJIMA N., HIROSAWA M., SASAMOTO S., NARUO K., KITMURA T.,  
 RA HOSOCHI T., MATSUOKA A., MURAKI A., NARAZAKI N., NARUO K., OKUDRA S.,  
 RA SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YANADA M., YASUDA M.,  
 RA TABATA S.;  
 RT "Sequence analysis of the genome of the unicellular cyanobacterium  
 Synechocystis sp. strain PCC6803. I. Sequence determination of the  
 entire genome and assignment of potential protein-coding regions.";  
 RL DNA Res. 3:109-136(1996).  
 DR EMBL: D0919; BAA17786.1; -.  
 DR PFAM: PF00355; Rieske, 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 469 AA; 52544 MW; 0887A65E CRC32;

Query Match 71.4%; Score 10; DB 13; Length 63;  
 Best Local Similarity 100.0%; Pred. No. 8e-06; DB 2; Length 469;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0; N mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFRHRW 5  
 |||||||  
 Db 605 AEFRHSSYM 614

RESULT 3  
 Q9W6Y8 PRELIMINARY; PRT; 95 AA.  
 ID Q9W6Y8;  
 AC 09W6Y8;  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
 DE ACETYLCHOLINESTERASE (FRAGMENT).  
 OS Torpedo californica (Pacific electric ray).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
 OC Elasmobranchii; Rajiformes; Torpedinidae; Torpedo; Torpedo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MAULE Y., CAMP S., GIBNEY G., RACHINSKY T.L., EKSTROEM T.J.,  
 RA TAYLOR P.; Submitted (OCT-1990) to the EMBL/GenBank/DBJ databases.  
 RL EMBL: X56517; CAB37951.1; -.  
 DR EMBL: X56516; CAB37951.1; JOINED.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 95 AA; 11752 MW; F7387712 CRC32;

Query Match 64.3%; Score 9; DB 13; Length 95;  
 Best Local Similarity 100.0%; Pred. No. 4e-05; DB 12; Length 149;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0; N mismatches 0; Indels 0; Gaps 0;

Qy 2 EFHRHSSYM 10  
 |||||||  
 Db 68 EFHRHSSYM 76

RESULT 4  
 P73738 PRELIMINARY; PRT; 469 AA.  
 AC P73738;  
 DT 01-FEB-1997 (TREMBLrel. 02, Created)  
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
 DE HYPOTHETICAL 5.5 KD PROTEIN.  
 OS Synecchocystis sp. (strain PCC 6803).  
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PCC6803;



|             |   |   |                                 |                       |  |                                       |
|-------------|---|---|---------------------------------|-----------------------|--|---------------------------------------|
| FT          | NON_TER   | 244                                     | 244                             | RA                    | GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L., JONES M., KERSHAW J., KIRSHNER A., MORTIMORE B., O CALLAGHAN M., O'LAISTEILLE P., LIGHTNING J., LLOYD C., MC MURRAY A., MORTIMORE B., O CALLAGHAN M., PARSONS J., PERCY C., RIKKEN L., ROOPRA A., SAUNDERS D., SHONKEEN R., SNALDON N., SMITH A., SONNHAMMER E., SPADEN R., SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSRTON R., WATSON A., WEINSTOCK L., WILKINSON SPROAT J., WORLDMAN P.; |                                       |
| SQ          | SEQUENCE  | 244 AA:                                 | 27027 MW;                       | RA                    | "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans."  |                                       |
| Query Match | Best Local Similarity   | 35.7%;                                  | Score 5; DB 12; Length 244;     | RA                    | Nature 368:32-38(1994).  |                                       |
|             | Matches   | 5;                                      | Pred. No. 18; Indels 0; Gaps 0; | RL                    | RT   |                                       |
| Qy          | 7   | SSYMV 11                                |                                 | DR                    | DR   |                                       |
| Db          | 71  | SSYMV 75                                |                                 | SEQUENCE              | 255 AA; 2960 MW; FACC3B217 CRC32;  |                                       |
| RESULT      | 10  |   |                                 |                       |  |                                       |
| TD          | P88358  | PRELIMINARY;                            | PRT;                            | 251 AA.               | Query Match  | 35.7%; Score 5; DB 5; Length 251;     |
| AC          | P88358;   |   |                                 |                       | Best Local Similarity  | 100 %; Pred. No. 19;                  |
| DT          | 01-MAY-1997   | (TREMBLrel. 03, Created)                | Matches                         | 0; Mismatches 0;      | Matches  | 0; Mismatches 0;                      |
| DT          | 01-MAY-1997   | (TREMBLrel. 03, Last sequence update)   | Qy                              | 2 EFHRW 6             | Indels 0; Gaps 0;  |                                       |
| DT          | 01-NOV-1998   | (TREMBLrel. 08, Last annotation update) | Db                              | 208 EFHRW 212         |  |                                       |
| DE          | ENVLOPE GLYCOPROTEIN (FRAGMENT).  |   |                                 |                       |  |                                       |
| GN          | ENV.  |   |                                 |                       |  |                                       |
| OS          | Human immunodeficiency virus type 1.  |   |                                 |                       |  |                                       |
| OC          | Human immunodeficiency virus; Retroviridae; Lentivirus.   |   |                                 |                       |  |                                       |
| RN          | [1]   |   |                                 |                       |  |                                       |
| RP          | SEQUENCE FROM N.A.  |   |                                 |                       |  |                                       |
| RC          | STRAIN=PATIENT H;   |   |                                 |                       |  |                                       |
| RX          | MEDLINE: 97184515   |   |                                 |                       |  |                                       |
| RA          | MCDONALD R.A., MAYERS D.L., CHUNG R.C.Y., WAGNER K.F., KIM S., BIRX D.L., MICHAEL N.L.;   |   |                                 |                       |  |                                       |
| RX          | ENVLOPE protein.  |   |                                 |                       |  |                                       |
| RX          | *Evolution of human immunodeficiency virus type 1 env sequence variation in patients with diverse rates of disease progression and cell function. ;   |   |                                 |                       |  |                                       |
| RT          | J. VIROL. 71:1871-1879(1996). ;   |   |                                 |                       |  |                                       |
| DR          | EMBL: U69434; AAC56745.1; -.  |   |                                 |                       |  |                                       |
| DR          | PFAM: PF00516; GP120; 1.  |   |                                 |                       |  |                                       |
| KW          | Envelope protein.   |   |                                 |                       |  |                                       |
| FT          | NON_TER   | 1                                       |                                 |                       |  |                                       |
| FT          | NON_TER   | 251                                     |                                 |                       |  |                                       |
| SQ          | SEQUENCE  | 251 AA;                                 | 27714 MW;                       | A06370E1 CRC32;       | Sequence FROM N.A.   | 35.7%; Score 5; DB 12; Length 262;    |
| Query Match | Best Local Similarity   | 35.7%;                                  | Score 5; DB 12; Length 251;     | Best Local Similarity | 35.7%; Score 5; DB 12; Length 262;   |                                       |
|             | Matches   | 100 %;                                  | Pred. No. 19;                   | Matches               | 100 %; Pred. No. 19;   |                                       |
|             | Matches   | 5;                                      | Indels 0; Gaps 0;               | Matches               | 5; Conservative 0; Mismatches 0;   |                                       |
| Qy          | 7   | SSYMV 11                                |                                 | Qy                    | 5 RWSSY 9  |                                       |
| Db          | 78  | SSYMV 82                                |                                 | Db                    | 59 RWSSY 63  |                                       |
| RESULT      | 11  |   |                                 |                       |  |                                       |
| Q22117      | ID  | 022117                                  | PRELIMINARY;                    | PRT;                  | 255 AA.  |                                       |
| AC          | Q22117;   |   |                                 |                       |  |                                       |
| DT          | 01-NOV-1996   | (TREMBLrel. 01, Created)                | ID                              | 097972                | PRELIMINARY;   |                                       |
| DT          | 01-NOV-1996   | (TREMBLrel. 01, Last sequence update)   | AC                              | 097972;               | PRT;   |                                       |
| DT          | 01-JAN-1999   | (TREMBLrel. 09, Last annotation update) | DT                              | 01-MAY-1999           | (TREMBLrel. 10, Created)   |                                       |
| DE          | T03F7.5 PROTEIN.  |   |                                 | DT                    | 01-MAY-1999  | (TREMBLrel. 10, Last sequence update) |
| DN          | T03F7.5.  |   |                                 | DE                    | INDOLETHYLAMINE N-METHYLTRANSFERASE.   |                                       |
| OS          | Caenorhabditis elegans.   |   |                                 | DN                    | INMT.  |                                       |
| OC          | Eukaryota; Metazoa; Nemata; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Pelodirinae; Caenorhabditis.   |   |                                 | OS                    | Oryctolagus cuniculus (Rabbit).  |                                       |
| RN          | [1]   |   |                                 | OC                    | Ornithodoros; Chordata; Craniata; Vertebrate; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  |                                       |
| RP          | SEQUENCE FROM N.A.  |   |                                 | RN                    | SEQUENCE FROM N.A.   |                                       |
| RA          | MORIMORE B.;  |   |                                 | RP                    | SEQUENCE FROM N.A.   |                                       |
| RL          | Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.   |   |                                 | RC                    | TISSUE-LUNG;   |                                       |
| RN          | [2]   |   |                                 | RX                    | MEMLINE; 99069450.   |                                       |
| RP          | SEQUENCE FROM N.A.  |   |                                 | RA                    | THOMPSON M.A., WEINSHILBOUM R.M.;  |                                       |
| RA          | MEDLINE: 94150718   |   |                                 | RX                    | "Rabbit lung indolethylamine N-methyltransferase. CDNA and gene cloning and characterization.";  |                                       |
| RA          | WILSON R., ALNSCOUGH R., ANDERSON K., BAYNES C., BERKS M., COPSEY T., COOPER J., COULSON A., BONFIELD J., BURTON J., CONNELL M., FAVELLO A., FULTON L., CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L., |   |                                 | RT                    | J. Biol. Chem. 273:34502-34510(1998).  |                                       |
| RA          | DR  | AF077838; AAC9792.1; -.                 |                                 | DR                    | AF077827; AAC9792.1; JOINED.   |                                       |
| EMBL        | AF077827;   |   |                                 | EMBL                  |  |                                       |

DR EMBL; AF077826; AAC97491.1; -.  
 KW Transferase; Nethyltransferase.  
 SQ SEQUENCE 263 AA; 28955 MW; CEA3D9F6 CRC32;

|                       |                 |               |           |             |
|-----------------------|-----------------|---------------|-----------|-------------|
| Query Match           | 35.7%           | Score 5;      | DB 8;     | Length 294; |
| Best Local Similarity | 100.0%          | Pred. No. 21; |           |             |
| Matches 5;            | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0;     |

QY 7 SSYMV 11  
 Db 202 SSYMV 206

Search completed: September 13, 2000, 02:27:31  
 Job time: 173 sec

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RESULT 14

|  |              |      |         |
|--|--------------|------|---------|
| Q52970   | PRELIMINARY; | PRT; | 285 AA. |
| ID Q52970  |              |      |         |
| AC Q52970;   |              |      |         |
| DT 01-NOV-1996 (TREMBLrel. 01, Created)                              |              |      |         |
| DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)                 |              |      |         |
| DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)               |              |      |         |
| DE NODULATION GENES NODA, NODB AND NODC.                             |              |      |         |
| OS Rhizobium meliloti.   |              |      |         |
| OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  |              |      |         |
| OC Rhizobiaceae; Sinorhizobium.                                      |              |      |         |
| RN [1]   |              |      |         |
| RP SEQUENCE FROM N.A.  |              |      |         |
| RX MEDLINE; 85087953.  |              |      |         |
| RA TOERER I., KONDOROSI E., STEPCKONSKI T., POSFAI J., KONDOROSI A.; |              |      |         |
| RT "Nucleotide sequence of Rhizobium meliloti nodulation genes .";   |              |      |         |
| RL Nucleic Acids Res;12:9509-9524(1984).                             |              |      |         |
| DR EMBL; X01649; CAA25807.1; -.                                      |              |      |         |
| SQ SEQUENCE 285 AA; 32342 MW; 157B9E20 CRC32;                        |              |      |         |

Query Match 35.7%; Score 5; DB 2; Length 285;  
 Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WSSYM 10  
 Db 86 WSSYM 90

RESULT 15

|  |              |      |         |
|--|--------------|------|---------|
| Q9XMG3   | PRELIMINARY; | PRT; | 294 AA. |
| ID Q9XMG3  |              |      |         |
| AC Q9XMG3;   |              |      |         |
| DT 01-NOV-1999 (TREMBLrel. 12, Created)  |              |      |         |
| DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)   |              |      |         |
| DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)   |              |      |         |
| DE ET2_C1 PROTEIN (FRAGMENT).  |              |      |         |
| GN ET2_C1.   |              |      |         |
| OS Epichloë typhina.   |              |      |         |
| OC Mitochondrion   |              |      |         |
| OG Hypocreales; Clavicipitaceae; Epichloë.   |              |      |         |
| OC Eukaryota; Fungi; Ascomycota; Euascomycetes; Pyrenomycetes;   |              |      |         |
| RN [1]   |              |      |         |
| RP SEQUENCE FROM N.A.  |              |      |         |
| RC STRAIN=PNG; PLASMID=MITOCHONDRIAL PLASMID;  |              |      |         |
| RX MEDLINE; 92145777.  |              |      |         |
| RA MOGEN K.L., STEGEL M.R., SCHARDL C.L.;  |              |      |         |
| RT "Linear DNA plasmids of the perennial ryegrass choker pathogen, Epichloë typhina (Clavicipitaceae)."; |              |      |         |
| RT Curr. Genet. 20:519-526(1991).  |              |      |         |
| DR EMBL; X57200; CAA40486.2; -.  |              |      |         |
| KW Mitochondrion.  |              |      |         |
| NON_TER 1  | 1            |      |         |
| FT NON_TER 294 AA; 35780 MW; 90A243F8 CRC32;   | 294          |      |         |
| SEQUENCE   |              |      |         |



Om of: US-09-155-076-1 to: EST: \* out\_format : pfs  
 Date: Sep 13, 2000 3:34 AM  
 About: Results were produced by the GenCore software, version 4.5,  
 Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:  
 -MODEL\_P2n.Node -DEVv1P  
 -Q/cgn2.1/USPTO\_spool/US09155076/runat\_29082000.092558\_16898/app\_query.fasta\_1.144  
 -DB=EST -QMPF=fastap -SUFFIX=rst -GAPEXT=4 500 -GAPEXT=0 050  
 -MINMATCH=1.00 -LOC\_PCL=0.000 -LOGEXT=0.000 -QGAPOP=4 .500  
 -QGAPEXT=0.050 -XGAPOP=60.000 -XGAPEXT=60.000 -FGAPOP=6.000  
 -DEPLEXT=7.000 -YGAPEXT=60.000 -YGAPEXT=60.000 -DELPOP=6.000  
 -DOALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15  
 -MODE=LOCAL -START=1 -MATRIX=C0190 -TRANS human0.cdt -LIST=45  
 -USER=US09155076\_@CGN1\_1\_1327 -NCPU=6 -ICPU=3 -LONGLOG -NO\_XLPXY  
 -WAIT -THREADS=1

Search information block:

Query: US-09-155-076-1

Query length: 14

Database: EST: \*

Database sequences: 5247842

Database length: -26905206

Search time (sec): 889.020000

WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPEXT=XGAPEXT=60.000

WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.000

score\_list:

| sequence            | Strd | Orig  | ZScore | EScore  | Len | Documentation   | Source |
|---------------------|------|-------|--------|---------|-----|---|--------|
| gb_est50:N90761     | +    | 14.00 | 309.28 | 2.1e-08 | 248 | N90761_zb22e03.s1 Soares_fetal_Lung_NbHL19W Human Embryo Ho |        |
| gb_est52:T128280    | +    | 14.00 | 309.13 | 2.2e-08 | 254 | T28280_EST31080 Human Embryo Ho                             |        |
| gb_es55:AI1764103   | -    | 14.00 | 307.01 | 2.8e-08 | 362 | AI764103_U1-R-YO-acry-11-04-0-U1                            |        |
| gb_est56:AI29586    | +    | 14.00 | 306.75 | 2.9e-08 | 378 | F21586_HSPD155_HM3 Homo sapi                                |        |
| gb_est14:AA933814   | +    | 14.00 | 306.72 | 3.0e-08 | 380 | AA933814_O1L_CGAP_K1  |        |
| gb_est44:AW612295   | +    | 14.00 | 306.66 | 3.0e-08 | 384 | AW612295_hh3a07_x1_NCI_CGAP_Lu                              |        |
| gb_est95:AA998511   | -    | 14.00 | 306.52 | 3.0e-08 | 393 | AA998511_U1-R-CO-le-h-11-0-U1-K1                            |        |
| gb_est25:AI17668112 | +    | 14.00 | 306.49 | 3.0e-08 | 395 | AI1766812_w189a12_x1_NCI_CGAP_K1                            |        |
| gb_est26:AI1847791  | -    | 14.00 | 306.49 | 3.0e-08 | 395 | AI1847791_U1-M-AK1-aev-f-02-0-U1                            |        |
| gb_est11:AA1360141  | +    | 14.00 | 306.25 | 3.1e-08 | 410 | AI1360141_qy83d10_x1_NCI_CGAP_B1                            |        |
| gb_est24:AI1690171  | +    | 14.00 | 306.25 | 3.1e-08 | 411 | AI1690171_tx23a02_x1_NCI_CGAP_Lu                            |        |
| gb_est7:AR401251    | +    | 14.00 | 306.22 | 3.2e-08 | 413 | AA401251_zv26b01_s1 Soares_total                            |        |
| gb_est45:AW653940   | +    | 14.00 | 305.12 | 3.6e-08 | 496 | AW653940_1087_MARC_1BOV_Bos_J                               |        |
| gb_est1:AR030863    | +    | 14.00 | 305.06 | 3.7e-08 | 501 | AA030863_mi45c07_r1 Soares_mous                             |        |
| gb_est2:AR118440    | +    | 14.00 | 304.91 | 3.7e-08 | 514 | AA118440_mi34a07_r1 Life_Tech_m                             |        |
| gb_est38:AW131312   | +    | 14.00 | 304.80 | 3.8e-08 | 523 | AW131312_ESP29a1333 Normalized_I                            |        |
| gb_est24:AI125377   | +    | 14.00 | 304.68 | 3.8e-08 | 534 | AI125377_mi45c07_Y1 Soares_mous                             |        |
| gb_est18:AI227851   | -    | 14.00 | 304.61 | 3.9e-08 | 540 | AI227851_ESP245456 Normalized_I                             |        |
| gb_est12:AI182369   | -    | 14.00 | 304.51 | 3.9e-08 | 549 | AI182369_mi15c07_x1 Soares_mous                             |        |
| gb_est53:WI9259     | -    | 12.00 | 262.35 | 8.8e-08 | 416 | WI9259_zb22e03.r1 Soares_fetal                              |        |
| gb_est48:J334547    | +    | 11.00 | 242.35 | 0.0001  | 302 | F34547_HSPD28467_HM3 Homo sapi                              |        |
| gb_est26:AI194432   | +    | 10.00 | 220.06 | 0.0020  | 223 | AI837078_U1-M-AK0-adc-b-02-0-U1                             |        |
| gb_est23:AI651194   | +    | 10.00 | 219.32 | 0.0022  | 364 | AI651194_wb0d09_x1_NCI_CGAP_Go                              |        |
| gb_est4:AA271549    | +    | 8.00  | 175.35 | 0.6142  | 373 | AA271549_vb4f09_r1 Soares_mous                              |        |
| gb_gss1:AA048995    | -    | 7.00  | 152.51 | 1.187   | 454 | AQ48995_HS_50461_B2_H07_SPE_R                               |        |
| gb_est47:C96701     | +    | 6.00  | 149.59 | 16.72   | 709 | C96701_C96701_Rice callus Orzya                             |        |
| gb_est27:AI194432   | +    | 6.00  | 136.02 | 95.24   | 176 | AT144432_bs01c12_Y1 Drosophila                              |        |
| gb_gss1:AO791533    | +    | 6.00  | 135.66 | 9.78    | 187 | AQ191533_HS_5269_A2_H03_T7A RPC                             |        |
| gb_est33:AV280727   | +    | 6.00  | 134.93 | 10.948  | 211 | AV280727_RIKEN full-16                                      |        |
| gb_est46:AW736001   | +    | 6.00  | 134.93 | 10.948  | 211 | AW736001_ESP331987_KV3 Medicago                             |        |
| gb_est18:AI182192   | +    | 6.00  | 134.68 | 11.06   | 220 | AI182192_xj71f12_x1 Soares_NFL                              |        |
| gb_est33:AV241723   | +    | 6.00  | 134.19 | 12.049  | 239 | AV241723_AV241723_RIKEN full-16                             |        |
| gb_gss17:BB90397    | +    | 6.00  | 133.48 | 131.95  | 269 | B90397_CIT_PRT-2163A5_TF CIT-HS                             |        |
| gb_gss1:AO791533    | -    | 6.00  | 133.35 | 131.21  | 275 | TO191533_Y139a11_s1 Soares_fetal                            |        |
| gb_est51:RH5464     | +    | 6.00  | 132.99 | 140.54  | 292 | R15464_HH161_F Adult heart, Cic                             |        |
| gb_est3:AV0494775   | +    | 6.00  | 132.97 | 140.91  | 293 | AQ0494775_AV0494775 Mus musculus                            |        |
| gb_gss1:AO86955     | +    | 6.00  | 132.93 | 141.65  | 295 | AQ86955_RPC1-11-260E20.TV RPC                               |        |
| gb_est35:AV349284   | -    | 6.00  | 132.91 | 142.02  | 300 | AV349284_AV249284 RIKEN full-16                             |        |
| gb_est32:AV184324   | +    | 6.00  | 132.83 | 143.49  | 300 | AV184324_AV184324 Yuji Kohara                               |        |

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|---------------------------|-----------------|--|--------|-------------|
| gb_est6:AA346027          | +               | 6.00   | 132.79 | 144.23      |
| gb_est26:AI184126         | -               | 6.00   | 132.75 | 144.59      |
| gb_est19:AI136528         | -               | 6.00   | 132.59 | 147.88      |
| gb_est5:AA296553          | +               | 6.00   | 132.59 | 147.88      |
| gb_est39:AW181786         | +               | 6.00   | 132.53 | 148.98      |
| gb_gss8:AO552303          | -               | 6.00   | 132.53 | 148.98      |
| seq_name: gb_est50:N90761 |                 |  |        |             |
| seq_documentation_block:  |                 |  |        |             |
| LOCUS                     |                 | 248 bp mRNA  |        |             |
| DEFINITION                |                 | NbH19W Homo sapiens cDNA clone IMAGE:302812_3, similar to gb:M5504 ACEYLCHOLINESTERASE PRECURSOR (HUMAN); mRNA sequence.   |        |             |
| ACCESSION                 |                 | N90761   |        |             |
| VERSION                   |                 | N90761.1 GI:14440488   |        |             |
| KEYWORDS                  |                 | EST.   |        |             |
| SOURCE                    |                 | human.   |        |             |
| ORGANISM                  |                 | Homo sapiens   |        |             |
| MATERIAL                  |                 | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.   |        |             |
| REFERENCE                 |                 | 1 (bases 1 to 248)   |        |             |
| AUTHORS                   |                 | Hillier,L., Clark,N., Dubuge,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marras,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P., Wilson,R.   |        |             |
| TITLE                     |                 | The WashU-Merck EST Project  |        |             |
| JOURNAL                   |                 | Unpublished (1995)   |        |             |
| COMMENT                   |                 | On Dec 30, 1997 this sequence version replaced gi:905921. Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LNLN; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Trace considered overall poor quality Possible reversed clone: polyT not found Seg primer: Empriimer High quality sequence stop: 1. Location/Qualifiers 1. 248 /organism="Homo sapiens" /db_xref="GDB:1247744" /db_xref="taxon:9006" /clone_id="Soares_fetal_lung_NbH19W" /dev_stage="19 weeks" /lab_host="DH10B (ampicillin resistant)" /note="Organ: lung; Vector: pT7T3 (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; strand: cDNA was primed with a Not I - Oligo(dT) primer double-stranded cDNA was selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pTT3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NbH19W." BASE COUNT 47 a 89 c 57 g 47 t 8 others ORIGIN |        |             |

US-09-155-076-1 x N90761 .. alignment\_block: US-09-155-076-1 x T28280 .. Align seg 1/1 to: N90761 from: 1 to: 248

1 AlaGluPheHisArgTrpSerSerTyrMetValHistRplys 14  
 ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 11 GCGGAGTTCACGGCTGAGCTCTACATGGTCACTGGAG 52

seq\_name: qb\_est52:T28280

seq\_documentation\_block:

LOCUS T28280 mRNA EST 06-SEP-1995  
 DEFINITION EST55080 Human Embryo Homo sapiens cDNA 5, end similar to  
 acetylcholinesterase (HT: 51:18), mRNA sequence.

ACCESSION T28280  
 VERSION T28280.1 GI:610378  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 254); Mammalia; Eutheria; Primates; Catarrini; Hominidae; Homo.  
 AUTHORS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fulcher, R.A., Bult, C.J., Lee, N., Kirness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Braxton, R.C., Chiu, M.W., Clayton, R.A., Cline, R.T., Cotton, M.D., Earle, R.-Aughey, J., Fine, L.D., Fitzgerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geeshaben, N.S.M., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinneijer, P.S., Merrick, J.M., Moreno-Palancas, R.F., McDonald, L.A., Nguyen, D.T., Pelegriño, S.M., Phillips, C.A., Ryder, S.E., Scott, J.I., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Coleman, T.A., Collins, E.-J., Dinkin, D., Fang, P., Ferrie, A., Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M., Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunisch, C., Ji, H., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C., Yu, G.-L., Rubin, S.M., Dillon, P.J., Fanon, M.R., Rosen, C.A., Hasektine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.

TITLE Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 83 Million Basepairs of cDNA Sequence

JOURNAL Nature 377, 3-174 (1995)  
 MEDLINE 96026280  
 COMMENT On May 10, 1995 this sequence version replaced gi:805490.  
 Other-ESTs: THC2076 Contact: Venter, JC  
 The Institute for Genomic Research  
 932 Clapper Rd, Gaithersburg, MD 20878  
 Tel: 3018699056  
 Fax: 3018699423  
 Email: tdbinfo@tcb.tigr.org

For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfo@tigr.org)

Insert Length: 1145 Std Error: 0.00  
 Seq primer: M13 Reverse  
 High quality sequence stop: 187.

FEATURES source

1..254 Location/Qualifiers  
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 /db\_xref="ATCC (lhost):101797"  
 /db\_xref="taxon:9606"  
 /clone\_lib="Human Embryo"

BASE COUNT 45 a 89 c 78 g 41 t 1 others  
 ORIGIN alignment\_scores:  
 Quality: 14.00 Length: 14  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

Align seg 1/1 to: T28280 from: 1 to: 254

1 AlaGluPheHisArgTrpSerSerTyrMetValHistRplys 14  
 ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 138 GCCGAGTTCACGGCTGAGCTCTACATGGTCACTGGAG 179

seq\_name: qb\_est25:AI764103

seq\_documentation\_block:

LOCUS AI764103 mRNA EST 25-JUN-1999  
 DEFINITION UI-R-Y0-acy-h-04-0-UI-3', mRNA sequence.

ACCESSION AI764103  
 VERSION AI764103.1 GI:5220038  
 KEYWORDS EST.  
 SOURCE Norway rat.  
 ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 362)  
 AUTHORS Bonaldo, M.F., Lennon, G., and Soares, M.B.  
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery  
 JOURNAL Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE 9704477  
 COMMENT Contact: Soares, MB  
 Program for Rat Gene Discovery and Mapping  
 University of Iowa  
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: msoares@blue.weeg.uiowa.edu  
 The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bona fide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the normalized Eye library cDNA Library Preparation: M.B. Soares Lab  
 Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 1-30, >POLY-A#Simple-repeat  
 Seq primer: M13 Forward  
 POLYA-Yes.

FEATURES source

1..362 Location/Qualifiers  
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 /strain="Sprague-Dawley"  
 /db\_xref="taxon:10116"  
 /clone="UI-R-Y0-acy-h-04-0-UI"  
 /clone.lib="UI-R-T0"  
 /dev\_stage="adult"  
 /lab.host="DH10B (Life Technologies)"  
 /note="Vector: pET3D-Pac (Pharmacia) with a modified PolyLinker; Site 1: Not I; Site 2: Eco RI; The UI-R-Y0 library is a subtracted library derived from an individually-tagged normalized whole-eye (minus the lens) library. The driver for the subtraction consisted of a pool of all previous libraries (UI-R-A0, UI-R-B0, UI-R-E1, UI-R-C0, and UI-R-C1). The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library (UI-R-Y0) was constructed as follows: PCR amplified cDNA inserts from previous library clones from which 3' ESTs had been derived were used as a driver in a hybridization with the normalized whole-eye library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to



alignment\_block:  
US-09-155-076-1 x AA933814 ...

Align seg 1/1 to: AA933814 from: 1 to: 380  
 1 AlagluPheHisArgTrpSerSerTyrMetValHistrpLys 14  
 ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 115 GCGGAGTTCCACCGCTGGAGCTCATGGTGACTGGAG 156

seq\_name: gb\_est14:AW612795

seq\_documentation\_block:  
 LOCUS AW612795 384 bp mRNA clone IMAGE:2956884 3'  
 DEFINITION similar to contains PTTR5.t3 PTTR5 repetitive element ;, mRNA sequence.

ACCESSION AW612795  
 VERSION AW612795.1  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE NCI- CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index

JOURNAL COMMENT Unpublished (1997)  
 Contact: Robert Straussberg, Ph.D.  
 Tel.: (301) 496-1550  
 Email: Robert.Straussberg@nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
 Eumann-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: image.lnl.gov/image/html/resources.shtml

Possible reversed clone: polyT not found  
 Seq primer: 400P from Gibco.  
 Location/Qualifiers 1 . 384  
 /organism="Homo sapiens"  
 /db\_xref="taxon:2956884"  
 /clone="IMAGE:2956884"  
 /clone\_lib="NCI-CGAP\_Lu24"  
 /lab\_host="DHL10B"  
 /issue\_type="carcinoind"

note="Organ: lung; Vector: PT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-Co library is a subtracted library derived from the UI-R-Al and UI-R-El libraries. The UI-R-Al library consisted of a mixture of individually tagged normalized libraries constructed from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, and muscle. The UI-R-El library consisted of a mixture of individually tagged normalized libraries constructed from 8, 12 and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-Co) was constructed as follows: PCR amplified cDNA inserts from a pool of UI-R-Al and UI-R-El clones from which 3 ESAs had been derived were used as a driver in a hybridization with the pooled UI-R-Al and UI-R-El library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxypatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-Co library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806,

FEATURES source  
 seq\_name: gb\_est14:AA998511  
 seq\_documentation\_block:  
 LOCUS AA998511 393 bp mRNA EST  
 DEFINITION UI-R-Co-le-h-11-0-U1-S1 UI-R-C0 Rattus norvegicus CDNA clone  
 ACCESSION AA998511  
 VERSION AA998511.1 GI:4290364  
 KEYWORDS EST.  
 SOURCE Rattus norvegicus  
 Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 393)  
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.  
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery  
 JOURNAL Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE 9704477  
 COMMENT On Jun 5, 1998 this sequence version replaced gi:3189162.  
 Contact: Soares, MB  
 Program for Rat Gene Discovery and Mapping  
 University of Iowa  
 tel: 319 335 9250  
 Fax: 319 335 9565  
 Email: msoares@blue.weeg.uiowa.edu  
 The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized adult Brain library. cDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone distribution: Clones will be available through Research Genetics. This clone is also available through the I.M.A.G.E. Consortium at LINL (info@image.lnl.gov). IMAGE ID=1774140  
 Seq primer: M13 Forward  
 POLYA-No.

FEATURES source  
 seq\_name: gb\_est14:AA998511  
 seq\_documentation\_block:  
 LOCUS AA998511 393 bp mRNA EST  
 DEFINITION UI-R-Co-le-h-11-0-U1-S1 UI-R-C0 Rattus norvegicus CDNA clone  
 ACCESSION AA998511  
 VERSION AA998511.1 GI:4290364  
 KEYWORDS EST.  
 SOURCE Rattus norvegicus  
 Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 393)  
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.  
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery  
 JOURNAL Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE 9704477  
 COMMENT On Jun 5, 1998 this sequence version replaced gi:3189162.  
 Contact: Soares, MB  
 Program for Rat Gene Discovery and Mapping  
 University of Iowa  
 tel: 319 335 9250  
 Fax: 319 335 9565  
 Email: msoares@blue.weeg.uiowa.edu  
 The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized adult Brain library. cDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone distribution: Clones will be available through Research Genetics. This clone is also available through the I.M.A.G.E. Consortium at LINL (info@image.lnl.gov). IMAGE ID=1774140  
 Seq primer: M13 Forward  
 POLYA-No.

FEATURES source  
 seq\_name: gb\_est14:AA998511  
 seq\_documentation\_block:  
 LOCUS AA998511 393 bp mRNA EST  
 DEFINITION UI-R-Co-le-h-11-0-U1-S1 UI-R-C0 Rattus norvegicus CDNA clone  
 ACCESSION AA998511  
 VERSION AA998511.1 GI:4290364  
 KEYWORDS EST.  
 SOURCE Rattus norvegicus  
 Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 393)  
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.  
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery  
 JOURNAL Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE 9704477  
 COMMENT On Jun 5, 1998 this sequence version replaced gi:3189162.  
 Contact: Soares, MB  
 Program for Rat Gene Discovery and Mapping  
 University of Iowa  
 tel: 319 335 9250  
 Fax: 319 335 9565  
 Email: msoares@blue.weeg.uiowa.edu  
 The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized adult Brain library. cDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone distribution: Clones will be available through Research Genetics. This clone is also available through the I.M.A.G.E. Consortium at LINL (info@image.lnl.gov). IMAGE ID=1774140  
 Seq primer: M13 Forward  
 POLYA-No.

FEATURES source  
 seq\_name: gb\_est14:AA998511  
 seq\_documentation\_block:  
 LOCUS AA998511 393 bp mRNA EST  
 DEFINITION UI-R-Co-le-h-11-0-U1-S1 UI-R-C0 Rattus norvegicus CDNA clone  
 ACCESSION AA998511  
 VERSION AA998511.1 GI:4290364  
 KEYWORDS EST.  
 SOURCE Rattus norvegicus  
 Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 393)  
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.  
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery  
 JOURNAL Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE 9704477  
 COMMENT On Jun 5, 1998 this sequence version replaced gi:3189162.  
 Contact: Soares, MB  
 Program for Rat Gene Discovery and Mapping  
 University of Iowa  
 tel: 319 335 9250  
 Fax: 319 335 9565  
 Email: msoares@blue.weeg.uiowa.edu  
 The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized adult Brain library. cDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone distribution: Clones will be available through Research Genetics. This clone is also available through the I.M.A.G.E. Consortium at LINL (info@image.lnl.gov). IMAGE ID=1774140  
 Seq primer: M13 Forward  
 POLYA-No.

alignment\_scores:  
 Quality: 14.00 Length: 14  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
 US-09-155-076-1 x AW612795 ..

Align seg 1/1 to: AW612795 from: 1 to: 384

BASE COUNT 80 a 1996" 92 c 130 g 91 t  
 ORIGIN alignment\_scores:  
 Quality: 14.00 Length: 14  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
 US-09-155-076-1 x AA998511/rev  
 Align seg 1/1 to reverse of: AA998511 from: 1 to: 393  
 1 AlAgluPheHisArgTrpSerSerTyrMetValHistRplys 14  
 ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 327 GCCGAGTTCCACGGCTGAGCTCATGGGCACTGGAAAG 286

seq\_name: gb\_est25:AI766812

seq\_documentation\_block:  
 LOCUS AI766812 395 bp mRNA EST 15-JUL-1999  
 DEFINITION wi8a12.x1 NCI-CGAP-Kid12 Bonbo sapiens cDNA PRECURSOR (HUMAN); mRNA  
 similar to gb:IM55040 ACETYLCHOLINESTERASE sequence.  
 ACCESSION AI766812  
 VERSION AI766812.1  
 KEYWORDS EST  
 SOURCE human  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 TITLE Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT On Apr 7, 1998 this sequence version replaced gi:3034669.  
 Contact: Robert Strausberg, Ph.D.  
 Tel: (301) 496-1550  
 Email: Robert\_Strausberg@nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 DNA Library Preparation: M. Bento Soares, Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
 Insert Length: 442 Std Error: 0.00  
 Seq primer: -40NP from Gibco.  
 Location/Qualifiers 1..395  
 /db\_xref="db\_xref=" "Organism="Homo sapiens"  
 /clone="clone=" "taxon="Mus musculus"  
 /clone="clone=" "strain="C57BL/6J"  
 /clone="clone=" "db\_xref=" "taxon:1090"  
 /clone="clone=" "host="DH10B"  
 /lab\_host="DH10B"  
 /note="note=" "organ="kidney; Vector: pMT3D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; Plasmid DNA from the normalized library NCI-CGAP-Kid5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneids 1323912-1325831, 1471368-1472903 and 1492104-149355). subtraction by Bento Soares and M.  
 BASE COUNT 64 a 155 c 107 g 69 t  
 ORIGIN

alignment\_scores:  
 Quality: 14.00 Length: 14  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
 US-09-155-076-1 x AI766812 ..

Align seg 1/1 to: AI766812 from: 1 to: 395  
 1 AlaGluPheHisArgTrpSerSerTyrMetValHistRplys 14  
 ||||| ||||| ||||| ||||| ||||| |||||  
 119 GCCGAGTTCCACGGCTGAGCTCATGGACTGGAG 160

seq\_name: gb\_est26:AI847791

seq\_documentation\_block:  
 LOCUS AI847791 395 bp mRNA EST 15-JUL-1999  
 DEFINITION UI-M-AK1-aev-f-02-0-UI-S1 NIH\_BMAP\_MHY\_N Mus musculus cDNA clone  
 EST.  
 ACCESSION AI847791  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 (bases 1 to 395)  
 Bonaldo,M.F., Lennon,G. and Soares,M.B.  
 Normalization and subtraction: two approaches to facilitate gene discovery  
 Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE 9704477  
 COMMENT On Apr 7, 1998 this sequence version replaced gi:3035605.  
 Contact: Chin, H  
 National Institute of Mental Health  
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD  
 20892-9643, USA  
 Tel: 301 443 1706  
 Fax: 301 443 9890  
 Email: mEST@mail.nih.gov  
 The sequence contained an oligo-dT track that was present in the sequence. This may represent a bona fide poly A strand cDNA and therefore this may represent the Not I site and the oligo-dT track served to verify it as a clone from the normalized hypothalamus library cDNA Library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined.  
 Seq Primer: M13 Forward  
 POLYA:Yes  
 FEATURES  
 source 1. .395  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:1090"  
 /clone="UI-M-AK1-aev-f-02-0-UI"  
 /clone="clone=" "lib="NIH\_BMAP\_MHY\_N"  
 /dev\_stage="7-32 days"  
 /lab\_host="DH10B (Life Technologies)"  
 /note="vector: pMT3D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; The NIH\_BMAP\_MHY\_N library is a normalized library constructed from mouse hypothalamus. The tag is a string of 5 nucleotides present between the Not I site and the oligo-dT track. The library was constructed as described by Bonaldo, Lennon and Soares, Genome Research 6:  
 791-806, 1998. Tissue provided by Ms. Annie Novakovich, Zivic-Miller Laboratories; TAG\_JIB=NIH\_BMAP\_MHY\_N;  
 TAG\_TISSUE=hypothalamus; TAG\_SEQ=CGGTAA"



1 AlaGluPheHisArgTrpSerSerTyrMetValHistrpys 14  
 J5-09-155-076-1 x AI690171 ..

Align seg 1/1 to: AI690171 from: 1 to: 411

1 AlaGluPheHisArgTrpSerSerTyrMetValHistrpys 14  
 119 GCGAGTTCCACCGCTGGACCTACATGGCACTGGAG 160

seq\_name: gb\_est7:AA401251

seq\_documentation\_block:  
 LOCUS AW653940 496 bp mRNA EST 05-APR-2000  
 DEFINITION Bos taurus CDNA 5', mRNA sequence.  
 ACCESSION AW653940  
 VERSION AW653940.1 GI:7419766  
 KEYWORDS EST, Bos taurus, Eukaryota, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Bovinae; Bovidae; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
 SOURCE Organism

REFERENCE Smith, T.P.J., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A. and Keele, J.W.

AUTHORS Design and use of four pooled tissue normalized cDNA libraries for EST discovery in cattle

TITLE Unpublished (2000)

JOURNAL Contact: Smith, T.P.J.

COMMENT USDA, ARS, US Meat Animal Research Center  
 PO Box 166, Clay Center, NE 68933-0166, USA  
 Tel: 402 762 4366  
 Fax: 402 762 4390  
 Email: smith@email.marc.usda.gov

ORGANISM Homo sapiens

REFERENCE Hillier, L., Allen, M., Bowles, T., Dubuke, T., Geissel, G., Jost, S., Kucaba, T., Iacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wyllie, T., Waterston, R. and Wilson, R.

AUTHORS WISHU-Merck EST Project 1997

TITLE Unpublished (1997)

JOURNAL On Jan 17, 1998 this sequence version replaced 91:2044207.

COMMENT Contact: Wilson RK

Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Possible reversed clone: PolyT not found

Seq primer: -A1m13 fwd. ET from Amersham.

Location/Qualifiers

FEATURES source

source

1. .413 "Homo sapiens"  
 /db\_xref="Taxon:9606"  
 /clone IMAGE:738569"  
 /clone\_lib="soares-total\_fetus\_Nb2HF8\_9w"  
 /dev\_stage="8-9 weeks",  
 /dev\_host="BH10",  
 /note="vector: pRT3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from pooled 8-9 week (total) fetus material with Not I - Oligo(dT) primer [5' TCTTACCAATTGCAAGTCGGAGCGGCCCTTAATTTTTTTTTT 3' ]. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I (Pharmacia), and Eco RI sites of the modified pRT3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT ORIGIN

68 a 163 c 111 g 71 t

FEATURES source

source

1. .413 "Homo sapiens"  
 /db\_xref="Taxon:9606"  
 /clone IMAGE:738569"  
 /clone\_lib="soares-total\_fetus\_Nb2HF8\_9w"  
 /dev\_stage="8-9 weeks",  
 /dev\_host="BH10",  
 /note="vector: pRT3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from pooled 8-9 week (total) fetus material with Not I - Oligo(dT) primer [5' TCTTACCAATTGCAAGTCGGAGCGGCCCTTAATTTTTTTTTT 3' ]. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I (Pharmacia), and Eco RI sites of the modified pRT3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT ORIGIN

68 a 163 c 111 g 71 t

Alignment\_scores:

Quality: 14.00 Length: 14  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

seq\_documentation\_block:  
 LOCUS AA030363 501 bp mRNA EST 21-AUG-1996  
 DEFINITION mi45c07.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:466416 5 similar to gb:M55040 ACETYLCHOLINESTERASE

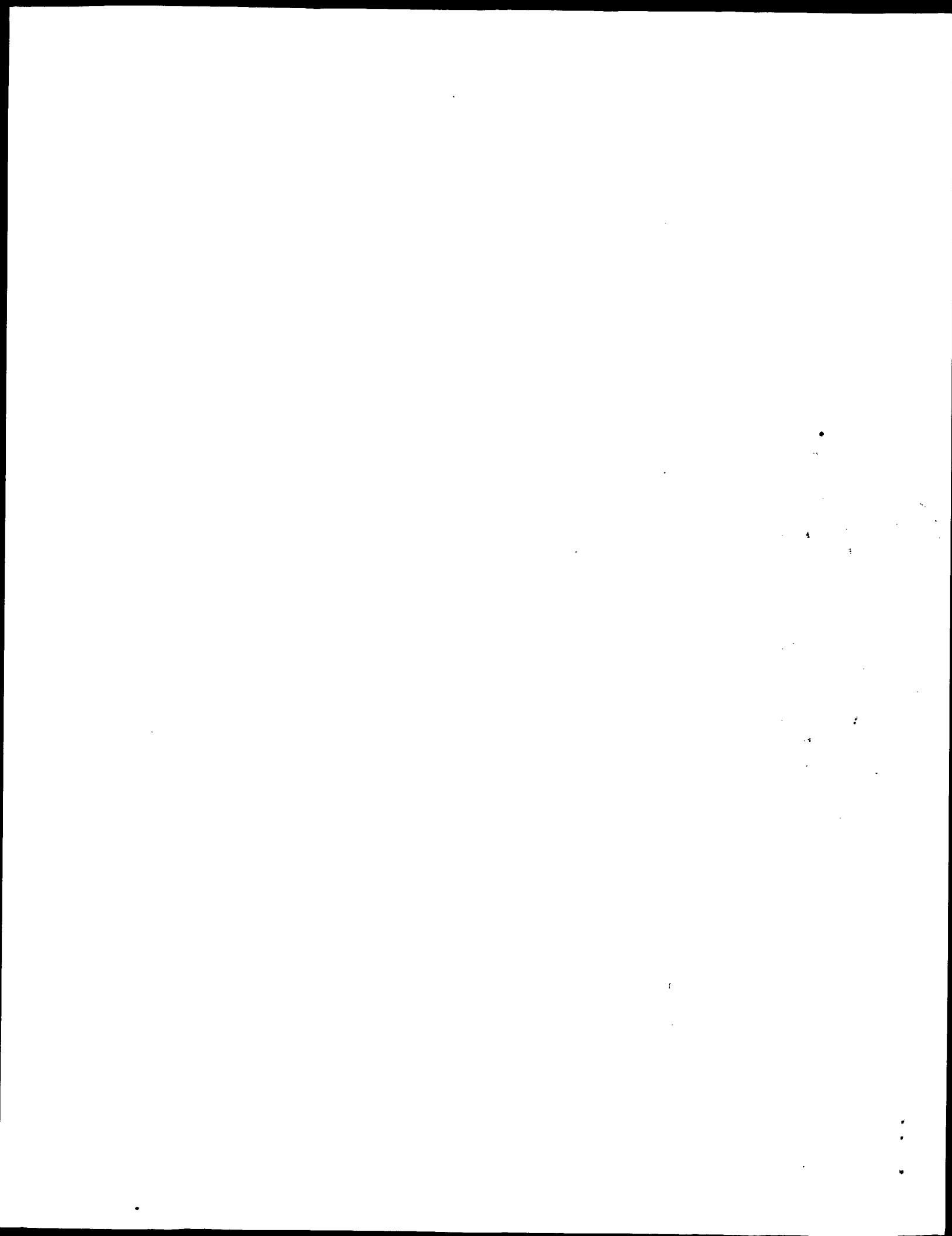
Align seg 1/1 to: AW653940 from: 1 to: 496

1 AlaGluPheHisArgTrpSerSerTyrNetvalHistrpys 14  
 118 GCGAGTTCCACCGCTGGACCTACATGGCACTGGAG 227

seq\_name: gb\_est1:AA030863

|                               |  |                           |                           |
|-------------------------------|--|---------------------------|---------------------------|
| PRECURSOR (HUMAN); gbi:X56518 | Mouse mRNA for acetylcholinesterase (MOUSE); mRNA sequence.  | EST                       | 19-Nov-1996               |
| ACCESSION                     | AA030863   |                           |                           |
| VERSION                       | AA030863.1   | GI:1500851                |                           |
| KEYWORDS                      | EST.   |                           |                           |
| SOURCE                        | Mouse  |                           |                           |
| ORGANISM                      | Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 501)  |                           |                           |
| REFERENCE                     | Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Scheibenbogen, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.   |                           |                           |
| AUTHORS                       | Unpublished (1996)   |                           |                           |
| TITLE                         | The WashU-HMMI Mouse EST Project   |                           |                           |
| JOURNAL                       | Contact: Marra M/Mouse EST Project   |                           |                           |
| COMMENT                       | WashU HMMI Mouse EST Project   |                           |                           |
|                               | Washington University School of MedicineP<br>4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108   |                           |                           |
|                               | TeL: 314 286 1800  |                           |                           |
|                               | Fax: 314 286 1810  |                           |                           |
|                               | Email: mouseest@watson.wustl.edu   |                           |                           |
|                               | This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  |                           |                           |
|                               | MGI:280292   |                           |                           |
|                               | Seq primer: -28M13 rev2 from Amersham  |                           |                           |
|                               | High quality sequence stop: 168.   |                           |                           |
| FEATURES                      | Location/Qualifiers  |                           |                           |
| source                        | 1..501   |                           |                           |
|                               | /organism="Mus musculus"   |                           |                           |
|                               | /strain="C57BL/6J"   |                           |                           |
|                               | /db_xref="taxon:10030"   |                           |                           |
|                               | /clone="IMAGE:66476"   |                           |                           |
|                               | /clone_1lib="Soares mouse embryo NDME13.5 14.5"  |                           |                           |
|                               | /sex="unknown"   |                           |                           |
|                               | /tissue_type="embryo"  |                           |                           |
|                               | /dev_stage="13.5-14.5dpc total fetus"  |                           |                           |
|                               | /lab_host="DH10B"  |                           |                           |
|                               | /note="Vector: PT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTTACCAATCTGACTGAGGGAGCGCCGGAAATTTCCTTTTTTTTTT-3'] on equal amounts of mRNA from 2 13.5dpc and 2 14.5dpc embryos (total RNA provided by Minoru Ko, Wayne State Univ., from 2 ); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo." |                           |                           |
| BASE COUNT                    | 97 a 163 c 138 g 103 t   |                           |                           |
| ORIGIN                        |  |                           |                           |
| alignment_scores:             | Quality: 14.00   | Length: 14                | Length: 14                |
|                               | Ratio: 1.000   | Gaps: 0                   | Gaps: 0                   |
| Percent Similarity: 100.000   | Percent Identity: 100.000  | Percent Identity: 100.000 | Percent Identity: 100.000 |
| alignment_block:              | US-09-155-076-1 x AAI18440 ..  |                           |                           |
|                               | Align seg 1/1 to: AAI18440   |                           |                           |
|                               | 1 AlagliuPhahisArgTrpSerSerTyrveta.Histplys 1  |                           |                           |
|                               | 202 GCGGAGTTCACCGGCTGGCTCATGTGCACTGGAG 243   |                           |                           |







PA (YISS ) YISSUM RES & DEV CO.  
 PI Shani M, Soreq H, Zukut H;  
 DR WPI: 95-31149/40.

PT Alternative forms of human acetyl cholinesterase (ChE) gene -  
 PT activity of organo:phosphate(s), etc. or as model of ChE imbalance  
 Disclosure; Fig 6, 55pp; English.

PS Human acetylcholinesterase (EC-3.1.1.7) is accumulated at  
 CC neuromuscular junctions where it serves a vital function in  
 modulating cholinergic neurotransmission. This alternative  
 spliced form of human AChE may be expressed in transgenic animals  
 which are used in an assay system for determining the anti-ChE  
 activity of organophosphates, carbamates, anti-ChE drugs, plant  
 CC glycoalkaloids and snake venoms.  
 Sequence 39 AA;

SEQ

Query Match 100.0%; Score 87; DB 1; Length 45;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYMHWK 14  
 Db 17 AEFHRWSSYMHWK 30

RESULT 4  
 W68144 standard; Protein: 45 AA.  
 ID W68144;  
 AC W68144;  
 DT 05-OCT-1998 (first entry)  
 DE Human AChE splice variant E1-4, 6.  
 KW Nuclease resistant; acetylcholinesterase; human; myasthenia gravis;  
 KW AChE; Parkinson's disease; Alzheimer's disease; central nervous system;  
 KW neuromuscular junction; cholinergic signalling; brain.  
 KW Homo sapiens.  
 OS WO9826062-A2.  
 PN 18-JUN-1998  
 PD 12-DEC-1997; U223598.  
 PF 21-JUL-1997; US-053334.  
 PR 12-DEC-1996; US-035266.  
 PR 13-FEB-1997; US-037777.  
 PR 02-MAY-1997; US-850347.  
 PA (YISS ) YISSUM RES & DEV CO.  
 PI Eckstein F, Friedman A, Kaufner D, Seidman S, Soreq H;  
 PT Synthetic nucleic acid sequence showing antisense Oligodeoxynucleotides -  
 PT directed against acetylcholinesterase, useful for treating  
 PT Parkinson's and Alzheimer's diseases and myasthenia gravis  
 PS Disclosure; Fig 12; 89pp; English.  
 CC This represents the amino acid sequence of a human acetylcholinesterase  
 CC (AChE) splice variant. The invention provides sequences shown in W41278  
 CC to W41285 that represent synthetic nucleic acid sequences shown in W41278  
 CC oligodeoxynucleotides which are capable of selectively modulating human  
 CC acetylcholinesterase (AChE) production. These oligonucleotides are  
 CC targeted to a splice junction in a splice variant of AChE mRNA and are  
 CC capable of selectively modulating human AChE production in the central  
 CC nervous system and neuromuscular junction. The invention also provides a  
 CC method for determining the efficacy of these human AChE specific  
 CC antisense oligonucleotides. These antisense oligonucleotides can be used  
 CC to restore balanced cholinergic signalling in the brain, particularly  
 CC related to learning and memory as well as stress disorders, Parkinson's  
 CC and Alzheimer's disease. They can also be used to reduce production and  
 CC therefore deposition of AChE in the neuromuscular junctions of patients  
 CC with e.g. myasthenia gravis. The oligonucleotides work effectively at low  
 CC doses while avoiding many of the side effects associated with Tacrine and  
 CC related cholinergic drugs for Alzheimer's disease and Pyridostigmine and  
 CC related drugs for myasthenia gravis.  
 SEQ Sequence 45 AA;

Query Match 100.0%; Score 87; DB 1; Length 45;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYMHWK 14  
 Db 17 AEFHRWSSYMHWK 30

RESULT 5  
 W74586 standard; Protein: 45 AA.  
 ID W74586;  
 AC W74586;  
 DT 21-DEC-1998 (first entry)  
 DE Amino acid sequence of the human AChE variant 1.  
 KW Nuclease resistance; inhibition; human; acetyl-cholinesterase; AChE;

PS

PT Increasing the permeability of the blood/brain barrier - using e.g.  
 PT adrenergic, atropine or acetylcholine esterase 14 splice variant  
 PT peptide, useful for imaging and/or treatment of central nervous  
 PT system disorders  
 Disclosure; Fig 2; 71pp; English.

CC The present sequence represents a C-terminal fragment of the human  
 acetylcholine esterase splice variant E1-4, 6 variant  
 CC comprises of residues encoded by exons 1-4 of AChE linked to residues  
 CC encoded by the alternatively spliced AChE exon 5. The invention claims  
 CC for the human acetylcholine esterase-14 (AChE-14) readthrough splice  
 CC variant (W48/97). The invention provides a pharmaceutical composition  
 CC for facilitating passage of compounds through the blood/brain barrier;  
 CC (BBB), comprising of AChE-14, 14 peptide (see W48/97) or AChE-14  
 CC analogues (such as the AChE E1-4, 6 variant) together with a  
 CC pharmaceutically acceptable carrier. The pharmaceutical composition  
 CC is claimed to facilitate a reversible disruption of the BBB allowing  
 CC transport of compounds through the BBB. The compounds, e.g. imaging  
 agents, antibiotics or chemotherapeutic drugs, are claimed to be  
 CC for the diagnosis and treatment of diseases or disorders of the CNS such  
 CC as infections, neurochemical disorders, brain tumours, gliomas, etc.  
 Sequence 45 AA;







DE Yeast delta-9 desaturase gene.  
 KW Delta-9 desaturase; fatty acids; seed oil; Zea maize;  
 KW Brassica rapa; Brassica napus; yeast; crops; ss.  
 OS Saccharomyces cerevisiae.  
 PN EP-561169-A.  
 PD 22-SEP-1993.  
 PF 12-MAR-1992; 301895.  
 PR 13-MAR-1992; US-850714.  
 PA (LUBR ) LUBRIZOL CORP.  
 PI Mehra-palta A, Poutre CG;  
 DR WPI: 93-296843/38.  
 DR N-PSDB: Q48731.  
 PT Plant seed contg. Yeast delta-9 desaturase gene - used to produce  
 PT oil with lower proportion of saturated fatty acids  
 PS Disclosure, Page 21-22; 32pp; English.  
 CC The yeast delta-9 desaturase gene was placed under the control of a  
 CC phaeolin promoter (normal or truncated) or 35S promoter to drive  
 CC expression in plant seeds transformed with the gene. Plant seeds  
 CC preferably used are Zea maize (a monocot plant) and Brassica rapa or  
 CC Brassica napus (dicots). Expression of the yeast delta-9 saturase  
 CC gene in any plant seed tissue could result in a decrease in  
 CC saturated fatty acids and an increase in monounsaturated fatty acids  
 CC in the seed oil.  
 SQ Sequence 510 AA;

Query Match 46.6%; Score 40.5; DB 1; Length 510;  
 Best Local Similarity 56.2%; Pred. No. 99;  
 Matches 9; Conservative 1; Mismatches 3; Indels 3; Gaps 2;

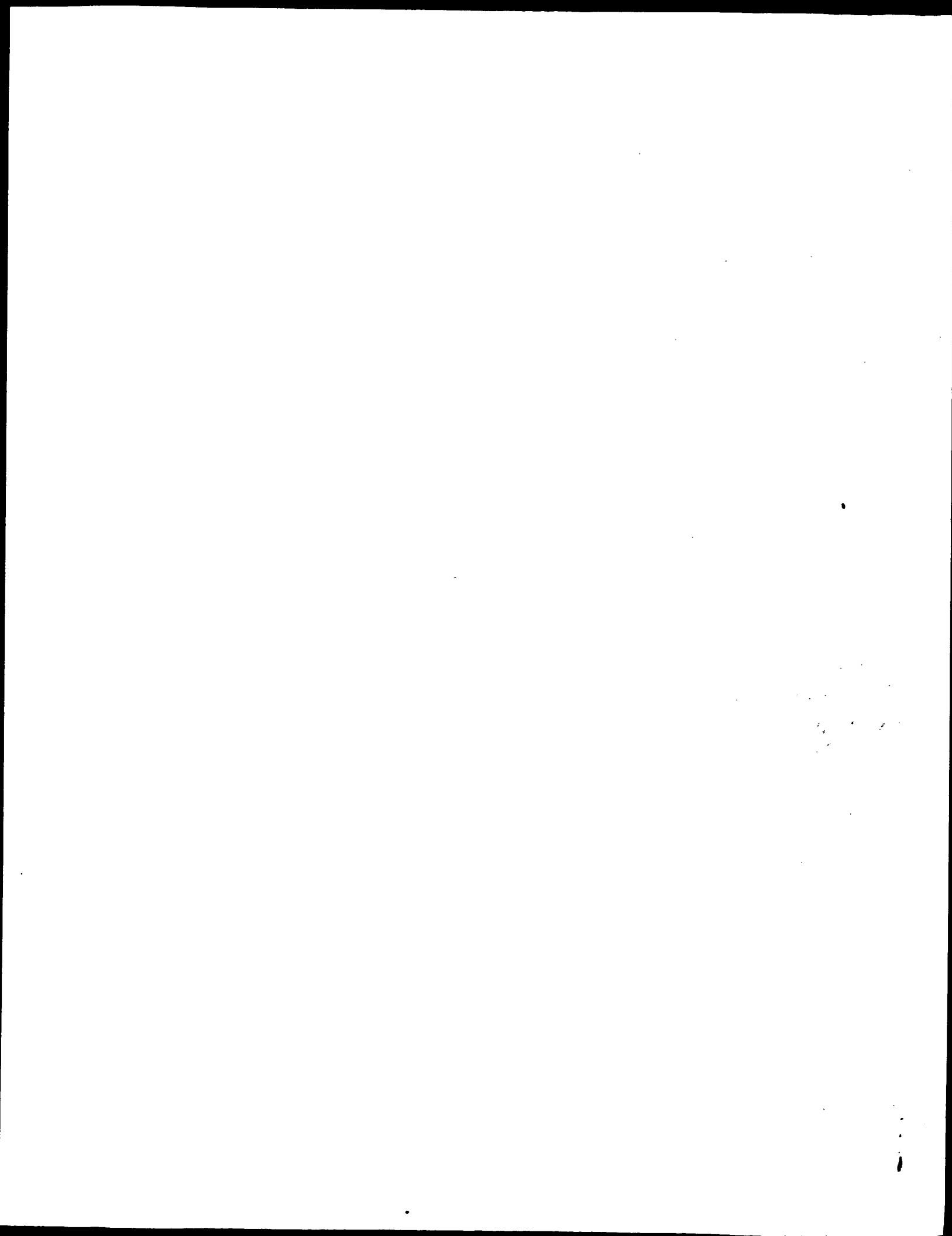
Qy 1 AEFHR-W\$-SYMVHW 13  
 Db 158 AGYHRLWHSRSYLSAHW 173

RESULT 15  
 R15441  
 ID R15441 standard; Protein; 124 AA.  
 AC R15441;  
 DT 25-FEB-1992 (first entry)  
 DE Heavy chain variable region of MAB 18B9.  
 KW HRV; ICAM-1; antigen-binding fragment; inflammation;  
 KW auto-immune disease.  
 OS Homo sapiens.  
 PN EP-459377-A.  
 PD 04-DEC-1991.  
 PF 25-MAY-1991; 201243.  
 PR 01-JUN-1990; US-532001.  
 PA (MERI ) MERCK & CO INC.  
 PI Colonna RJ, Condar JH, Tomassini JE, Sardana VV;  
 DR WPI: 91-355850/49.  
 PT Microbially expressed portions of monoclonal antibody - can block  
 PT attachment of rhinovirus ligands to inter-cellular adhesion  
 PT molecule (ICAM-1)  
 PR Claim 1; Page 20; 28pp; English.  
 PS This is one of six antibody fragments from MAB's specific for domain  
 CC 1 of ICAM-1. The peptide fragments can be used to treat or prevent  
 CC rhinovirus infection. See R15437-R15443.  
 SQ Sequence 124 AA;

Query Match 46.0%; Score 40; DB 1; Length 124;  
 Best Local Similarity 38.5%; Pred. No. 27;  
 Matches 5; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AEFHRSSSYMHW 13  
 Db 24 ASGHTFTSFVHW 36





GenCore version 4.5  
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OM protein - protein search, using sw mode

Run on: September 13, 2000, 02:19:42 ; Search time 14:59 Seconds  
(without alignments)  
14.709 Million cell updates/sec

Title: US-09-155-076-1  
Perfect score: 87  
Sequence: 1 AEFHRSSSYMHWK 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 152396 seqs, 15329161 residues

Total number of hits satisfying chosen parameters: 152396

Minimum DB seq length: 0  
Maximum DB seq length: 1000000

Post-processing: Minimum Match 100%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:  
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2: /cgna\_6/ptodata/2/1aa/5B\_COMBO.pep:  
3: /cgna\_6/ptodata/2/1aa/6\_COMBO.pep:  
4: /cgna\_6/ptodata/2/1aa/BCTUS\_COMBO.pep:  
5: /cgna\_6/ptodata/2/1aa/backfiles1.pep:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

| Result No. | Score | Query Match | Length | DB ID              | Description        |
|------------|-------|-------------|--------|--------------------|--------------------|
| 1          | 87    | 100.0       | 40     | 2 US-08-370-156-25 | Sequence 25, Appli |
| 2          | 87    | 100.0       | 45     | 2 US-08-370-156-7  | Sequence 7, Appli  |
| 3          | 87    | 100.0       | 45     | 2 US-08-370-156-8  | Sequence 8, Appli  |
| 4          | 87    | 100.0       | 614    | 1 US-07-732-162A-2 | Sequence 2, Appli  |
| 5          | 87    | 100.0       | 614    | 2 US-08-370-156-2  | Sequence 2, Appli  |
| 6          | 87    | 100.0       | 614    | 3 US-08-446-100-19 | Sequence 19, Appli |
| 7          | 87    | 100.0       | 614    | 3 US-08-446-100-20 | Sequence 20, Appli |
| 8          | 87    | 100.0       | 614    | 3 US-08-446-100-21 | Sequence 21, Appli |
| 9          | 87    | 100.0       | 614    | 3 US-08-446-100-23 | Sequence 22, Appli |
| 10         | 87    | 100.0       | 614    | 3 US-08-446-100-24 | Sequence 23, Appli |
| 11         | 87    | 100.0       | 614    | 3 US-08-446-100-25 | Sequence 25, Appli |
| 12         | 87    | 100.0       | 614    | 3 US-08-814-095-2  | Sequence 19, Appli |
| 13         | 87    | 100.0       | 614    | 4 PCT-US92-05106-2 | Sequence 2, Appli  |
| 14         | 80    | 92.0        | 575    | 1 US-08-348-920-1  | Sequence 1, Appli  |
| 15         | 80    | 92.0        | 575    | 1 US-08-348-920-2  | Sequence 2, Appli  |
| 16         | 62    | 71.3        | 572    | 5 5200183-5        | Patent No. 5200183 |
| 17         | 62    | 71.3        | 573    | 5 5215909-12       | Patent No. 5215909 |
| 18         | 62    | 71.3        | 602    | 3 US-08-446-100-1  | Sequence 1, Appli  |
| 19         | 62    | 71.3        | 602    | 3 US-08-446-100-2  | Sequence 2, Appli  |
| 20         | 62    | 71.3        | 602    | 3 US-08-446-100-3  | Sequence 3, Appli  |
| 21         | 62    | 71.3        | 602    | 3 US-08-446-100-4  | Sequence 4, Appli  |
| 22         | 62    | 71.3        | 602    | 3 US-08-446-100-5  | Sequence 5, Appli  |
| 23         | 62    | 71.3        | 602    | 3 US-08-446-100-6  | Sequence 6, Appli  |
| 24         | 62    | 71.3        | 602    | 3 US-08-446-100-7  | Sequence 7, Appli  |
| 25         | 62    | 71.3        | 602    | 3 US-08-446-100-8  | Sequence 8, Appli  |
| 26         | 62    | 71.3        | 602    | 3 US-08-446-100-9  | Sequence 9, Appli  |
| 27         | 62    | 71.3        | 602    | 3 US-08-446-100-10 | Sequence 10, Appli |
| 28         | 62    | 71.3        | 602    | 3 US-08-446-100-11 | Sequence 11, Appli |

**ALIGNMENTS**

---

RESULT 1  
US-08-370-156-25  
; Sequence 25, Application US/08370156  
; Patent No. 5912780  
; GENERAL INFORMATION:  
; APPLICANT: Soreq, Hermona  
; APPLICANT: Zukut, Haim  
; APPLICANT: Shani, Moshe  
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR  
; TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Reising, Ethington, Barnard & Perry  
; STREET: P.O. Box 4390  
; CITY: Troy  
; STATE: Michigan  
; COUNTRY: US  
; ZIP: 48099  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/370,156  
; FILING DATE: 5/3/98  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kohn, Kenneth I.  
; REGISTRATION NUMBER: 30,955  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (810) 689-3500  
; TELEFAX: (810) 689-4071  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQ ID NO: 25  
; LENGTH: 40 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-370-156-25  
; Query Match Score 87; DB 2; Length 40;  
; Best Local Similarity 100.0%; Pred. No. 5.2e-06;  
; Matches 14; Conservative 0; Mismatches 0; Index 0;  
; Gaps 0;

Qy : 1 AEFHRSSSYMHWK 14  
Db : 1 AEFHRSSSYMHWK 14  
Db : 12 AEFHRSSSYMHWK 25

RESULT 2  
US-08-370-156-7  
Sequence 7, Application US/08370156  
GENERAL INFORMATION:  
Patent No. 5932780  
APPLICANT: Soreq, Hermona  
APPLICANT: Shani, Moshe  
APPLICANT: Zakut, Haim  
TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR  
TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSSEE: Reisinger, Ethlington, Barnard & Perry  
STREET: P.O. Box 4390  
CITY: Troy  
STATE: Michigan  
COUNTRY: US  
ZIP: 48099  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/370,156  
FILING DATE:  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Kohn, Kenneth I.  
REGISTRATION NUMBER: 30,955  
REFERENCE/DOCKET NUMBER: P-307 (Mulford)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (810) 689-3500  
TELEFAX: (810) 689-4071  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-370-156-7

Query Match 100.0%; Score 87; DB 2; Length 45;  
Best Local Similarity 100.0%; Pred. No. 5.8e-06; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSMVHK 14  
Db 17 AEFHRWSSMVHK 30

RESULT 3  
US-08-370-156-8  
Sequence 8, Application US/08370156  
GENERAL INFORMATION:  
Patent No. 5932780  
APPLICANT: Soreq, Hermona  
APPLICANT: Shani, Moshe  
APPLICANT: Zakut, Haim  
TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR  
TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSSEE: Reisinger, Ethlington, Barnard & Perry  
STREET: P.O. Box 4390  
CITY: Troy  
STATE: Michigan  
ZIP: 48099  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

Query Match 100.0%; Score 87; DB 1; Length 614;  
 Best Local Similarity 100.0%; Pred. No. 6.3e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OP 1 AEFHRWSSYMWHK 14  
 | | | | | | | | | | | |  
 Db 586 AEFHRWSSYMWHK 599

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RESULT 5  
 US-08-370-156-2  
 ; Sequence 2, Application US/08370156  
 ; Patent No. 5532780  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Soreq, Hermona  
 ; APPLICANT: Zalut, Haim  
 ; APPLICANT: Shani, Moshe  
 ; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR  
 ; NUMBER OF SEQUENCES: 27  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Reisinger, Ethlington, Barnard & Perry  
 ; STREET: P.O. Box 4390  
 ; CITY: Troy  
 ; STATE: Michigan  
 ; COUNTRY: US  
 ; ZIP: 48099  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/370,156  
 ; FILING DATE:  
 ; CLASSIFICATION: 536  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Kohn, Kenneth I.  
 ; REGISTRATION NUMBER: 30,955  
 ; REFERENCE/DOCKET NUMBER: P-307 (Mulford)  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (810) 689-3500  
 ; TELEFAX: (810) 689-4071  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 614 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-08-370-156-2

Query Match 100.0%; Score 87; DB 2; Length 614;  
 Best Local Similarity 100.0%; Pred. No. 6.3e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OP 1 AEFHRWSSYMWHK 14  
 | | | | | | | | | | | |  
 Db 586 AEFHRWSSYMWHK 599

---

RESULT 6  
 US-08-446-100-19  
 ; Sequence 19, Application US/08446100  
 ; Patent No. 6001625  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Broomfield, Clarence A  
 ; APPLICANT: Millard, Charles B  
 ; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases  
 ; NUMBER OF SEQUENCES: 31  
 ; CORRESPONDENCE ADDRESS:

Query Match 100.0%; Score 87; DB 1; Length 614;  
 Best Local Similarity 100.0%; Pred. No. 6.3e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OP 1 AEFHRWSSYMWHK 14  
 | | | | | | | | | | | |  
 Db 586 AEFHRWSSYMWHK 599

---

RESULT 7  
 US-08-446-100-20  
 ; Sequence 20, Application US/08446100  
 ; Patent No. 6001625  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Broomfield, Clarence A  
 ; APPLICANT: Millard, Charles B  
 ; APPLICANT: Lockridge, Oksana  
 ; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases  
 ; NUMBER OF SEQUENCES: 31  
 ; CORRESPONDENCE ADDRESS:  
 ; STREET: 9669 A Main Street, P.O. Box 2509  
 ; CITY: Fairfax  
 ; STATE: VA  
 ; COUNTRY: US  
 ; ZIP: 22031  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/446-100  
 ; FILING DATE: 19-MAY-1995  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:

NAME: Hendricks, Glenna  
 REGISTRATION NUMBER: 32,535  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 425-4250  
 TELEFAX: (703) 425-2167  
 INFORMATION FOR SEQ ID NO: 20;  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 614 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: unknown  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: YES  
 ANTI-SENSE: YES  
 FRAGMENT TYPE: N-terminal  
 ORIGINAL SOURCE:  
 ORGANISM: human esterases  
 US-08-446-100-20

Query Match Score 100.0%; DB 3; Length 614;  
 Best Local Similarity 100.0%; Pred. No. 6.3e-05;  
 Matches 14; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

RESULT 9  
 US-08-446-100-22  
 Sequence 22, Application US/08446100  
 Patent No. 6001625  
 GENERAL INFORMATION:  
 APPLICANT: Broomfield, Clarence A  
 APPLICANT: Millard, Charles B  
 APPLICANT: Lockridge, Oksana  
 ADDRESS: Hendricks and Assoc.  
 STREET: 9669 A Main Street, P.O. Box 2509  
 CITY: Fairfax  
 STATE: VA  
 COUNTRY: US  
 ZIP: 22031  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/446,100  
 FILING DATE: 19-MAY-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Hendricks, Glenna  
 REGISTRATION NUMBER: 32,535  
 REFERENCE/DOCKET NUMBER: broomfield  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 425-4250  
 TELEFAX: (703) 425-2767  
 INFORMATION FOR SEQ ID NO: 22;  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 614 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: unknown  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: YES  
 ANTI-SENSE: YES  
 FRAGMENT TYPE: N-terminal  
 ORIGINAL SOURCE:  
 ORGANISM: human esterases  
 US-08-446-100-22

Query Match Score 100.0%; DB 3; Length 614;  
 Best Local Similarity 100.0%; Pred. No. 6.3e-05;  
 Matches 14; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

RESULT 10  
 US-08-446-100-23

Qy 1 AEFHRWSSYVHWK 14  
 Db 586 AEFHRWSSYVHWK 599

Sequence 23, Application US/08446100  
 Patent No. 6001625  
 GENERAL INFORMATION:  
 APPLICANT: Broomfield, Clarence A  
 APPLICANT: Millard, Charles B  
 APPLICANT: Lockridge, Oksana  
 TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases  
 NUMBER OF SEQUENCES: 31  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Hendricks and Assoc.  
 STREET: 9669 A Main Street, P.O. Box 2509  
 CITY: Fairfax  
 STATE: VA  
 COUNTRY: US  
 ZIP: 22031

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/446,100  
 FILING DATE: 19-MAY-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Hendricks, Glenna  
 REGISTRATION NUMBER: 32,535  
 REFERENCE/DOCKET NUMBER: broomfield  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 425-250  
 TELEFAX: (703) 425-2767  
 INFORMATION FOR SEQ ID NO: 25:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 614 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: unknown  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: YES  
 ANTI-SENSE: YES  
 FRAGMENT TYPE: N-terminal  
 ORIGINAL SOURCE:  
 ORGANISM: human esterases  
 US-08-446-100-25

Query Match 100.0%; Score 87; DB 3; Length 614;  
 Best Local Similarity 100.0%; Pred. No. 6.3e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0;  
 Gaps 0;

QY 1 AEFHRNSSYAHWK 14  
 Db 586 AEFHRNSSYAHWK 599

RESULT 12  
 US-08-814-095-2  
 Sequence 2, Application US/08814095  
 Patent No. 6025183  
 GENERAL INFORMATION:  
 APPLICANT: Soreq, Hermona  
 APPLICANT: Zakut, Haim  
 APPLICANT: Shani, Moshe  
 TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR  
 NUMBER OF SEQUENCES: 7  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: KOHN & ASSOCIATES  
 STREET: 30500 No. 6025183thwestern Highway, Suite 410  
 CITY: Farmington Hills  
 STATE: Michigan  
 COUNTRY: U.S.  
 ZIP: 48334  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/814,095  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Montgomery, Irene N.  
 REGISTRATION NUMBER: 38,972  
 REFERENCE/DOCKET NUMBER: 2391.00066  
 TELECOMMUNICATION INFORMATION:  
 STREET: Fairfax  
 STATE: VA  
 COUNTRY: US  
 ZIP: 22031  
 COMPUTER READABLE FORM:

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 614 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens

• US-08-814-095-2

RESULT 13

Query Match 100.0%; Score 87; DB 3; Length 614;  
 Best Local Similarity 100.0%; Pred. No. 6.3e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRSSSYMHWK 14  
 Db 586 AEFHRSSSYMHWK 599

Sequence 1, Application US/08348920  
 Patent No. 5695750  
 GENERAL INFORMATION:  
 APPLICANT: Doctor, Bhupandra P.  
 APPLICANT: Maxwell, Donald  
 APPLICANT: Saxena, Ashima  
 APPLICANT: Radic, Zoran  
 APPLICANT: Taylor, Palmer  
 TITLE OF INVENTION: Compositions for use to Deactivate  
 NUMBER OF SEQUENCES: 2  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: John F. Moran  
 STREET: Off. of Command Judge Adv., HQ USAMRDC, Fort  
 STREET: Off. of Command Judge Adv., HQ USAMRDC, Fort  
 CITY: Frederick  
 STATE: MD  
 COUNTRY: US  
 ZIP: 21702-5012  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/348,920  
 FILING DATE: 25-NOV-1994  
 CLASSIFICATION: 424  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Hendricks, Glenna  
 REGISTRATION NUMBER: 32,535  
 REFERENCE/DOCKET NUMBER: doc348,920  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (301) 619-7807  
 TELEFAX: 301-619-7714  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 575 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: unknown  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: internal  
 US-08-348-920-1

Query Match 92.0%; Score 80; DB 10; Length 575;  
 Best Local Similarity 92.3%; Pred. No. 0.00054;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EEFHRSSSYMHWK 14  
 Db 548 EEFHRSSSYMHWK 560

RESULT 15

US-08-348-920-2

Sequence 2, Application US/08348920  
 Patent No. 5695750  
 GENERAL INFORMATION:  
 APPLICANT: Doctor, Bhupandra P.  
 APPLICANT: Maxwell, Donald  
 APPLICANT: Saxena, Ashima  
 APPLICANT: Radic, Zoran  
 APPLICANT: Taylor, Palmer  
 TITLE OF INVENTION: Compositions for use to Deactivate  
 NUMBER OF SEQUENCES: 2  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: John F. Moran  
 STREET: Off. of Command Judge Adv., HQ USAMRDC, Fort

Query Match 100.0%; Score 87; DB 4; Length 614;  
 Best Local Similarity 100.0%; Pred. No. 6.3e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 586 AEFHRSSSYMHWK 599

RESULT 14

US-08-348-920-1

Wed Sep 13 08:11:30 2000

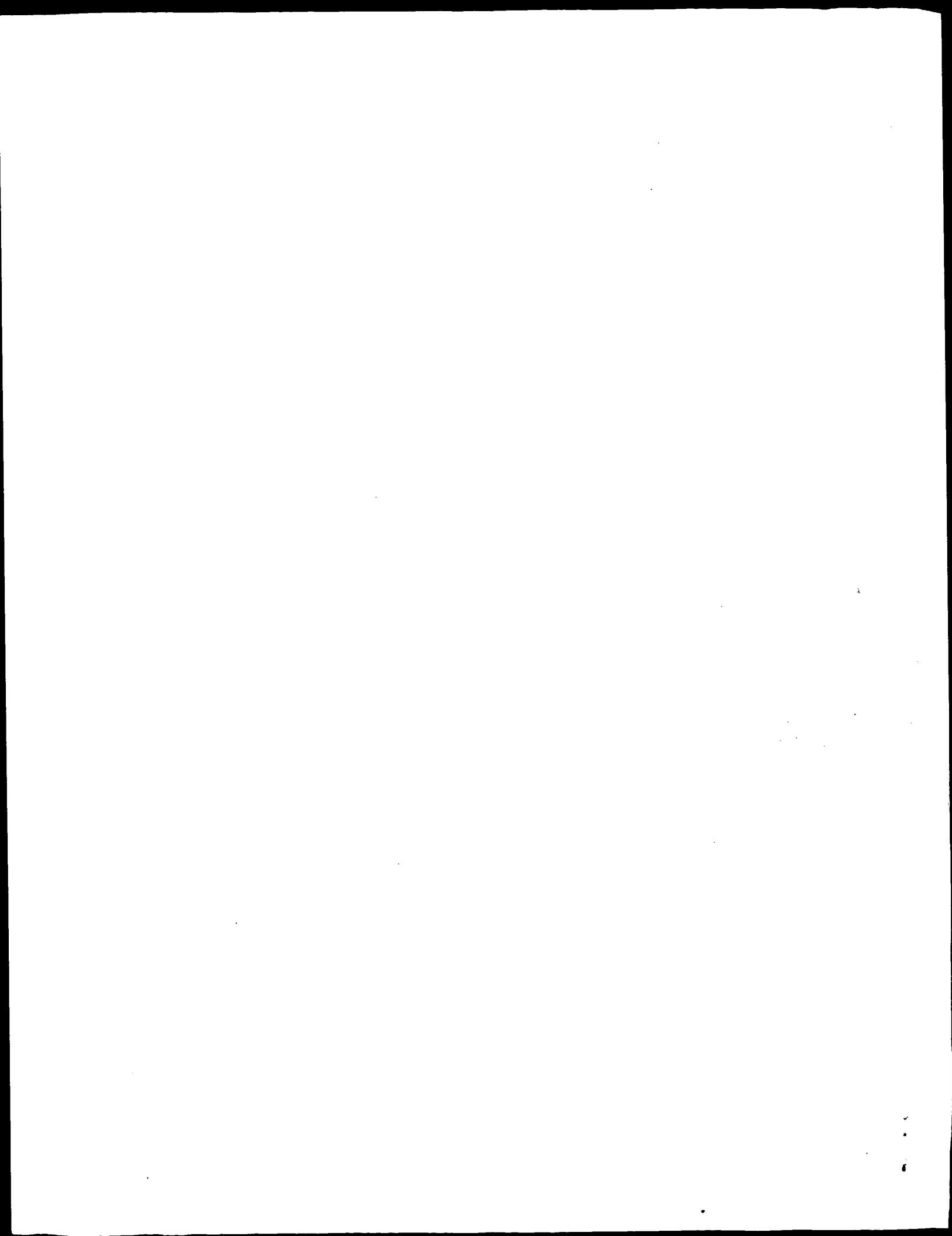
us-09-155-076-1\_1.rai

Page 7

; STREET: Detrick  
; ; CITY: Frederick  
; STATE: MD  
; COUNTRY: US  
; ZIP: 21702-5012  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/348,920  
; FILING DATE: 25-NOV-1994  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hendricks, Glenna  
; REGISTRATION NUMBER: 32,535  
; REFERENCE/DOCKET NUMBER: doc348,920  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 619-7807  
; TELEFAX: 301-619-7714  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 575 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; US-08-348-920-2

Query Match Score 80; DB 1; Length 575;  
Best Local Similarity 92.3%; Pred. No. 0.00054;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 2 EFHRWSSMVMHVK 14  
Db 548 EFHRWSSMVMHVK 560

Search completed: September 13, 2000, 02:22:01  
Job time: 139 sec



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 Date: Sep 13, 2000 2:56 AM  
 About: Results were produced by the Gencore software, version 4.5,  
 Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:  
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 -O=/con2.1/DUSPTO\_spool/US09155076/runat\_29082000\_092505.15746/app\_query.fasta\_1.144  
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Search information block:

Query: US-09-155-076-1

Query length: 14

Database: GenEmbl:\*

Database sequences: 972840

Database length: 89238106

Search time (sec): 757.400000

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| LOCUS                    | BTACHE4  | -          | -      | -      | ! AC006734 | Caenorhabditis elegans           |
| DEFINITION               | Bos taurus acetylcholinesterase T-subunit precursor (AChE) gene, exon 6 and partial cds.   | -          | -      | -      | ! AC012008 | Homo sapiens cDNA clone AC023283 |
| ACCESSION                | AF061816   | -          | -      | -      | 167300     |                                  |
| VERSION                  | AF061816.1   | GI:3746574 | -      | -      | 2.9e+03    |                                  |
| KEYWORDS                 | 4 of 4   | -          | -      | -      | 4.6e+03    |                                  |
| SEGMENT                  | Bos taurus   | -          | -      | -      | 257599     |                                  |
| SOURCE                   | Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovine; Bos.           | -          | -      | -      | -          |                                  |
| REFERENCE                | 1 (bases 1 to 140)   | -          | -      | -      | -          |                                  |
| AUTHORS                  | Mendelson,I., Kronman,C., Ariel,N., Shafferman,A. and Velan,B.   | -          | -      | -      | -          |                                  |
| TITLE                    | Bovine acetylcholinesterase: cloning, expression and characterization  | -          | -      | -      | -          |                                  |
| JOURNAL                  | Biochem. J. 334 (Pt 1), 251-259 (1998)   | -          | -      | -      | -          |                                  |
| MEDLINE                  | 98359754   | -          | -      | -      | -          |                                  |
| REFERENCE                | 2 (bases 1 to 140)   | -          | -      | -      | -          |                                  |
| AUTHORS                  | Mendelson,I., Kronman,C., Ariel,N., Shafferman,A. and Velan,B.   | -          | -      | -      | -          |                                  |
| TITLE                    | Direct Submission  | -          | -      | -      | -          |                                  |
| JOURNAL                  | Submitted (28-ABR-1998) Biochemistry and Molecular Genetics, Israel Institute for Biological Research, Po Box 19, Ness Ziona 70450, Israel | -          | -      | -      | -          |                                  |
| FEATURES                 | Location/Qualifiers  | -          | -      | -      | -          |                                  |
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|                          | /codon_start=3   | -          | -      | -      | -          |                                  |
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seq\_name: gb\_pr3:HUMACHE04

seq\_documentation\_block:  
 LOCUS HUMACHE04 475 bp DNA PRI 14-JUN-1995  
 DEFINITION Human acetylcholinesterase (ACHE) gene, exon 6.  
 ACCESSION L22562  
 VERSION L22562.1 GI:8622302  
 KEYWORDS acetylcholinesterase.  
 SEGMENT 4 of 4  
 SOURCE Homo sapiens DNA.

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (sites)  
 AUTHORS Soerg, H.E., Ben-Ariz, R., Prody, C.A., Seidman, S., Gmatt, A., Neville, L., Lieman-Hurwitz, J., Lev-Lehman, E., Ginzerberg, D., Lapidot-Lifson, Y. and Zukut, H.

TITLE Molecular cloning and construction of the coding region for human acetylcholinesterase reveals a G + C-rich attenuating structure  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (24), 9888-9892 (1990)

MEDLINE 91088577  
 REFERENCE 2 (sites)  
 AUTHORS Li, Y., Camp, S., Rachinsky, T.L., Getman, D. and Taylor, P.

TITLE Gene structure of mammalian acetylcholinesterase. Alternative exons dictate tissue-specific expression  
 JOURNAL J. Biol. Chem. 266 (34), 23083-23090 (1991)

MEDLINE 92078174  
 REFERENCE 3 (bases 1 to 475)  
 AUTHORS Bartels, C.F., Zelinski, T. and Lockridge, O.

TITLE Mutation at codon 322 in the human acetylcholinesterase (ACHE) gene accounts for YT blood group polymorphism  
 JOURNAL Am. J. Hum. Genet. 52 (5), 928-936 (1993)

MEDLINE 93256075  
 COMMENT On Jun 15, 1995 this sequence version replaced gi:857448.  
 Reference [1] reports bases 142-480.  
 Reference [J. Biol. Chem. 266, 23083-23090 (1991)] reports bases 132-141;

Reference [3] reports bases 1-131\*\*.  
 Location/Qualifiers  
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 US-09-155-076-1 x OC05036 ..  
 Align seg 1/1 to: OC05036 from: 1 to: 1947

1 AlaGluPheHisArgTrpSerSerTyrMetValHistPlys 14  
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1666 CGGAAGTTCCACCGCTGGACTCCATAGTGGACTGAAAG 1707

seq\_name: gb\_ro:S50879

seq\_documentation\_block:  
 LOCUS S50879 2066 bp mRNA  
 DEFINITION acetylcholinesterase T subunit [rats, mRNA Partial, 2066 nt].

1 AlaGluPheHisArgTrpSerSerTyrMetValHistPlys 14  
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169 GCGAGTTCACCGCTGGACTCTACAGTGGACTGAAAG 210

seq\_name: gb\_om:OCU05036

seq\_documentation\_block:  
 LOCUS OC05036 1947 bp mRNA  
 DEFINITION Oryctolagus cuniculus acetylcholinesterase mRNA, partial cds.  
 ACCESSION U05036  
 VERSION U05036.1 GI:576446  
 KEYWORDS acetylcholinesterase.  
 SOURCE Oryctolagus cuniculus.  
 ORGANISM Oryctolagus cuniculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Lagomorpha; Leporidae; Oryctolagidae.  
 REFERENCE 1 (bases 1 to 1947)  
 AUTHORS Jbilo, O., Lhermitte, Y., Toutant, J. and Chatonnet, A.  
 TITLE Acetylcholinesterase and Butyrylcholinesterase expression in adult rabbit tissues and during development  
 JOURNAL Eur. J. Biochem. 225, 115-124 (1994)  
 MEDLINE 95010096  
 REFERENCE 2 (bases 1 to 1947)  
 AUTHORS Chatonnet, A.  
 TITLE Direct Submission  
 JOURNAL Submitted [13-JAN-1994] Arnaud Chatonnet, Physiologie Animale, Institut National de la Recherche Agronomique, Place Viala, Montpellier, 34060 France  
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 POLYA\_site 1946 .. 655 c 660 g 333 t  
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 BASE COUNT 299 a  
 Percent Similarity: 100.000  
 Percent Identity: 100.000

ACCESSION S50879  
 VERSION S50879\_1  
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 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 REFERENCE 1 (bases 1 to 2086)  
 AUTHORS Legay,C., Bon,S., Vernier,P., Coussen,F., and Massoulie,J.  
 TITLE Cloning and expression of a rat acetylcholinesterase subunit:  
 generation of multiple molecular forms and complementarity with a  
 Torpedo collagenic subunit  
 J. Neurochem. 60 (1), 337-346 (1993)  
 JOURNAL 93107932  
 MEDLINE GenBank staff at the National Library of Medicine created this  
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 REMARK This sequence comes from Fig. 1.  
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 Ratio: 6.214 Gaps: 0  
 Percent Similarity: 100.000 Identity: 100.000

alignment\_block: US-09-155-076-1 x S50879 ..

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1 AlaGlupheHisArgTrpSerSerTyrMetValHistTrpLys 14  
 1756 GCCGAGTTCCACCGCTGGAGCTCATGGACTGGAG 1797

seq\_name: gb\_prz:MMACHE

seq\_documentation\_block:

LOCUS MMACHE  
 DEFINITION Human acetylcholinesterase (ACHE) mRNA, complete cds.  
 ACCESSION M55040  
 VERSION M55040\_1 GI:177974  
 KEYWORDS acetylcholinesterase.  
 SOURCE Human 21-week old fetus DNA, and cDNA to mRNA.  
 ORGANISM Homo sapiens  
 Eukaryote; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 2218)  
 AUTHORS Soere,H.E., Ben-Azzi,R., Prody,C.A., Seidman,S., Gnatt,A., Neville,L., Lieman-Hurwitz,J., Lev-Lehman,E., Ginzberg,D., Lapidot-Lifson,Y. and Zukut,H.

TITLE Direct Submission (30-OCT-1990) Taylor P., University of California, San  
 Diego, Department of Pharmacology, La Jolla, CA 92093-0556  
 REFERENCE 2 (bases 1 to 2089)  
 AUTHORS Rachinsky,T.L., Camp,S., Li,Y., Ekstrom,T.J., Newton,M. and  
 Taylor,P.  
 TITLE Molecular cloning of mouse acetylcholinesterase: tissue  
 distribution of alternatively spliced mRNA species  
 JOURNAL Neuron 5 (3), 317-327 (1990)  
 MEDLINE 90380429  
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 Percent Similarity: 100.000 Identity: 100.000

alignment\_block: US-09-155-076-1 x MMACHE ..

Align seg 1/1 to: MMACHE from: 1 to: 2089

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 1756 GCCGAGTTCCACCGCTGGAGCTCATGGACTGGAG 1797

seq\_name: gb\_prz:MMACHE

seq\_documentation\_block:

LOCUS MMACHE  
 DEFINITION Mouse mRNA for acetylcholinesterase.  
 ACCESSION X56518  
 VERSION X56518\_1 GI:49844  
 KEYWORDS acetylcholinesterase.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
 Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 2089)  
 AUTHORS Taylor,P.

**TITLE** Molecular cloning and construction of the coding region for human acetylcholinesterase reveals a G + C-rich attenuating structure  
**JOURNAL** Proc. Natl. Acad. Sci. U.S.A. 87 (24), 9688-9692 (1990)  
**MEDLINE** 91088577  
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  LDYDGFRFLVQAEVTYLVEVMNVRGAFLSPSRGLFHRAPGNGVLLDORALQWQENV  
  AAFGSDPTSVLFESESAGASVGMHLLSPSPRLFHRAPGNGVLLDORALQWQENV  
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  DGDFEISDTPALINGDFRGLQVLYGVKDEGFLFVYGAPEFSKDESLTSRAEFLIA  
  GVRGVPVOSDLSAEAVYLHYTOMLHPDPARALEREALDVYDHNTVCPLAQLAGRLA  
  AQGRARYAYTEFHASTLSWPLJNGVPGYEETFFIGPLDSDRNTAAEKFAQLML  
  RYWANFARTGDPNBRDKAPQNPYTAGAQVVSQSLDRPLVERRGLRAQCAFWRFL  
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3.10. . 1998  
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**BASE COUNT** 355 a  
**ORIGIN** 680 g  
**sig\_peptide**  
**BASE COUNT** 355 a  
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  **Ratio:** 6.214   **Gaps:** 0  
  **Percent Similarity:** 100.000   **Percent Identity:** 100.000  
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Align seg 1/1 to: HUMACHE from: 1 to: 2218  
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DEFINITION Sequence 5 from patent US 5891725.  
ACCESSION AR070205  
VERSION AR070205.1 GI:7221093  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.

**REFERENCE** 1 (bases 1 to 2256)  
**AUTHORS** Soreq, H., Zakut, H. and Eckstein, F.  
**TITLE** Synthetic antisense oligodeoxyribonucleotides and pharmaceutical compositions containing them  
**JOURNAL** Patent: US 5891725-A 5 06-APR-1999;  
**FEATURES** Location/Qualifiers  
**source** 1. . 2256  
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**ORIGIN** 680 g  
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1 AlagluPheHisArgTrpSerSerTyrMetValHistRplys 14  
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**seq\_name:** gb\_pat:AR070205

**seq\_documentation\_block:** AR070207 3016 bp DNA  
**LOCUS** AR070207 Sequence 6 from patent US 5891725.  
**DEFINITION** Sequence 6 from patent US 5891725.  
**ACCESSION** AR070207  
**VERSION** AR070207.1 GI:7221094  
**KEYWORDS** Unknown.  
**SOURCE** Unknown.  
**ORGANISM** Unknown.

**seq\_documentation\_block:** AR070206 3096 bp DNA  
**LOCUS** AR070206 Sequence 6 from patent US 5891725.  
**DEFINITION** Sequence 6 from patent US 5891725.  
**ACCESSION** AR070206  
**VERSION** AR070206.1 GI:7221094  
**KEYWORDS** Unknown.  
**SOURCE** Unknown.  
**ORGANISM** Unknown.

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Unclassified.
1 (bases 1 to 3096)
Sores, H., and Eckstein, F.
Synthetic antisense oligodeoxynucleotides and pharmaceutical
compositions containing them
Patent: US 5891725-A 6 06-APR-1999;
Location/Qualifiers
1. 3096
    /organism="unknown"
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alignment_scores:
    Quality: 87.00          Length: 14
    Ratio: 6.214             Gaps: 0
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seq_name: gb_om:AF053485
seq_documentation_block:
    LOCUS AF053485 bp      DNA
    DEFINITION Felis catus acetylcholinesterase glycoprophospholipid-anchored f
    precursor (ACHE) and acetylcholinesterase collagen-tailed or
    globular form precursor (ACHE) genes, complete cds.
    ACCESSION AF053485
    VERSION AF053485.1
    GI:3003019
    SOURCE cat.
    ORGANISM Felis catus
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
    Eutheria; Carnivora; Fissipedia; Felidae; Felis.
    1 (bases 1 to 3958)
    Bartels, C.F., Xie, W.-H., Miller-Lindholm, A.K. and Lockridge, O.
    Sequence and characterization of domestic cat acetylcholinest
    and butyrylcholinesterase
    Unpublished
    2 (bases 1 to 3958)
    Bartels, C.F., Xie, W.-H., Miller-Lindholm, A.K. and Lockridge, O.
    Direct Submission
    Submitted (12-MAR-1998) Eppley Institute, University of Nebraska
    Medical Center, 600 S. 42nd St., Omaha, NE 68198-6805, USA
    JOURNAL
    FEATURES source
    REFERENCE
    AUTHORS
    TITLE
    JOURNAL
    FEATURES source
    mRNA
    mRNA
    gene
    CDS

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GGDPMSVTLRESEAGASAVGMHLSPPSRGFLDHFVHLQAPNGWATVGEARRA  
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| BASE COUNT | 723 | a | 1256 | c | 1205 | g | 772 | t | 2 | Others |
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 Quality: 87.00 Length: 14  
 Ratio: 6.214 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

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 US-09-155-076-1 x AF053485 ..

Align seq 1/1 to: AF053485 from: 1 to: 3958

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| 1    | AlaGluPheHisArgTrpSerSerTyrNetValHistRPrLyS 14 |
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seq\_name gb\_pr3:HOMACHEB

seq\_documentation\_block:

|  |   |           |     |     |             |
|--|---|-----------|-----|-----|-------------|
| LOCUS  | HOMACHEB                                      | 4185 bp   | DNA | PRI | 23-JUN-1995 |
| DEFINITION   | Homo sapiens acetylcholinesterase (ACHE) gene |           |     |     |             |
| ACCESSION  | I42812  |           |     |     |             |
| VERSION  | I42812.1                                      | GI:851682 |     |     |             |
| KEYWORDS   | acetylcholinesterase.                         |           |     |     |             |
| SOURCE   | Homo sapiens DNA.                             |           |     |     |             |
| ORGANISM   | Homo sapiens                                  |           |     |     |             |
| Eukaryota; Primates; Chordata; Craniata; Vertebrata; Mammalia; |   |           |     |     |             |
| Buthera; Primates; Catarrhini; Hominidae; Homo.                |   |           |     |     |             |
| 1 (sites)  |   |           |     |     |             |

Bartels,C.F., Zelinski,T. and Lockridge,O.  
Mutation at codon 322 in the human acetylcholinesterase (ACHE) gene  
accounts for YT blood group polymorphism  
Am. J. Hum. Genet. 52 (5), 928-936 (1993)  
93256075

REFERENCE 2 (bases 1 to 4185)  
AUTHORS Bartels,C.F., Moriarity,P.L., Becker,R.E., Robbs,R.S.,  
TITLE Sorenson,R.C., Mountjoy,C.P. and Lockridge,O.  
Polymerase sites in the acetylcholinesterase gene of patients with  
Alzheimer's disease  
Unpublished (1995)  
Location/Qualifiers

JOURNAL FEATURES

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 3239. .3991  
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 ORIGIN Gaps: 0  
 Percent Identity: 100.000

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 Quality: 87.00 Length: 14  
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alignment\_block:  
 US-09-155-076-1 X HUMACHEB  
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seq\_documentation\_block:  
 LOCUS HSAF002993 34921 bp DNA PRI 01-JAN-1998  
 DEFINITION Homo sapiens cDNA from 7q22, complete sequence.  
 ACCESSION AF002993  
 VERSION AF002993.1 GI:2735699  
 KEYWORDS HTG.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 (bases 1 to 34921)  
 REFERENCE Drescher,B., Rosenthal,A., Hinzmann,B. and Korner,M.  
 AUTHORS Drescher,B., Rosenthal,A., Hinzmann,B. and Korner,M.  
 TITLE Genomic sequencing in 7q22 revealed a novel arsenite resistance  
 gene  
 Unpublished (1997)  
 2 (bases 1 to 34921)  
 REFERENCE Drescher,B., Rosenthal,A., Hinzmann,B. and Korner,M.  
 AUTHORS Direct Submission  
 TITLE JOURNAL Submitted (07-MAY-1997) Genome Analysis, Institute of Molecular  
 Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany  
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 exon 1474. .1572  
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 exon 1657. .174  
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 evidence-not\_experimental Ratio: 6.214 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

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ORIGIN

alignment\_block: US-09-155-076-1 x HSAF002993/review

Align seg 1/1 to reverse of: HSAF002993 from: 1 to: 34921

1 AlaglupheHisArgTrpSerSerTyrMetValHistIlePlys 14  
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seq\_name: gb\_htg929:AC011895

seq\_documentation\_block:  
 LOCUS AC011895 175155 bp DNA HTG 21-APR-2000  
 DEFINITION Homo sapiens chromosome 7 clone RP11-126L15, WORKING DRAFT  
 SEQUENCE, 3 unordered pieces.

ACCESSION AC011895  
 VERSION AC011895\_3 GI:7630854  
 KEYWORDS HTGS PHASE1; HTGS\_DRAFT.  
 SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 1 (bases 1 to 175155)  
 Waterston,R.H.  
 The sequence of Homo sapiens clone  
 Unpublished  
 2 (bases 1 to 175155)

Waterston, R. H.  
 TITLE Direct Submission  
 JOURNAL Submitted (15-OCT-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA  
 On Apr 21, 2000 this sequence version replaced gi:6136444.

Center: Washington University Genome Sequencing Center  
 Center code: WUGSC  
 Web site: <http://genome.wustl.edu/gsc/index.shtml>

Project Information -----  
 Project name: H\_NH0126L15  
 Summary Statistics -----  
 Sequencing vector: M13; 748

Sequencing vector: Plasmid; 268

Chemistry: Dye-primer ET; 67% of reads  
 Chemistry: Dye-terminator Big Dye; 33% of reads

Assembly program: Phrap; version 0.390319

Consensus quality: 175580 bases at least Q40  
 Consensus quality: 173920 bases at least Q30  
 Consensus quality: 174136 bases at least Q20

Insert size: 180000; agarose-fp  
 Insert size: 179555; sum-of-contigs  
 Quality coverage: 7.01 in Q20 bases; agarose-fp  
 Quality coverage: 7.40 in Q20 bases; sum-of-contigs

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 This is a 'working draft' sequence. It currently  
 \* consists of 3 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

\* 1 28804: contig of 28804 bp in length  
 \* 28904: gap of unknown length  
 \* 28905 93340: contig of 64436 bp in length  
 \* 93341 93440: gap of unknown length  
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Location/Qualifiers

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FEATURES source

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 Quality: 87.00 Length: 14  
 Ratio: 6.214 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block: US-09-155-076-1 x AC011895/review  
 Align seg 1/1 to reverse of: AC011895 from: 1 to: 175155

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       135235 GCCGAGTTCCACCGCTGGACTCTACATGGTCACTGGAAAG 135194

seq\_name: gb\_htg929:AC011895

seq\_documentation\_block:  
 LOCUS AF030422 4472 bp DNA VRT 20-NOV-1997  
 DEFINITION Electrophorus electricus acetylcholinesterase catalytic subunit precursor gene, complete cds.  
 ACCESION AF030422  
 VERSION AF030422.1 GI:2613035  
 KEYWORDS electric eel.  
 SOURCE Electrophorus electricus  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii; Neopterygii; Teleostei; Bteleoste; Ostariophysi; Gymnotiformes; Gymnotoidei; Electricphoridae; Electrophorus.

REFERENCE 1 (bases 1 to 4472)  
 AUTHORS Simon,S. and Massoulie,J.  
 TITLE Cloning and expression of acetylcholinesterase from Electrophorus  
 JOURNAL J. Biol. Chem. (1997) In press  
 REFERENCE 2 (bases 1 to 4472)  
 AUTHORS Simon,S. and Massoulie,J.  
 TITLE Direct Submission  
 JOURNAL Submitted (15-OCT-1997) Neurobiology, Ecole Normale Supérieure, 45 Rue d'Ulm, Paris 75005, France  
 FEATURES Location/Qualifiers  
 1 4472 /protein\_id="AAB86606.1"  
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 /chromosome="7"  
 /region="pnl1-126L15"

BASE COUNT 1234 a 1234 g 983 g 1351 t 3700 )





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OM of: US-09-155-076-1 to: N_Geneseq_36: * out_format : pfs
Date: Sep 13, 2000 2:58 AM

About: Results were produced by the GenCore software, version 4.5.
Copyright (C) 1993-2000 Compugen Ltd.

Command line parameters:
 -MODEL=frame+_D2n model -DEV=xlp
 -Q=/cgn2/_USP10_spool/US09155016/runat_29082000_092505_15779/app_que
 -DB=N_Geneseq_36 -QFNT=fastaP -SUFFIX=ring -GAPOF=12.000
 -GAPEXT=-1.000 -MINMATCH=0.100 -LOOPFCI=0.000
 -QGAPEXT=4.000 -QGAPOF=0.000 -LOOPEXT=0.000
 -FGAPOF=4.500 -FGAPEXT=0.050 -XGAPOF=10.000 -XGAPEXT=0.500
 -DFGAPOF=6.000 -DFGAPEXT=7.000 -YGAPOF=10.000 -YGAPEXT=0.500
 -DELOF=6.000 -DELEXT=7.000 -START=-1 -MATRIX=blosum62
 -TRANS=human40_cdi -LIST=45 -DOCALIGN=200 THR_SCORE_PCT
 -THR_MAX=0 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
 -NORM=ext -MINLEN=0 -MAXLEN=1000000 -USERID=US09155076 @CGN1_1.75
 -NCPU=6 -ICPU=3 -LONGLOG -NO_XLPPX -WAIT -THREADS=1

Search information block:
Query: US-09-155-076-1
Query length: 14
Database: N_Geneseq_36:*
Database sequences: 311585
Database length: 125016042
Search time (sec): 75.68000000000000

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N\_Geneseq\_36:Q12851 + 42.00 108.14 201.16 821 ! A niger PGII promoter, sigma  
 ID C05999 standard; DNA; 1800 BP.  
 AC Q05999;  
 DT 16-JAN-1991 (first entry)  
 DE Sequence encoding foetal human acetylcholinesterase (hAChE).  
 KW Organophosphorous poisoning; OP; cancer; leukaemia;  
 KW megakaryocytopoiesis; ovarian cancer; ds.  
 OS Homo sapiens.  
 PH Key  
 FT Location/Qualifiers  
 CDS 1..1500  
 FT /tag= a  
 FT 1501..1800  
 FT /\*tag= b  
 PN EP-388906-A.  
 PD 26-SEP-1990.  
 PR 20-MAR-1990; 105274.  
 PR 21-MAR-1990; IL-089703.  
 PA (YISS ) YISUM RES DEV CO.  
 PI Soreq H, Zakut H;  
 DR P-PSDB; R06990.  
 PT Human acetyl:cholinesterase DNA and prodn. of recombinant hAChE -  
 PT for treatment of organo-phosphorous poisoning and diagnosis of haemo-  
 PT cytotoxic disorders and ovarian carcinomas.  
 PS Disclosure: Fig 1C; 47PP; English.  
 CC hAChE is useful as an active pharmaceutical component for the  
 CC prophylaxis and treatment of organophosphorous poisoning, and  
 CC post-surgical apnea due to succinylcholine administration.  
 CC CDNA probe to the sequence may be used in diagnosis of various  
 CC leukemias, abnormal megakaryocytopoiesis and ovarian carcinomas.  
 CC Bases given as N are obscured in the patent specification.  
 SQ sequence 1800 BP; 330 A; 602 C; 539 G; 326 T;

alignment\_scores:  
 Quality: 87.00 Length: 14  
 Ratio: 6.214 Gaps: 0  
 Percent Similarity: 100.000 Identity: 100.000

alignment\_block:  
 US-0155-076-1 x Q05999 ...

Align seg 1/1 to: Q05999 from: 1 to: 1800

1 AlagliuPheHisArgTrpSerTyrMetValHistpRlys 14  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 1414 GCGAGTCACCGCTCACATGAGTCAGTGACTGGRAG 1455

seq\_name: N\_Geneseq\_36:Q05998

seq\_documentation\_block:  
 ID C05998 standard; DNA; 2253 BP.  
 AC Q05998;  
 DT 16-JAN-1991 (first entry)  
 DE Sequence encoding human acetylcholinesterase (hAChE).  
 KW Organophosphorous poisoning; OP; cancer; leukaemia;  
 KW megakaryocytopoiesis; ovarian cancer; ds.  
 OS Homo sapiens.  
 PN EP-388906-A.  
 PD 26-SEP-1990.  
 PR 20-MAR-1990; 105274.  
 PA (YISS ) YISUM RES DEV CO.  
 PI Soreq H, Zakut H;  
 DR P-PSDB; R06989.  
 DR WPI; 90-291865/39.

PT Human acetylcholinesterase DNA and prodn. of recombinant hAChE -  
 PT for treatment of organo-phosphorous poisoning and diagnosis of haemo-  
 PS cytopenic disorders and ovarian carcinomas.  
 Claim 5; Page 25; 47pp; English.  
 Gene product is useful as an active pharmaceutical component for the  
 prophylaxis and treatment of organophosphorous poisoning, and post-  
 surgical aphex due to succinylcholine administration.

CC CDNA probe to the sequence may be used in diagnosis of various

CC leukaemias, abnormal megakaryocytopoiesis and ovarian carcinomas.

SQ Sequence " 2253 BP; 390 A; 740 C; 694 G; 429 T;

alignment\_scores:  
 Quality: 87.00 Length: 14  
 Ratio: 6.214 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
 US-09-155-076-1 x Q05998 ..

Align seg 1/1 to: Q05998 from: 1 to: 2253

1 AlaglupheHisArgTrpSerTyrMetValHistRlys 14  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

1912 GCCAAGTTCACCCCTGGACCTCATGGCACTGGAAAG 1953

seq\_name: N\_Geneseq\_36:Q99002

seq\_documentation\_block:  
 ID 099002 standard; DNA; 2256 BP.

AC Q99002; 1996 (first entry)

DE Human acetylcholinesterase (AChE) gene.

KW Acetylcholinesterase; acetyl cholinesterase; EC-3.1.1.7;

KW chromosome-7q22; acetylcholine-hydrolyzing enzyme; ss.

OS Homo sapiens.

Location/Qualifiers

FT cds 160 . 2206 /\*tag= a

PN W09523158-A1.

PD 28-AUG-1995; 002806.

PF 28-FEB-1995; US-202755.

PR 28-FEB-1994; US-370156.

PA (KOHN/ ) KOHN K I.

PA (YISS ) YISSIM RES & DEV CO.

PI Shani M.; Soreq H.; Zukut H.;

WPI: 95-311199/40.

DR P-PSDB; R80726.

PT Alternative forms of human acetyl cholinesterase system for evaluating anti-ChE expressed in transgenic animal assay system for evaluating anti-ChE activity of organophosphate(s), etc. or as model of ChE imbalance.

PT This DNA sequence encoding human acetylcholinesterase is useful for producing transgenic animals which express AChE. The transgenic animals are in turn useful as an assay system for determining the anti-ChE activity of organophosphates, carbamates, anti-ChE drugs, plant glycoalkaloids and snake venoms. This gene contains a promoter region, 6 exons (E1 to E6) and 4 introns (I1-I4).

SQ Sequence 2256 BP; 390 A; 757 C; 680 G; 429 T;

alignment\_scores:  
 Quality: 87.00 Length: 14  
 Ratio: 6.214 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
 US-09-155-076-1 x Q99002 ..

Align seg 1/1 to: Q99002 from: 1 to: 2256

1 AlaglupheHisArgTrpSerTyrMetValHistRlys 14  
 ||||| ||||| ||||| ||||| ||||| ||||| |||||

1792 GCAGGATTCATCCCTGAAACATTACATGTTGACTGGAAA 1833

seq\_name: N\_Geneseq\_36:N60111

seq\_documentation\_block:  
 ID N60111 standard; CDNA; 2445 BP.

AC N60111; 1991 (first entry)

DE Sequence encoding a protein having human cholinesterase (ChE) activity.

KW Organophosphorous poisoning; therapy; prophylaxis; diagnosis;

KW pseudocholinesterase deficiency; ss.

OS Homo sapiens.

Location/Qualifiers

FT cds 1 . 1908 /\*tag= a



PR 05-JAN-1996; US-009861.  
PA (HUMA - HUMAN GENOME SCI INC.  
PI Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA,  
Rosen CA;  
PI WPI: 97-374922/35.  
PCT Polynucleotide(s) and proteins derived from *Staphylococcus aureus*  
PCT stored on computer readable medium and used in the production of  
PCT anti-S. aureus vaccines  
PCT Claim 1: Page 745-750; 3271pp; English.  
CCS This sequence represents one of 5191 *Staphylococcus aureus* DNA sequences  
CCC of the invention. The DNA sequences are recorded on a computer readable  
CCC medium, preferably selected from a floppy or hard disk, random access  
CCC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using  
CCC the S. aureus DNA sequences allows putative functions to be assigned so  
CCC that protein-encoding or regulatory regions of commercial, therapeutic or  
CCC industrial importance can be obtained. Specifically, sequences which are  
CCC likely to encode antigens have been identified and these polypeptides can  
CCC be used in a vaccine composition against S. aureus infection. The  
CCC polypeptides can also be used in a kit for the immunodetection of  
CCC S. aureus in a sample. S. aureus is implicated in numerous human diseases,  
CCC including cellulitis, eyelid infections, food poisoning, osteomyelitis,  
CCC skin and surgical wound infections, scalded skin syndrome, toxic shock  
CCC syndrome, etc. Organisms transformed with the DNA sequences can be used  
CCC for recombinant production of the polypeptides. The new DNA sequences  
CCC (and their fragments) are useful as primers or probes for isolating  
CCC homologues of any of the S. aureus DNA sequences contained on the  
CCC computer readable medium. Sequence 10320 BP; 3071 A; 1531 G; 3449 T;

```

alignment_scores:
    Quality: 55.00          Length: 11
    Ratio: 5.000             Gaps: 0
    Percent Similarity: 100.000 Percent Identity: 45.455

alignment_block:
US-09-155-076-1 x V74454/rev .. .
Align seg 1/1 to reverse of: V74454 from: 1 to: 10320

```

can be genetically engineered into insect larvae food and plants for insect control. Claim 38; Page 229-231; 276pp; English.

This genomic DNA sequence encodes the 62.9 kDa *TcBaiii* insecticidal toxin protein (see WI7899) of *Photorhabdus luminescens* W-14. It is derived from a full-length clone (see T68836) obtained from a genomic library. A 280.6 kDa protein (see WI7871) is processed proteolytically into *TcBaiii* (see WI8302) and *TcBaiii* components. Claimed toxins of *P. luminescens* (see WI7871, WI7884-89, WI7899-900, WI18301-06) can be produced by recombinant DNA methods and applied to or genetically engineered into, insect larvae food and plants for insect control. The *Photorhabdus* toxins are particularly effective against southern corn rootworm, Colorado potato beetle, western corn rootworm, meal worm, black weevil and turf grub (*Coleoptera*), beet armyworm, black cutworm, cabbage looper, codling moth, corn earworm, European corn borer, tobacco hornworm and tobacco budworm (*Lepidoptera*), and are also active against insects of the orders Hymenoptera, Diptera, Acarina and Homoptera. (All claimed).

| Sequence | 1722 BP; | 461 A; | 368 C; | 446 G; | 447 T; |
|----------|----------|--------|--------|--------|--------|
| 58       |          |        |        |        |        |

alignment\_scores:  
    Quality: 50.50  
    Ratio: 4.208  
Percent Similarity: 85.714

```

Align seg 1/1 to: T68847 from: 1 to: 1722
      1 Ala Glu Lphe His Arg Trp Ser Tyr Met Val His Trp Lys 14
      ||| : : : : | | | : : : : | | | : : : : | | | : : : : | | |
      1187 GCACGGTTCAT ... TGGCAGGGTTATGATTCACGGAG 1224

```

```

seq_documentation_block:
  ID V29987 standard; DNA; 1722 BP.
  AC V29987;
  DT 07-19-1995 (first entry)
  DE tbalphaI gene from the tcb genomic region encoding protein TcbA.
  KW Photorhabdus luminescens W-14; nematode; symbiotic; toxin
  KW Heterorhabditis; tca; tcb; tcc; tcd; insecticidal activity; toxic
  KW Lepidoptera; Coleoptera; Hymenoptera; Diptera; Acarina; Rootworm; Colorado potato beetle; beet
  KW Homoptera; Southern; Western; rootworm; mealworm; boll weevil; turf grub; beetle armyworm; black cutworm; cabbage looper; codling moth; corn earworm; European corn borer; tobacco hornworm; budworm; ds.
  KW Photorhabdus luminescens.
  Location/Qualifiers
  Key
  FRN
  CDS
  1..1722
  /tag= a

```

(DOWC ) DOWELANCO.  
PA (WISC ) WISCONSIN ALUMNI RES FOUND.  
PA Blackburn MB, Bowen DJ, Ciche TA, Ensign JC, Fating R,  
PA French-Constant RH, Guo L, Hey TD, Merlo DJ, Orr GL,  
PA Petell J, Roberts JL, Rochelleau TA, Schoonover S,  
PA Strickland JA, Sukhapinda K;  
PA WPI 98-19427/16.  
DR P-PSDB; W36559.  
DR Isolated toxins from *Photorhabdus luminescens* strains - useful for  
PP control of insect pests  
PP Claim 38; Pages 253-261; 321pp; English.  
ES The present sequence encodes a protein named TcbAII of the bacterium  
CC *Photorhabdus luminescens* (W-14). This is a symbiotic bacterium of the

nematodes of the *Heterorhabditis* genus. The bacterium has at least 4 distinct genomic regions, tca, tcb, tcc, and tcd. Peptide products are produced from these regions that are associated with insecticidal activity. The native toxins are secreted proteins. The proteins are toxic to insects upon exposure and especially when ingested. The nucleic acid sequence can be used to produce transgenic plants, baculoviruses or microbial hosts for toxin production. They can be used to control insects pests from the Lepidoptera, Coleoptera, Hymenoptera, Diptera, Dicynoptera, Acarina or Homoptera orders, especially the Southern or Western corn rootworm, Colorado potato beetle, mealworm, boll weevil, turf grub, beetle armyworm, black cutworm, cabbage looper, codling moth, corn earworm, European corn borer or tobacco hornworm or budworm. sequence 11722 BP; 461 A; 368 C; 445 G; 368 C; 445 G; sequence

CCC borer, tobacco hornworm and tobacco budworm (*Lepidoptera*), and  
CC are also active against insects of the orders Hymenoptera, Diptera  
CC Dicrystoptera, Acarina and Homoptera. (All claimed).  
SQ Sequence 7515 BP; 2146 A; 1483 C; 1765 G;  
T; 2121 T;

|                   |                            |                          |
|-------------------|----------------------------|--------------------------|
| alignment_scores: | Quality: 50.50             | Length: 14               |
|                   | Ratio: 4.208               | Gaps: 1                  |
|                   | Percent Similarity: 85.714 | Percent Identity: 57.143 |

alignment\_block:  
US-09-155-076-1 x T68836 ..

`alignment_scores:`  
`Quality: 50.50`  
`Ratio: 4.208`  
`Percent_Similarity: 85.714`  
`Length: 14`  
`Gaps: 1`  
`Percent_Identity: 57.143`

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..:alignment_block:
US-09-155-076-1 x V29987
Align seg 1/1 to: V29987 from: 1
1 AlaGluPhenHisArgTriPsrSerTyr
   ||:::||||| |:::||: :::
1187 GCACGGTTCA...TGGCAGTGGCTT
eq_name: N_GenSeq_36:r68836
eq_documentation_block:

```

```

eq_name: N_Geneseq_36:r68836
eq_documentation_block:
D T68836 standard; DNA; 7515 BP.
C T68836;
W 29-JAN-1998 (first entry)
E Photorhabdus luminescens insect toxin protein TcBa DNA.
Insecticide; toxin; pest control; biological control;
W Photorhabdus luminescens; TcBa; Southern corn rootworm;
W Colorado potato beetle; Western corn rootworm; meal worm;
W beet armyworm; black cutworm;
W cabbage looper; codling moth; corn earworm; European corn borer;
W tobacco hornworm; tobacco budworm; Lepidoptera; Hymenoptera;
W Diptera, Dicthyoptera; Acarina; Homoptera; ds
S Photorhabdus luminescens strain W-14 (ATCC 55397).

```

U 13-PAI-1397.  
U 06-NOV-1996; US-00031.  
R 28-AUG-1996; US-705484.  
R 06-NOV-1995; US-007255.  
R 28-FEB-1996; US-600423.  
A (WISC ) WISCONSIN ALUMNI RES FOUND.  
I Blackburn MB, Bowen DJ, Cliche TA, Ensign JC, Fatig R;  
I Ffrench-Constant RH, Guo L, Hey TD, Mario DJ, Orr GL;  
I Petell J, Roberts JL, Rochleau TA, Schoonover S;

CC tobacco hornworm and tobacco budworm (*Lepidoptera*), and  
 CC are also active against species of the orders Hymenoptera, Diptera,  
 CC Dicrystoptera, Acarina and Homoptera. (All claimed.)  
 Sequence 7515 BP; 2146 A; 1483 C; 1765 G; 2121 T;  
 SQ alignment\_scores:  
 Quality: 50.50 Length: 14  
 Ratio: 4.208 Gaps: 1  
 Percent Similarity: 85.714 Percent Identity: 57.143  
 alignment\_block: US-09-155-076-1 x T68836 ..  
 Align seg 1/1 to: T68836 from: 1 to: 7515  
 1 AlagliuPheHisArgGrrSerSerTyrMetValHistPlys 14  
 |||:||||||| |:::|||:|||:|||:|||:|||:|||:|||:|||:  
 6980 GCACGCGTTCTAT...TGGCAGTGTTATGATTCACTGGAA 7018  
 seq\_name: N\_Geneseq\_36:v29985  
 seq\_documentation\_block:  
 ID V29985 standard; DNA: 7515 BP.  
 AC V29985;  
 DT 07-AUG-1998 (first entry)  
 tcba Gene from the tcb genomic region encoding protein Tcba.  
 CC Photorhabdus luminescens W-14; nematode; symbiotic;  
 CC Heterorhabditis; tca; tcb; tcc; tcd; insecticidal activity; toxin;  
 CC Lepidoptera; Coleoptera; Hymenoptera; Diptera; Dictyoptera; Acarina;  
 CC Homoptera; Southern; Western corn rootworm; Colorado potato beetle;  
 CC mealworm; boll weevil; turf grub; beetle armyworm; black cutworm;  
 CC cabbage looper; coding moth; corn earworm; European corn borer;  
 CC Tobacco hornworm; budworm; ds.  
 CC Photorhabdus luminescens.  
 Key CDS  
 Location/Qualifiers  
 1..7515  
 /tag= a  
 W09808932-A1.  
 05-MAR-1998.  
 05-MAY-1997; U07657.  
 06-NOV-1996; WO-U18003.  
 (DOWC ) DOWELANCO.  
 (WISC ) WISCONSIN ALUMNI RES FOUND.  
 PA Blackburn MB, Bowen DJ, Cicchetti TA, Ensign JC, Fatig R,  
 FF French-Constant RH, Guo L, Hey TD, Merlo DJ, Orr GL,  
 PE Petrelli J, Roberts JL, Rocheleau TA, Schoonover S,  
 SR Strickland JA, Sukhapinda K;  
 WPI; 98-17942/16.  
 P-PSDB: W56557.  
 Isolated toxins from *Photorhabdus luminescens* strains - useful for  
 control of insect pests  
 Claim 38; Pages 154-162; 321pp; English.  
 The present sequence encodes a protein named Tcba of the bacterium  
 Photorhabdus luminescens (W-14). This is a symbiotic bacterium of  
 nematodes of the Heterorhabditis genus. The bacterium has at least  
 distinct genomic regions, tca, tcb, tcc, and tcd. Peptide products  
 produced from these regions that are associated with insecticidal  
 activity. The native toxins are secreted proteins. The proteins are  
 toxic to insects upon exposure and especially when ingested. The  
 nucleic acid sequence can be used to produce transgenic plants,  
 baculoviruses or microbial hosts for toxin production. They can be  
 used to control insect pests from the Lepidoptera, Coleoptera, Hymenoptera  
 Diptera, Dicrystoptera, Acarina or Homoptera orders, especially the  
 Southern or Western corn rootworm, Colorado potato beetle, mealworm,  
 boll weevil, turf grub, beetle armyworm, black cutworm, cabbage looper,  
 coding moth, corn earworm, European corn borer or tobacco hornworm  
 or budworm. SEQ 7515 BP: 2149 A: 1484 C: 1760 G: 2122 T;

alignment\_scores:  
 Quality: 50.50 Length: 14  
 Ratio: 4.208 Gaps: 1  
 Percent Similarity: 85.714 Percent Identity: 57.143

alignment\_block:  
 US-09-155-076-1 x V29985 ..

Align seg 1/1 to: V29985 from: 1 to: 7515

1 AlaGluIleHisArgTrpSerSerTyrMetValHisTrpLys 14  
 ||||:||||| .|||:|||:||||:||||:|||||  
 6980 GCACGGTTTCAT...TGCGAGTGTATGATTCACTGGAG 7018

seq\_name: N\_Geneseq\_36:y21209\_02

seq\_documentation\_block:  
 Continuation (3 of 17) of V21209 from base 200001 (Methanococcus jannaschii circular chr  
 WP Sequence split into 17 fragments LOCUS V21209 Accession V21209

|               |        |         |
|---------------|--------|---------|
| Fragment Name | Begin  | End     |
| WP            | 1      | 110000  |
| WP            | 210001 | 210000  |
| WP            | 210002 | 310000  |
| WP            | 210003 | 410000  |
| WP            | 210004 | 510000  |
| WP            | 210005 | 610000  |
| WP            | 210006 | 710000  |
| WP            | 210007 | 810000  |
| WP            | 210008 | 910000  |
| WP            | 210009 | 1010000 |
| WP            | 210010 | 1110000 |
| WP            | 210011 | 1210000 |
| WP            | 210012 | 1310000 |
| WP            | 210013 | 1410000 |
| WP            | 210014 | 1510000 |
| WP            | 210015 | 1610000 |
| WP            | 210016 | 1664976 |

alignment\_scores:  
 Quality: 49.00 Length: 13  
 Ratio: 4.900 Gaps: 0  
 Percent Similarity: 76.923 Percent Identity: 53.846

alignment\_block:  
 US-09-155-076-1 x V21209\_02 ..

Align seg 1/1 to: V21209\_02 from: 1 to: 110000

1 AlaGluIleHisArgTrpSerSerTyrMetValHisTrp 13  
 ||||:||||| .|||:|||:||||:||||:|||||  
 40708 GCAGTGTATTATATGGTAGTTATCCATGG 40746

seq\_name: N\_Geneseq\_36:y21209\_02

seq\_documentation\_block:  
 ID V26068 standard; cDNA to mRNA; 4868 BP.  
 AC V26068 ..  
 DT 22-JUL-1998 (first entry)  
 DE Human canalicular multispecific organic anion transporter gene.  
 KW Human canalicular multispecific organic anion transporter; cMOAT;  
 KW diagnosis; Dubin-Johnson Syndrome; cancer; tumour; ss.  
 OS Homo sapiens.

|     |  |
|-----|--|
| Key | Location/Qualifiers  |
| FH  | 38..4675   |
| FT  | *tag= a  |
| FT  | /product= "cMOAT"  |
| FT  | /note= "canalicular multispecific organic anion transporter" |

PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
 DR WPI; 98-28872/26.  
 DR P-PSDB; W55966.  
 PT Human cMOAT gene and its cDNA - useful in diagnosis of Dubin-Johnson syndrome.  
 PS Claim 1; Page 4-6; 16pp; Japanese.  
 CC The present sequence encodes the human canalicular multispecific organic anion transporter (cMOAT). The human cMOAT gene expresses a mRNA of 6.5 kb and is present in the band 4 of the region 2 in the long arm of the tenth human chromosome. The cMOAT gene and the cDNA can be used for the diagnosis and the treatment of Dubin-Johnson syndrome.  
 CC Sequence 4868 BP; 1148 C; 1132 A; 1135 G; 1263 T;

alignment\_scores:  
 Quality: 48.00 Length: 13  
 Ratio: 5.33 Gaps: 0  
 Percent Similarity: 69.231 Percent Identity: 46.154

alignment\_block:  
 US-09-155-076-1 x V26068 ..

Align seg 1/1 to: V26068 from: 1 to: 4868

1 AlaGluIleHisArgTrpSerSerTyrMetValHisTrp 13  
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 4105 TCAGATTATCATTGATGGAGATATTGCTCCATGG 4143

seq\_name: N\_Geneseq\_36:y21209\_02

seq\_documentation\_block:  
 ID T94023 standard; cDNA; 5586 BP.  
 AC T94023;  
 DT 01-APR-1998 (first entry)  
 DE Human canalicular multispecific organic anion transporter protein.  
 KW Canalicular multispecific organic anion transporter protein;  
 KW cMOAT protein; ATP-binding cassette transporter family; ABC transporter;  
 KW hepatobiliary excretion; multidrug resistance-associated protein;  
 KW cMOAT protein activity; multidrug resistance-related protein; MDR-1;  
 KW Dubin-Johnson disease; Rotor disease; ss.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT FT 102..4739 /\*tag= a  
 PN W09731111-A2.  
 PD 28-AUG-1997.  
 PF 01-APR-1997; NL0079.  
 PR 22-FEB-1996; EP-200460.  
 PA (MEDI-) ACAD MEDISCH CENT AMSTERDAM.  
 PA (HETN-) HET NEDERLANDS KANKER INST.  
 PA (INTR-) INTRONENE BV.  
 PI Borst P, Bosma PJ, Evers R, Oude Elferink RP,  
 PI Paulusma CC;  
 DR W33362.  
 PT DNA encoding human and rat canalicular multispecific organic anion transporter proteins - useful for diagnosis and treatment of  
 PT transporter diseases and Rotor disease  
 PT Dublin-Johnson disease and Rotor disease  
 PS Claim 4; Fig 1A; 10pp; English.  
 CC The present cDNA sequence encodes a novel canalicular multispecific organic anion transporter (cMOAT) protein, isolated from a human lambda gt11 liver cDNA library. The protein is a new member of the ATP-binding cassette (ABC) transporter family. The ATP dependent cMOAT transporter system mediates hepatobiliary excretion in the liver. cMOAT may be a liver-specific homologue of multidrug resistance-associated protein. The nucleic acids are used to provide cells with cMOAT protein activity. cMOAT protein activity in cells can be enhanced by increasing the level of glutathione, glucuronide and/or sulphate. Antisense constructs, especially derived from another multidrug resistance (MDR)-related protein, e.g. MDR-1, to the nucleic acids and vectors can be used to decrease the level of cMOAT in a cell. The nucleic acids and proteins can be used especially in diagnosis of Dubin-Johnson disease, Rotor disease or another disease involving cMOAT. The cMOAT gene may also be





OM of: US-09-155-076-1 to: Issued\_Patents\_NA: \* out\_format : pfs  
 Date: Sep 13, 2000 2:43 AM  
 About: Results were produced by the GenCore software, version 4.5,  
 Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:  
 -MODEL="frame\_p2n model" -DVF=x1D  
 -Q:/cgn2\_6/pool/US09155016/runat\_29082000\_092505\_15762/app\_query.fasta\_1.144  
 -DB=Issued\_Patents\_NA -QFMT=fastaP -SUFIX=rni -GAPOP=11.000  
 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPEXT=0.000  
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Query: US-09-155-076-1  
 Query length: 14  
 Database: Issued\_Patents\_NA: \*  
 Database sequences: 241080  
 Database length: 6877915  
 Search time (sec): 59.330000

## score\_list:

| Sequence  | Strd | Orig  | ZScore | Escore  | Len   | Documentation | Quality | Length: | Gaps: |
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| /cgn2_6/podata/2/ina/5C_COMB.seq;US-08-314-095-1    | +    | 87.00 | 232.41 | 1.9e-05 | 2256  |               | 87.00   | 14      | 0     |
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| Sequence 24, Application US/08370156   |   | Sequence 24, Application US/08370156   |  | Sequence 24, Application US/08370156   |  | Sequence 24, Application US/08370156   |  | Sequence 24, Application US/08370156   |   |
| Patent No. 5932780   |   | Patent No. 5932780   |  | Patent No. 5932780   |  | Patent No. 5932780   |  | Patent No. 5932780   |   |
| GENERAL INFORMATION:   |   | GENERAL INFORMATION:   |  | GENERAL INFORMATION:   |  | GENERAL INFORMATION:   |  | GENERAL INFORMATION:   |   |
| APPLICANT: Soreq, Hermona  |   | APPLICANT: Soreq, Hermona  |  | APPLICANT: Soreq, Hermona  |  | APPLICANT: Soreq, Hermona  |  | APPLICANT: Soreq, Hermona  |   |
| APPLICANT: Zakut, Haim   |   | APPLICANT: Zakut, Haim   |  | APPLICANT: Zakut, Haim   |  | APPLICANT: Zakut, Haim   |  | APPLICANT: Zakut, Haim   |   |
| APPLICANT: Shani, Moshe  |   | APPLICANT: Shani, Moshe  |  | APPLICANT: Shani, Moshe  |  | APPLICANT: Shani, Moshe  |  | APPLICANT: Shani, Moshe  |   |
| TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR ANTICHOLINESTERASE SUBSTANCES |   | TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR ANTICHOLINESTERASE SUBSTANCES |  | TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR ANTICHOLINESTERASE SUBSTANCES |  | TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR ANTICHOLINESTERASE SUBSTANCES |  | TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR ANTICHOLINESTERASE SUBSTANCES |   |
| NUMBER OF SEQUENCES: 27  |   | NUMBER OF SEQUENCES: 27  |  | NUMBER OF SEQUENCES: 27  |  | NUMBER OF SEQUENCES: 27  |  | NUMBER OF SEQUENCES: 27  |   |
| CORRESPONDENCE ADDRESS:  |   | CORRESPONDENCE ADDRESS:  |  | CORRESPONDENCE ADDRESS:  |  | CORRESPONDENCE ADDRESS:  |  | CORRESPONDENCE ADDRESS:  |   |
| ADDRESSEE: Reising, Ethington, Barnard & Perry                                       |   | ADDRESSEE: Reising, Ethington, Barnard & Perry                                       |  | ADDRESSEE: Reising, Ethington, Barnard & Perry                                       |  | ADDRESSEE: Reising, Ethington, Barnard & Perry                                       |  | ADDRESSEE: Reising, Ethington, Barnard & Perry                                       |   |
| STREET: P.O. Box 4390  |   | STREET: P.O. Box 4390  |  | STREET: P.O. Box 4390  |  | STREET: P.O. Box 4390  |  | STREET: P.O. Box 4390  |   |
| CITY: TROY   |   | CITY: TROY   |  | CITY: TROY   |  | CITY: TROY   |  | CITY: TROY   |   |
| STATE: Michigan  |   | STATE: Michigan  |  | STATE: Michigan  |  | STATE: Michigan  |  | STATE: Michigan  |   |
| ZIP: 48099   |   | ZIP: 48099   |  | ZIP: 48099   |  | ZIP: 48099   |  | ZIP: 48099   |   |
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| SOFTWARE: Patent Release #1-0, version #1.30   |   | SOFTWARE: Patent Release #1-0, version #1.30   |  | SOFTWARE: Patent Release #1-0, version #1.30   |  | SOFTWARE: Patent Release #1-0, version #1.30   |  | SOFTWARE: Patent Release #1-0, version #1.30   |   |
| CURRENT APPLICATION DATA:  |   | CURRENT APPLICATION DATA:  |  | CURRENT APPLICATION DATA:  |  | CURRENT APPLICATION DATA:  |  | CURRENT APPLICATION DATA:  |   |
| APPLICATION NUMBER: US/08/370/156  |   | APPLICATION NUMBER: US/08/370/156  |  | APPLICATION NUMBER: US/08/370/156  |  | APPLICATION NUMBER: US/08/370/156  |  | APPLICATION NUMBER: US/08/370/156  |   |
| FILING DATE:   |   | FILING DATE:   |  | FILING DATE:   |  | FILING DATE:   |  | FILING DATE:   |   |
| CLASSIFICATION: 536  |   | CLASSIFICATION: 536  |  | CLASSIFICATION: 536  |  | CLASSIFICATION: 536  |  | CLASSIFICATION: 536  |   |
| ATTORNEY/AGENT INFORMATION:  |   | ATTORNEY/AGENT INFORMATION:  |  | ATTORNEY/AGENT INFORMATION:  |  | ATTORNEY/AGENT INFORMATION:  |  | ATTORNEY/AGENT INFORMATION:  |   |
| NAME: Kohn, Kenneth I.   |   | NAME: Kohn, Kenneth I.   |  | NAME: Kohn, Kenneth I.   |  | NAME: Kohn, Kenneth I.   |  | NAME: Kohn, Kenneth I.   |   |
| REGISTRATION NUMBER: 30,955  |   | REGISTRATION NUMBER: 30,955  |  | REGISTRATION NUMBER: 30,955  |  | REGISTRATION NUMBER: 30,955  |  | REGISTRATION NUMBER: 30,955  |   |
| REFERENCE/DOCKET NUMBER: P-307 (Mulford)   |   | REFERENCE/DOCKET NUMBER: P-307 (Mulford)   |  | REFERENCE/DOCKET NUMBER: P-307 (Mulford)   |  | REFERENCE/DOCKET NUMBER: P-307 (Mulford)   |  | REFERENCE/DOCKET NUMBER: P-307 (Mulford)   |   |
| TELECOMMUNICATION INFORMATION:   |   | TELECOMMUNICATION INFORMATION:   |  | TELECOMMUNICATION INFORMATION:   |  | TELECOMMUNICATION INFORMATION:   |  | TELECOMMUNICATION INFORMATION:   |   |
| TELEPHONE: (810) 689-3500  |   | TELEPHONE: (810) 689-3500  |  | TELEPHONE: (810) 689-3500  |  | TELEPHONE: (810) 689-3500  |  | TELEPHONE: (810) 689-3500  |   |
| TELEFAX: (810) 689-0711  |   | TELEFAX: (810) 689-0711  |  | TELEFAX: (810) 689-0711  |  | TELEFAX: (810) 689-0711  |  | TELEFAX: (810) 689-0711  |   |
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TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES  
 NUMBER OF SEQUENCES: 27  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Reising, Ethington, Barnard & Perry  
 STREET: P.O. Box 4390  
 CITY: Troy  
 STATE: Michigan  
 COUNTY: US  
 ZIP: 48099  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/370,156  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Kohn, Kenneth I.  
 REGISTRATION NUMBER: 30,955  
 REFERENCE/DOCKET NUMBER: P-307 (Mulford)  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (810) 689-3500  
 TELEFAX: (810) 689-4071  
 LENGTH: 1215 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 FEATURE:  
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 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
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seq\_documentation\_block:  
 Sequence 1, Application PC/TUSS9206106  
 GENERAL INFORMATION:  
 APPLICANT: Fischer, Meir  
 TITLE OF INVENTION: ENZYMATIICALLY ACTIVE RECOMBINANT HUMAN  
 ACETYLCHOLINESTERASE AND USES THEREOF  
 NUMBER OF SEQUENCES: 2  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: John P. White, Esq.  
 STREET: 30 Rockefeller Plaza  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10112  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US92/06106  
 FILING DATE: 19920722  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: White, John P.  
 REGISTRATION NUMBER: 28,678  
 REFERENCE/DOCKET NUMBER: 39304-B-PCT/JPW/EAB  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 977-9550  
 TELEFAX: (212) 664-0525  
 TELEX: 42253 COOP U  
 INFORMATION FOR SEQ ID NO: 1:

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SEQUENCE CHARACTERISTICS:
LENGTH: 1845 base pairs
TYPE: NUCLEIC ACID
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

FEATURE: NAME/KEY: CDS
LOCATION: 1..1842
PCT-US92-06106-1

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Percent Similarity: 100.000 Percent Identity: 100.000
US-08-318-826A-5

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Patent No. 5932750

GENERAL INFORMATION:
APPLICANT: Soreq, Hermona
APPLICANT: Zakut, Haim
APPLICANT: Shani, Moshe
TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Reisinger, Eckstein, Barnard & Perry
STREET: P.O. Box 4390
CITY: Troy
STATE: Michigan
COUNTRY: US
ZIP: 48099
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,156
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: P-307 (Millford)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810) 681-3500
TELEFAX: (810) 689-4071
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2256 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
HYPOTHETICAL: NO
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
ANTI-SENSE: NO
ORGANISM: Homo sapiens
ORIGINAL SOURCE: Homo sapiens

alignment_scores:
Quality: 87.00 Length: 14
Ratio: 6.214 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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Align seg 1/1 to: US-08-370-156-1

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seq\_name: /cgn2\_6/ptodata/2/ina/6\_COMB.seq:US-08-814-095-1

seq\_documentation\_block:

Sequence 1, Application US/08814095

Patent No. 6025183

GENERAL INFORMATION:

APPLICANT: Soreq, Hermona

APPLICANT: Zakut, Haim

APPLICANT: Shani, Moshe

TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTANCES

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: KOHN & ASSOCIATES

STREET: 30500 NO. 6025183western Highway, Suite 410

CITY: Farmington Hills

STATE: Michigan

COUNTRY: U.S.

ZIP: 48334

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/814,095

FILING DATE:

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Kohn, Kenneth I.

REGISTRATION NUMBER: 30,955

REFERENCE/DOCKET NUMBER: 2391.00001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (248) 539-5050

TELEFAX: (248) 539-5055

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 3016 base pairs

REFERENCE/DOCKET NUMBER: 2391.00006

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: 160..2010

OTHER INFORMATION: /note= "Splice Variant: Exons 1, 2,  
                           3, 4, 5 and 6"

US-08-318-826A-7

alignment\_scores:

Quality: 87.00 Length: 14  
       Ratio: 6.214 Gaps: 0  
       Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-155-076-1 x US-08-814-095-1 ..

Align seg 1/1 to: US-08-814-095-1 from: 1 to: 2256

align seg 1/1 to: US-08-814-095-1 x US-09-155-076-1 ..

1 AlaGluPheHisArgTrpSerSerTyrMetValHistRlys 14  
       ||||||| ||||| ||||| ||||| |||||  
   1915 GCGAAGTCCACCGCTGACTCTACATGGTGCAG 1956

seq\_name: /cgn2\_6/ptodata/2/ina/5C\_COMB.seq:US-08-318-826A-7

seq\_documentation\_block:

APPLICANT: Zakut, Haim  
 APPLICANT: Shani, Moshe  
 TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR  
 TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES  
 NUMBER OF SEQUENCES: 27  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Reising, Ethington, Barnard & Perry  
 STREET: P.O. Box 4390  
 CITY: TROY  
 STATE: Michigan  
 COUNTRY: US  
 ZIP: 48099

COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US-08/814,095  
 FILING DATE:  
 CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:  
 NAME: Mongomery, Ilene N.  
 REGISTRATION NUMBER: 38,972  
 REFERENCE/DOCKET NUMBER: 2391,00066  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (248) 539-5050  
 TELEFAX: (248) 539-5055  
 INFORMATION FOR SEQ ID NO: 5:  
 DESCRIPTION: "Alternatively spliced AChE  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3016 base pairs  
 TYPE: nucleic acid  
 ORGANISM: Homo sapiens  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: other nucleic acid  
 DESCRIPTION: /desc = "Alternatively spliced AChE  
 ORIGINAL SOURCE:  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 160..2010  
 US-08-814-095-5

alignment\_scores:  
 Quality: 87.00 Length: 14  
 Ratio: 6.214 Gaps: 0  
 Percent Similarity: 100.000 Identity: 100.000

alignment\_block:  
 US-09-155-076-1 x US-08-814-095-5 ..

Align seg 1/1 to: US-08-370-156-5 from: 1 to: 3016  
 US-09-155-076-1 x US-08-370-156-5 ..

Align seg 1/1 to: US-08-370-156-5 from: 1 to: 3016  
 US-09-155-076-1 x US-08-370-156-5 ..

seq\_name: /cgn2\_6/ptodata/2/ina/5C\_COMB.seq:US-08-318-826A-6

seq\_documentation\_block:  
 Sequence 5, Application US/08814095  
 GENERAL INFORMATION:  
 Patient No. 6025183  
 APPLICANT: Soreq, Hermona  
 APPLICANT: Zakut, Haim  
 APPLICANT: Shani, Moshe  
 TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR  
 TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTANCES  
 NUMBER OF SEQUENCES: 7  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: KOHN & ASSOCIATES  
 STREET: 30500 No. 6025183thwestern Highway, Suite 410  
 CITY: Farmington Hills  
 STATE: Michigan  
 COUNTRY: U.S.  
 ZIP: 48334

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/318,826A  
 FILING DATE: 7/1/2000  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Kohn, Kenneth I.  
 REGISTRATION NUMBER: 30,955  
 REFERENCE/DOCKET NUMBER: 2391.000001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (248) 539-5050  
 TELEFAX: (248) 539-5055  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3096 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA to mRNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 160..1959  
 OTHER INFORMATION: /note/ "splice variant: Exons 1, 2, 3, 4, 5 and the translated portion of Intron 4 (readthrough)"  
 OTHER INFORMATION: /note/ "splice variant: Exons 1, 2, 3, 4, 5 and the translated portion of Intron 4 (readthrough)"  
 US-08-318-826A-6

alignment\_scores:  
 Quality: 87.00 Length: 14  
 Ratio: 6.214 Gaps: 0  
 Percent Identity: 100.000

alignment\_block:  
 US-09-155-076-1 x US-08-318-826A-6 ..

Align seg 1/1 to: US-08-318-826A-6 from: 1 to: 3096

1 AlaGluPheHisArgTrpSerSerTyrMetValHistRplys 14  
 |||||Phe|||H|||S|||A|||G|||L|||U|||S|||R|||T|||r|||S|||e|||r|||S|||e|||r|||T|||y|||M|||e|||t|||V|||a|||l|||H|||i|||s|||t|||R|||p|||l|||y|||s 14  
 2755 GCCGAGTTCCACGGCTTGAGTCCTAGTGTGACTGGAAAG 2796

seq\_name: /cgn2\_6/ptodata/2/ins/6\_COMB.seq:US-08-814-095-3

seq\_documentation\_block:  
 Sequence 3, Application US/08814095  
 Patent No. 6025183

GENERAL INFORMATION:  
 APPLICANT: Soreq, Hermona  
 APPLICANT: Zakut, Haim  
 APPLICANT: Shani, Moshe  
 TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR ANTI-CHOLINESTERASE SUBSTANCES  
 NUMBER OF SEQUENCES: 7  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: KOHN & ASSOCIATES  
 STREET: 30500 N. 605183thwestern Highway, Suite 410  
 CITY: Farmington Hills  
 STATE: Michigan  
 COUNTRY: U.S.  
 ZIP: 48334

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentn Release #1.0, version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/814,095  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Montgomery, Irene N.  
 REGISTRATION NUMBER: 38,972  
 REFERENCE/DOCKET NUMBER: 2391.00066  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (248) 539-5050  
 TELEFAX: (248) 539-5055  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3096 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: other nucleic acid

APPLICATION NUMBER: US/08/370,156  
 FILING DATE:  
 CLASSIFICATION: 536  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Kohn, Kenneth I.

DESCRIPTION: /desc = "Alternatively spliced AChE comprising exons 2', 3', 4 and 5 as well as the translated portion of Intron 4 (readthrough)"

ORIGINAL SOURCE: /organism: Homo sapiens

NAME/KEY: CDS

LOCATION: 160..1959

US-08-814-095-3

alignment\_scores:

|                     |         |
|---------------------|---------|
| Quality:            | 87.00   |
| Percent Similarity: | 100.000 |
| Ratio:              | 6.214   |
| Length:             | 14      |
| Gaps:               | 0       |
| Identity:           | 100.000 |

Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
US-09-155-076-1 x US-08-814-095-3 ..

Align seg 1/1 to: US-08-814-095-3 from: 1 to: 3096

1 AlagliurheHisArgTrpSerSerTyrMetValHistRlys 14  
||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
2755 GCCGAGTTCCACCGCTGGAGCTCATGGTCACTGGANG 2796

seq\_name: /cgn2\_6/ptodata/2/lna6\_COMBO.seq:US-08-814-095-7

seq\_documentation\_block:

Sequence 7, Application US/08814095

GENERAL INFORMATION:  
Patent No. 6025183

APPLICANT: Soeq, Hermona

APPLICANT: Zakut, Haim

APPLICANT: Shariv, Moshe

TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR ANTI-CHOLINESTERASE SUBSTANCES

NUMBER OF SEQUENCES: 7

ADDRESSEE: Kohn & ASSOCIATES

STREET: 30500 No. 6025183thwestern Highway, Suite 410

CITY: Farmington Hills

STATE: Michigan

COUNTRY: U.S.

ZIP: 48334

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/08/814,095

FILING DATE: CLASSIFICATION 800

ATTORNEY/AGENT INFORMATION:  
NAME: Montgomery, Ilene N.

REGISTRATION NUMBER: 38,972

REFERENCE/DOCKET NUMBER: 2391.00006

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (248) 539-5050

TELEFAX: (248) 539-5055

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:  
LENGTH: 35060 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: Other nucleic acid

DESCRIPION: /desc = "Cosmid including AChE gene and ARs gene"

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE: Homo sapiens

POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 7q22

FEATURE:  
NAME/KEY: promoter

LOCATION: 4089..224644

OTHER INFORMATION: /function= "AChE Promotor"  
OTHER INFORMATION: /standard\_name= "AChE Promotor"

FEATURE:  
NAME/KEY: exon

LOCATION: 22465..22537

OTHER INFORMATION: /function= "non-translated"  
OTHER INFORMATION: /gene= "AChE"  
OTHER INFORMATION: /number= 1

FEATURE:  
NAME/KEY: exon

LOCATION: 24090..251177

IDENTIFICATION METHOD: experimental

OTHER INFORMATION: /function= "translation start"  
OTHER INFORMATION: 24110"

OTHER INFORMATION: /evidence= EXPERIMENTAL

OTHER INFORMATION: /gene= "AChE"

FEATURE:  
NAME/KEY: exon

LOCATION: 25524..26009

IDENTIFICATION METHOD: experimental

OTHER INFORMATION: /evidence= EXPERIMENTAL

OTHER INFORMATION: /gene= "AChE"  
OTHER INFORMATION: /number= 2

FEATURE:  
NAME/KEY: exon

LOCATION: 27005..27274

IDENTIFICATION METHOD: experimental

OTHER INFORMATION: /evidence= EXPERIMENTAL

OTHER INFORMATION: /gene= "AChE"  
OTHER INFORMATION: /number= 3

FEATURE:  
NAME/KEY: exon

LOCATION: 27255..28007

IDENTIFICATION METHOD: experimental

OTHER INFORMATION: /evidence= EXPERIMENTAL

OTHER INFORMATION: /gene= "AChE"  
OTHER INFORMATION: /number= 4

FEATURE:  
NAME/KEY: exon

LOCATION: 27385..27387

IDENTIFICATION METHOD: experimental

OTHER INFORMATION: /evidence= EXPERIMENTAL

OTHER INFORMATION: /gene= "AChE"  
OTHER INFORMATION: /number= 5

FEATURE:  
NAME/KEY: terminator

LOCATION: 28129..28131

FEATURE:  
NAME/KEY: exon

LOCATION: 28008..28129

IDENTIFICATION METHOD: experimental

OTHER INFORMATION: /evidence= EXPERIMENTAL

OTHER INFORMATION: /gene= "AChE"  
OTHER INFORMATION: /number= 6

FEATURE:  
NAME/KEY: terminator

LOCATION: 28129..28131

FEATURE:  
NAME/KEY: exon

LOCATION: complement (34092..34358)

OTHER INFORMATION: /function= "arsenite resistance"  
OTHER INFORMATION: /gene= "AR"  
OTHER INFORMATION: /number= 2

FEATURE:  
NAME/KEY: exon

LOCATION: complement (33779..33963)

OTHER INFORMATION: /gene= "Ar"  
OTHER INFORMATION: /number= 3

FEATURE: exon  
 LOCATION: complement (33493..33591)  
 OTHER INFORMATION: /gene= "AR"  
 OTHER INFORMATION: /number= 4

FEATURE: exon  
 NAME/KEY: OTHER INFORMATION: /gene= "AR"  
 LOCATION: complement (33297..33408)  
 OTHER INFORMATION: /number= 5

FEATURE: exon  
 LOCATION: complement (32959..33094)  
 OTHER INFORMATION: /gene= "AR"  
 OTHER INFORMATION: /number= 6

FEATURE: exon  
 LOCATION: complement (32569..32628)  
 OTHER INFORMATION: /gene= "AR"  
 OTHER INFORMATION: /number= 7

FEATURE: exon  
 LOCATION: complement (32386..32468)  
 OTHER INFORMATION: /gene= "AR"  
 OTHER INFORMATION: /number= 8

FEATURE: exon  
 LOCATION: complement (31894..32080)  
 OTHER INFORMATION: /gene= "AR"  
 OTHER INFORMATION: /number= 9

FEATURE: exon  
 LOCATION: complement (31363..31534)  
 OTHER INFORMATION: /gene= "AR"  
 OTHER INFORMATION: /number= 10

FEATURE: exon  
 LOCATION: complement (31131..31284)  
 OTHER INFORMATION: /gene= "AR"  
 OTHER INFORMATION: /number= 11

FEATURE: exon  
 LOCATION: complement (30816..31011)  
 OTHER INFORMATION: /gene= "AR"  
 OTHER INFORMATION: /number= 12

FEATURE: exon  
 LOCATION: complement (30470..30626)  
 OTHER INFORMATION: /gene= "AR"  
 OTHER INFORMATION: /number= 13

FEATURE: exon  
 LOCATION: complement (30187..30274)  
 OTHER INFORMATION: /gene= "AR"  
 OTHER INFORMATION: /number= 14

FEATURE: exon  
 LOCATION: complement (29945..30073)  
 OTHER INFORMATION: /gene= "AR"  
 OTHER INFORMATION: /number= 15

FEATURE: exon  
 LOCATION: complement (29664..29856)  
 OTHER INFORMATION: /gene= "ARS"  
 OTHER INFORMATION: /number= 16

US-08-814-095-7

alignment\_scores:  
 Quality: 87.00 Length: 14  
 Ratio: 6.214 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

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alignmnet\_block: US-09-155-076-1 x US-08-814-095-7 ..  
 Align seg 1/1 to: US-08-814-095-7 from: 1 to: 35060  
 1 AlaGluPheHisArgTrpSerSerTyrMetValHistIleTrp 14  
 1 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 28039 GCCGAGTTCCACCGCTGGAGCTCATGGACTGAAAG 28080

seq\_name: /cgn2.6/ptodata/2/ina/5C-COMB.seq;US-08-318-826A-9

seq\_documentation\_block:  
 ; Sequence 9, Application US/08318826A  
 ; Patent No. 5891725  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Soeq, Hermona  
 ; APPLICANT: Zabut, Haim  
 ; ECKSTEIN, Fritz  
 ; TITLE OF INVENTION: Synthetic Antisense  
 ; Oligodeoxynucleotides and Pharmaceutical Compositions  
 ; TITLE OF INVENTION: Containing Them  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Kohn & Associates  
 ; STREET: 30300 No. 5891725thwestern Hwy., Suite 410  
 ; CITY: Farmington Hills  
 ; STATE: Michigan  
 ; COUNTRY: US  
 ; ZIP: 48334  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/318,826A  
 ; FILING DATE:  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Kohn, Kenneth I.  
 ; REGISTRATION NUMBER: 30,955  
 ; REFERENCE/DOCNET NUMBER: 2391.00001  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (248) 539-5050  
 ; TELEX: (248) 539-1055  
 ; INFORMATION FOR SEQ ID NO: 9:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 2381 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA to mRNA  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Homo sapiens  
 ; DEVELOPMENTAL STAGE: fetal  
 ; TISSUE TYPE: Brain, Liver  
 ; POSITION IN GENOME:  
 ; MAP POSITION: 3q26  
 ; FEATURE:  
 ; NAME/KEY: mat\_peptide  
 ; LOCATION: 160..1881  
 ; IDENTIFICATION METHOD: experimental  
 ; OTHER INFORMATION: /EC\_number= 3.1.1.8  
 ; /evidence= EXPERIMENTAL  
 ; OTHER INFORMATION: /gene= "BCH"  
 ; OTHER INFORMATION: /note= "butyrylcholinesterase mature peptide"  
 ; FEATURE:  
 ; NAME/KEY: sig\_peptide  
 ; LOCATION: 76..159  
 ; FEATURE:  
 ; NAME/KEY: mRNA

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; LOCATION: 1..2381
; FEATURE: CDS
; NAME/KEY: US-08-318-826A-9
; LOCATION: 76..1884

alignment_scores:
    Quality: 62.00          Length: 14
    Ratio: 5.167            Gaps: 0
Percent Similarity: 85.714   Percent Identity: 64.286

alignment_block:
US-09-155-076-1 x US-08-318-826A-9  ..

Align seg 1/1 to: US-08-318-826A-9 from: 1 to: 2381
1 AlagliuPheHisArgTrpSerSerTyrMetValHistPlys 14
||| | | | | | | | | | | | | | | | | | | | | | | |
1792 GCAGGATTCCATGCCTGAAACATTACATGATGACTGGARA 1833
```



| Result No. | Score | Query | Match | Length | DB     | ID | Description   |
|------------|-------|-------|-------|--------|--------|----|---|
| 1          | 87    | 100.0 | 583   | 2      | S10712 |    | acetylcholinesterase (EC 3.1.1.7) - bovine  |
| 2          | 87    | 100.0 | 584   | 2      | S48724 |    | C;Species: Bos primigenius taurus (cattle)  |
| 3          | 87    | 100.0 | 614   | 2      | JH0811 |    | C;Date: 21-Nov-1993 #sequence_change 23-Mar-1995  |
| 4          | 87    | 100.0 | 614   | 2      | A39256 |    | C;Accession: S10712; A39734; B39734; R;Doctor, B.P.; Chapman, T.C.; Christner, C.E.; Deal, C.D.; de la Hoz, D.M.; Gentry, FEBs Lett. 266, 121-127, 1990 |
| 5          | 87    | 100.0 | 614   | 2      | JH0314 |    | A;Title: Complete amino acid sequence of fetal bovine serum acetylcholinesterase and  |
| 6          | 80    | 92.0  | 596   | 1      | ACRE   |    | A;Reference number: S10712; MUID:90306335   |
| 7          | 80    | 92.0  | 599   | 1      | A38868 |    | A;Accession: S10712   |
| 8          | 65    | 74.7  | 767   | 2      | S47639 |    | A;Residues: 1-15, R',17-38 <DOC>  |
| 9          | 62    | 71.3  | 602   | 1      | ACHU   |    | R;Roberts, W.L.; Doctor, B.P.; Foster, J.D.; Rosenberry, T.L.   |
| 10         | 61    | 70.1  | 581   | 2      | C39768 |    | J. Biol. Chem. 266, 7481-7487, 1991   |
| 11         | 61    | 70.1  | 603   | 2      | S70849 |    | R;Bon, S.; Chang, J.Y.; Strosberg, A.D.   |
| 12         | 44    | 50.6  | 260   | 2      | T12393 |    | FEBs Lett. 209, 205-212, 1986   |
| 13         | 43    | 49.4  | 516   | 2      | S67037 |    | A;Title: Identical N-terminal peptide sequences of asymmetric forms and of low-salt-s   |
| 14         | 42    | 48.3  | 1792  | 2      | T09878 |    | inesterase.   |
| 15         | 41    | 47.1  | 397   | 2      | A75137 |    | A;Reference number: A91370; MUID:87030761   |
| 16         | 41    | 47.1  | 1323  | 2      | T30253 |    | A;Accession: B39734   |
| 17         | 40.5  | 46.6  | 510   | 1      | S64059 |    | A;Residues: 1-38 <R02>  |
| 18         | 40    | 46.0  | 90    | 2      | PH1152 |    | R;Experimental source: fetal serum  |
| 19         | 40    | 46.0  | 184   | 2      | JC2104 |    | R;Bon, S.; Chang, J.Y.; Strosberg, A.D.   |
| 20         | 40    | 46.0  | 245   | 2      | S64351 |    | F;32/265/350/464/341/Binding site: carbohydrate (Asn) (covalent) #status predicted  |
| 21         | 40    | 46.0  | 450   | 2      | A64346 |    | F;203/Active site: Ser #status predicted  |
| 22         | 40    | 46.0  | 1350  | 2      | T30241 |    | Query Match 100.0%; Score 87; DB 2; Length 583;   |
| 23         | 40    | 46.0  | 1995  | 2      | T08166 |    | Best Local Similarity 100.0%; Pred. No. 4.8e-06;  |
| 24         | 39.5  | 45.4  | 469   | 2      | S74825 |    | Mismatches 0; Indels 0; Gaps 0;   |
| 25         | 39    | 45.4  | 542   | 2      | T02379 |    | Qy 1 AEFRWSSYVMVHK 14   |
| 26         | 39    | 44.8  | 100   | 2      | T09856 |    | Dq. 555 AEFRWSSYVMVHK 558   |
| 27         | 39    | 44.8  | 138   | 1      | HYMST  |    | IG heavy chain pre  |
| 28         | 39    | 44.8  | 226   | 2      | D4591  |    | membrane protein M  |
| 29         | 39    | 44.8  | 226   | 2      | S37434 |    | membrane glycoprot  |

Query Match 100.0%; Score 87; DB 2; Length 584;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYMYHWK 14  
 JH0811 ||||||| | | | | | | | |  
 Db 556 AEFHRWSSYMYHWK 569

RESULT 3  
 acetylcholinesterase (EC 3.1.1.7) catalytic chain precursor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Accession: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 18-Jun-1999  
 C:Accession: JH0811  
 R:Legay, C.; Bon, S.; Vernier, P.; Couussen, F.; Massoulie, J.  
 J:Neurochem, 60, 337-346, 1993  
 A:Title: Cloning and expression of a rat acetylcholinesterase subunit: generation of mul  
 A:Reference number: JH0811; MUID:93107932  
 A:Accession: JH0811  
 A:Residues: 1-614 <LEG>  
 A:Cross-references: GB:550879; PIDN:9262092; PIDN:AA24586.1; PID:9262093  
 A:Experimental source: striatum  
 C:Comment: This protein is responsible for hydrolysis of acetylcholine at cholinergic synapses  
 C:Superfamily: cholinesterase; cholinesterase homology  
 C:Keywords: carboxylic ester hydrolase; glycoprotein; membrane protein; muscle; nerve; n  
 F:1-31/Domain: signal sequence #status predicted <SG>  
 F:32-61/Domain: acetylcholinesterase catalytic chain #status predicted <CAT>  
 F:53-569/Domain: cholinesterase homology <CHE>  
 F:100-127,208-303,440-560/Disulfide bonds: #status predicted  
 F:234,478/Active site: Ser, Glu, His #status predicted  
 F:296,381,495/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 87; DB 2; Length 614;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYMYHWK 14  
 A39256 ||||||| | | | | | | | |  
 Db 586 AEFHRWSSYMYHWK 599

RESULT 4  
 acetylcholinesterase (EC 3.1.1.7) precursor, brain splice form - human  
 C:Species: Homo sapiens (man)  
 C:Accession: A39256; SO3959  
 R:Soreq, H.; Ben-Aziz, R.; Prody, C.A.; Seidman, S.; Gnatt, A.; Neville, L.; Lieman-Hurw  
 Proc. Natl. Acad. Sci. U.S.A. 87, 9688-9692, 1990  
 A:Title: Molecular cloning and construction of the coding region for human acetylcholine  
 A:Reference number: A39256; MUID:91088577  
 A:Accession: A39256

C;Accession: A00773; A60820; A31862; B31962; A23902; B41117; S15677  
 R;Schumacher, M.; Camp, S.; Maule, Y.; Newton, M.; MacPhee-Quigley, K.; Taylor, S.S.; F.  
 A;Title: Primary structure of *Torpedo californica* acetylcholinesterase deduced from its  
 C;Reference number: A00773; MUID:86118676  
 A;Molecule type: mRNA  
 A;Cross-references: GB:X03439; NID:964389  
 A;Experimental source: electric organ  
 A;Note: Parts of this sequence, including the amino and carboxyl ends of the mature protein  
 R;Schumacher, M.; Camp, S.; Maule, Y.; Newton, M.; MacPhee-Quigley, K.; Taylor, S.S.; F.  
 Ped. Proc. 45, 2976-2981, 1986  
 A;Title: Primary structure of acetylcholinesterase: implications for regulation and function  
 A;Reference number: A60820; MUID:87034662  
 A;Accession: A60820  
 A;Molecule type: mRNA  
 A;Residues: 22-596 <SC2>  
 R;Schumacher, M.; Maule, Y.; Camp, S.; Taylor, P.  
 J. Biol. Chem. 263, 18979-18987, 1988  
 A;Title: Multiple messenger RNA species give rise to the structural diversity in acetylcholinesterase  
 A;Reference number: A92701; MUID:89066695  
 A;Accession: A31962  
 A;Molecule type: mRNA  
 A;Residues: 1-23 <SC3>  
 A;Cross-references: EMBL:X03439; NID:964389  
 A;Experimental source: clones AChE-11 and AChE-18  
 A;Note: revision to sequence A00773  
 A;Accession: B31962  
 A;Molecule type: DNA; mRNA  
 A;Cross-references: GB:X03439; NID:964389  
 A;Experimental source: clone AChE-1  
 R;MacPhee-Quigley, K.; Weise, C.; Raba, R.; Aaviksaar, A.; Hucho, F.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 6117-6121, 1991  
 J. Biol. Chem. 260, 12185-12189, 1985  
 A;Title: Primary structures of the catalytic subunits from two molecular forms of acetylcholinesterase  
 A;Reference number: A23902; MUID:86008285  
 A;Accession: A23902  
 A;Molecule type: protein  
 A;Residues: 22, B, 24-45-214-237 <MAC>  
 A;Note: active site Ser identification  
 R;Kreienkamp, H.J.; Weise, C.; Raba, R.; Aaviksaar, A.; Hucho, F.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 6117-6121, 1991  
 A;Title: Anionic subsites of the catalytic center of acetylcholinesterase from *Torpedo*  
 A;Reference number: A41117; MUID:91296772  
 A;Accession: B41117  
 A;Molecule type: protein  
 A;Residues: 100-108 <FRE>  
 A;Note: substrate binding site  
 R;Maule, Y.; Camp, S.; Gibney, G.; Rachinsky, T.L.; Ekstroem, T.J.; Taylor, P.  
 Neuron 4, 289-301, 1990  
 A;Title: Single gene encodes glycophospholipid-anchored and asymmetric acetylcholinesterase  
 A;Reference number: PS0113; MUID:90166618  
 A;Accession: S15677  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 557-596 <NAU>  
 A;Cross-references: EMBL:X56516  
 R;MacPhee-Quigley, K.; Vedick, T.S.; Taylor, P.; Taylor, S.S.  
 J. Biol. Chem. 261, 13565-13570, 1986  
 A;Title: Profile of the disulfide bonds in acetylcholinesterase  
 A;Reference number: A3099; MUID:87008586  
 R;Sussman, J.L.; Harel, M.; Silman, I.  
 submitted to the Brookhaven Protein Data Bank, October 1991  
 A;Reference number: A50061; PDB:1ACE  
 A;Contents: annotation; disulfide bonds  
 R;Sussman, J.L.; Harel, M.; Silman, I.  
 Science 253, 872-879, 1991  
 A;Title: Atomic structure of acetylcholinesterase from *Torpedo californica*: a prototypic  
 A;Reference number: A3098; MUID:912443928  
 A;Contents: annotation; X-ray crystallography, 2.8 angstroms, residues 26-481, 511-555 of  
 R;Sussman, J.L.; Harel, M.; Frolow, F.; Oefner, C.; Goldman, A.; Toker, L.; Silman, I.

C;Comment: Synapses usually contain this lls (asymmetric) form of cholinesterase with homotetramer occurs on the outer surfaces of cell membranes, including those of erythrocytes. Homotetramer is disulfide linked homodimer; 18S form is homotetramer, a dimer  
 C;Function:  
 A;Description: hydrolyzes acetylcholine to choline and acetate  
 A;Pathway: neurotransmitter degradation  
 C;Superfamily: cholinesterase; cholinesterase homology  
 C;Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; membrane  
 F;1-21/Domain: Signal sequence #status Predicted <SC1>  
 F;22-59/Domain: acetylcholinesterase, lls form #status experimental <SC1>  
 F;51-554/Product: acetylcholinesterase, lls form #status experimental <NAT>  
 F;51-554/Domain: cholinesterase homology <CHE>  
 F;80-478/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F;88-115,215-286,422-542/Disulfide bonds: #status experimental  
 F;105/Binding site: substrate (Trp) #status experimental  
 F;221/Active site: Ser #status experimental  
 F;348-461/Active site: Glu, His #status predicted  
 F;437/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F;593/Disulfide bonds: interchain (#status experimental  
 A;Molecule type: mRNA  
 A;Residues: 22-596 <SC2>  
 R;Schumacher, M.; Maule, Y.; Camp, S.; Taylor, P.  
 J. Biol. Chem. 263, 18979-18987, 1988  
 A;Title: Multiple messenger RNA species give rise to the structural diversity in acetylcholinesterase  
 A;Reference number: A92701; MUID:89066695  
 A;Accession: A31962  
 A;Molecule type: mRNA  
 A;Residues: 1-23 <SC3>  
 A;Cross-references: EMBL:X03439; NID:964389  
 A;Experimental source: clones AChE-11 and AChE-18  
 A;Note: revision to sequence A00773  
 A;Accession: B31962  
 A;Molecule type: DNA; mRNA  
 A;Cross-references: GB:X03439; NID:964414; PID:CRA29047.1; PID:964415  
 A;Experimental source: clone AChE-1  
 R;MacPhee-Quigley, K.; Weise, C.; Raba, R.; Taylor, P.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 6117-6121, 1991  
 J. Biol. Chem. 260, 12185-12189, 1985  
 A;Title: Primary structures of the catalytic subunits from two molecular forms of acetylcholinesterase  
 A;Reference number: A23902; MUID:86008285  
 A;Accession: A23902  
 A;Molecule type: protein  
 A;Residues: 22, B, 24-45-214-237 <MAC>  
 A;Note: substrate binding site  
 R;Kreienkamp, H.J.; Weise, C.; Raba, R.; Aaviksaar, A.; Hucho, F.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 6117-6121, 1991  
 A;Title: Anionic subsites of the catalytic center of acetylcholinesterase from *Torpedo*  
 A;Reference number: A41117; MUID:91296772  
 A;Accession: B41117  
 A;Molecule type: protein  
 A;Residues: 100-108 <FRE>  
 A;Note: active site Ser identification  
 R;Maule, Y.; Camp, S.; Gibney, G.; Rachinsky, T.L.; Ekstroem, T.J.; Taylor, P.  
 Neuron 4, 289-301, 1990  
 A;Title: Single gene encodes glycophospholipid-anchored and asymmetric acetylcholinesterase  
 A;Reference number: PS0113; MUID:90166618  
 A;Accession: S15677  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 557-596 <NAU>  
 A;Cross-references: EMBL:X56516  
 R;MacPhee-Quigley, K.; Vedick, T.S.; Taylor, P.; Taylor, S.S.  
 J. Biol. Chem. 261, 13565-13570, 1986  
 A;Title: Profile of the disulfide bonds in acetylcholinesterase  
 A;Reference number: A3099; MUID:87008586  
 R;Sussman, J.L.; Harel, M.; Silman, I.  
 submitted to the Brookhaven Protein Data Bank, October 1991  
 A;Reference number: A50061; PDB:1ACE  
 A;Contents: annotation; X-ray crystallography, 2.8 angstroms, residues 26-481, 511-555 of  
 R;Sussman, J.L.; Harel, M.; Frolow, F.; Oefner, C.; Goldman, A.; Toker, L.; Silman, I.  
 Science 253, 872-879, 1991  
 A;Title: Atomic structure of acetylcholinesterase from *Torpedo californica*: a prototypic  
 A;Reference number: A3098; MUID:912443928  
 A;Contents: annotation; X-ray crystallography, 2.8 angstroms, residues 26-481, 511-555 of  
 R;Sussman, J.L.; Harel, M.; Silman, I.  
 Science 253, 872-879, 1991  
 A;Title: Atomic structure of acetylcholinesterase to choline and acetate  
 A;Pathway: neurotransmitter degradation  
 C;Superfamily: cholinesterase; cholinesterase homology

C; Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; neurotransmitter  
 F;-24;/Domain: signal sequence #status predicted <SIG>  
 F;54-554/Product: acetylcholinesterase #status predicted <MAT>  
 F;83-440,481,557/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F;91-118,278-289,426-515/Disulfide bonds: #status predicted  
 F;24,351,467/Active site: Ser, Glu, His #status predicted  
 F;556/Disulfide bonds: interchain #status predicted

Query Match 92.0%; Score 80; DB 1; Length 599;  
 Best Local Similarity 92.3%; Pred. No. 5.9e-05; 0; Gaps 0;  
 Matches 12; Conservative 0; Indels 0;

Qy 2 EFHRWSSYMHWK 14  
 Db 572 EFHRWSSYMHWK 584

RESULT 8

S4 639 acetylcholinesterase (EC 3.1.1.7) - chicken  
 C;Species: Gallus gallus (chicken)  
 C;Cross-references: 10-Nov-1995 #text\_change 17-Mar-2000  
 C;Accession: S47639  
 R;Randall, W.R.; Rimer, M.; Gough, N.R.  
 Biochim. Biophys. Acta 1218, 453-456, 1994  
 A;Title: Cloning and analysis of chicken acetylcholinesterase transcripts from muscle and brain  
 A;Reference number: S47639; MUID:94323539  
 A;Molecule type: mRNA  
 A;Residues: 1-767 <RAN>  
 A;Cross-references: EMBL:U03472; NID:9623031; PID:9424115  
 C;Superfamily: cholinesterase; cholinesterase homology  
 C;Keywords: carboxylic ester hydrolase

Query Match 92.0%; Score 80; DB 1; Length 599;  
 Best Local Similarity 92.3%; Pred. No. 5.9e-05; 0; Gaps 0;  
 Matches 12; Conservative 0; Indels 0;

Qy 2 EFHRWSSYMHWK 14  
 Db 740 EFHRWSSYMHWK 752

RESULT 9

ACHU cholinesterase (EC 3.1.1.8) precursor - human  
 N;Alternate names: acetylcholine acylhydrolase; butyrylcholinesterase; choline esterase II  
 C;Species: Homo sapiens (man)  
 C;Date: 30-Jun-1987 #sequence\_revision 23-Feb-1996 #text\_change 02-Sep-1997  
 C;Accession: S47639; A33163; A33387; A34665; A00772  
 R;Arpagaus, M.; Kott, M.; Vatsis, K.P.; Bartels, C.F.; La Du, B.N.; Lockridge, O.  
 Biochemistry 29, 124-131, 1990  
 A;Title: Structure of the gene for human butyrylcholinesterase. Evidence for a single cDNA  
 A;Reference number: A33769; MUID:9022557  
 A;Accession: A33769  
 A;Molecule type: DNA  
 A;Residues: MSVOSNLQAGAAASCISPKYIMFTPKLCHLCCRESEIN',-1-602 <ARP>  
 A;Cross-references: GB:M32391; GB:J02879  
 A;Note: two ATG codons found upstream of Met-1 do not lie in a favorable context for translation  
 R;Prody, C.A.; Zevin-Sorkin, D.; Gnatt, A.; Goldberg, O.; SoREQ, H.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 3555-3559, 1987  
 A;Title: Isolation and characterization of full-length cDNA clones coding for cholinesterase  
 A;Reference number: A26613; MUID:872231856  
 A;Accession: A26613  
 A;Molecule type: mRNA  
 A;Residues: 1-133, 'D'-135-602 <PRO>  
 R;McTiernan, C.; Adkins, S.; Chatonnet, A.; Vaughan, T.A.; Bartels, C.F.; Kott, M.; Rose, J.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 6682-6686, 1987  
 A;Title: Brain cDNA clone for human cholinesterase.  
 A;Reference number: A33887; MUID:88016155

A;Accession: A33887  
 A;Molecule type: mRNA  
 A;Residues: MSVOSNLQAGAAASCISPKYIMFTPKLCHLCCRESEIN',-1-602 <MCT>  
 A;Note: two ATG codons found upstream of Met-1 do not lie in a favorable context for translation  
 R;Nogueira, C.P.; McGuire, M.C.; Grzeser, C.; Bartels, C.F.; Arpagaus, M.; Van der Spiegel, I.L.  
 Am. J. Hum. Genet. 46, 934-942, 1990  
 A;Title: Identification of a frameshift mutation responsible for the silent phenotype  
 A;Reference number: A34668; MUID:9022779  
 A;Accession: A34668  
 A;Molecule type: DNA  
 A;Residues: 143-145, 'VSNWNLLTFTCL' <NOG>  
 A;Note: frameshift mutant in codon for residue 145 (Gly)  
 R;Lockridge, O.; Bartels, C.F.; Vaughan, T.A.; Wong, C.K.; Johnson, L.L.  
 J. Biol. Chem. 262, 549-557, 1987  
 A;Title: Complete amino acid sequence of human serum cholinesterase.  
 A;Reference number: A00772; MUID:87109144  
 A;Accession: A00772  
 A;Molecule type: protein  
 A;Residues: 29-602 <LOC>  
 A;Experimental source: plasma  
 C;Comment: Cholinesterase is present in most cells (except erythrocytes).  
 C;Genetics:  
 A;Gene: GDB:BCHE; CHE1  
 A;Cross-references: OMIM:120558; OMIM:177400  
 A;Map position: 3q26.1-3q26.2  
 A;Introns: 506/2; 562/1  
 C;Function:  
 A;Description: hydrolyzes acetylcholines to choline and a carboxylic acid  
 A;Note: this cholinesterase is highly reactive with organophosphate esters  
 C;Superfamily: cholinesterase; cholinesterase homology  
 C;Keywords: carboxylic ester hydrolase; glycoprotein; homotetramer  
 F;1-28/Domain: signal sequence #status predicted <SIG>  
 F;29-602/Domain: cholinesterase #status experimental <HAT>  
 P;56-556/Domain: cholinesterase homology <CHE>  
 P;45-85,134-269,284-369,483-509,514/Binding site: carbohydrate (Asn) (covalent) #stat  
 F;226/Active site: Ser #status experimental  
 F;226/Active site: Ser #status experimental

RESULT 10

C39768 cholinesterase (EC 3.1.1.8) - rabbit  
 N;Alternate names: butyrylcholinesterase  
 C;Species: Oryctolagus cuniculus (domestic rabbit)  
 C;Date: 14-Feb-1992 #sequence\_revision 01-Mar-1996  
 C;Accession: S10255; C37768  
 R;Jbilio, O.; Chatonnet, A.  
 Nucleic Acids Res. 18, 3990, 1990  
 A;Title: Complete sequence of rabbit butyrylcholinesterase.  
 A;Reference number: S10255; MUID:90328526  
 A;Accession: S10255  
 A;Molecule type: DNA  
 A;Residues: 1-581 <JB1>  
 A;Cross-references: EMBL:X52090; PID:91476; PID:CAA36308.1; PID:g137027  
 R;Arpagaus, M.; Chatonnet, A.; Masson, P.; Newton, M.; Vaughn, T.A.; Bartels, C.F.;  
 J. Biol. Chem. 266, 6966-6974, 1991  
 A;Title: Use of the polymerase chain reaction for homology probing of butyrylcholinesterase  
 A;Reference number: A39768; MUID:91201348  
 A;Accession: C39768  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 75-215 <ARP>  
 A;Cross-references: GB:M62779; PID:9164788; PID:AAA31169.1; PID:g164789  
 C;Genetics:

A; Introns: 485/2; 541/1  
 C; Superfamily: cholinesterase; cholinesterase homology  
 C; Keywords: carboxylic ester hydrolase; glycoprotein  
 F; 35-535/Domain: cholinesterase homology <CHE>

Query Match 70.1%; Score 61; DB 2; Length 581;  
 Best Local Similarity 64.3%; Pred. No. 0.049; Gaps 0;  
 Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 AEFHRWSYMYWK 14  
 Db 552 AGFHRWNYMMAWK 565

RESULT 11

S70849

cholinesterase (EC 3.1.1.8) - mouse

N; Alternate names: butyrylcholine esterase

C; Species: Mus musculus (house mouse)

C; Date: 29-Oct-1996 #sequence\_revision 08-Nov-1996 #text\_change 18-Jun-1999

R; Taylor, P.

Submitted to the EMBL Data Library, August 1992

A; Reference number: S70849

A; Accession: S70849

A; Molecule type: nucleic acid

A; Residues: 1-603 &lt;TA&gt;

A; Cross references: EMBL:M99492; NID:9191579; PID:AAA37328.1; PID:gi191580

R; Rachinski, T.L.; Camp, S.; Li, Y.; Ekstroem, T.J.; Newton, M.; Taylor, P.

Neuron 5, 317-327, 1990

A; Title: Molecular cloning of mouse acetylcholinesterase: tissue distribution of alterna

A; Reference number: JH0314; MUID:90380429

A; Accession: S15680

A; Status: nucleic acid sequence not shown

A; Molecule type: nucleic acid

A; Residues: 30-128, 'P', 130-603 &lt;RAC&gt;

A; Cross references: EMBL:M99492

R; Arpagaus, M.; Chatonet, A.; Masson, P.; Newton, M.; Vaughan, T.A.; Bartels, C.F.; Noj

J. Biol. Chem. 266, 6566-6574, 1991.

A; Title: Use of the polymerase chain reaction for homology probing of butyrylcholinester

A; Reference number: A39768; MUID:91201348

A; Accession: A39768

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 97-128, 'P', 130-237 &lt;ARP&gt;

C; Superfamily: cholinesterase; cholinesterase homology

C; Keywords: carboxylic ester hydrolase; glycoprotein

F; 57-557/Domain: cholinesterase homology &lt;CHE&gt;

Query Match 70.1%; Score 61; DB 2; Length 603;

Best Local Similarity 64.3%; Pred. No. 0.05; Gaps 0;

Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AEFHRWSYMYWK 14

Db 574 AGFHRWNSYMMHQ 587

RESULT 12

T12393 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Arabidopsis thaliana chloroplast

C; Species: chloroplast Arabidopsis thaliana (mouse-ear cress)

C; Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 11-Jan-2000

C; Accession: T12393

R; Galloway, G.L.; Malmberg, R.L.; Price, R.A.

Mol. Biol. 15, 1312-1320, 1998

A; Title: Phylogenetic utility of the nuclear gene arginine decarboxylase: an example fro

A; Reference number: Z16357; MUID:99003705

A; Accession: T12393

A; Status: preliminary; translated from GB/EMBL/DDJB

A; Molecule type: DNA

A; Residues: 1-260 &lt;GAL&gt;

A; Cross references: EMBL:AF064654; NID:gi366917; PID:gi366918; MUID:AAC68593.1

C; Genetics:

A; Genomic: chloroplast

A; Note: ndhF

C; Superfamily: NADH dehydrogenase (ubiquinone) chain 5

C; Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

Query Match 70.1%; Score 61; DB 2; Length 581;

Best Local Similarity 64.3%; Pred. No. 0.049; Gaps 0;

Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AEFHRWSYMYWK 14

Db 552 AGFHRWNYMMAWK 565

RESULT 13

S67037

SNP3 protein - yeast (Saccharomyces cerevisiae)

N; Alternate names: protein O3527; protein YOR149c

C; Species: Saccharomyces cerevisiae

C; Date: 12-Jul-1996 #sequence\_revision 12-Jul-1996 #text\_change 06-Feb-1998

C; Accession: S67037; S13750

R; Bordone, R.; Camasses, A.; Madanta, A.; Martin, R.P.; Poch, O.; Tarassov, I.A.; WI

submitted to the Protein Sequence Database, July 1996

A; Reference number: S67032

A; Molecule type: DNA

A; Residues: 1-516 &lt;BOR&gt;

A; Cross references: EMBL:Z75057; NID:gi1420374; PID:gi1420375; MIPS:YOR149

A; Experimental source: strain S288C

R; Irie, K.; Araki, H.; Oshima, Y.

Mol. Genet. 225, 257-265, 1991

A; Title: Mutations in a Saccharomyces cerevisiae host showing increased holding stab

A; Reference number: S13750; MUID:gi1172125

A; Accession: SGD:S503

A; Molecule type: DNA

A; Residues: 1-121, 'IK', 124-162, 'G', 164-168, 'R', 170-278, 'L', 280-516 &lt;IR1&gt;

A; Cross references: ENSEMBL:X58121; NID:gi4497; PID:gi4498

C; Genetics:

A; Gene: SGD:SMP3

A; Cross references: SGD:S0005675; MIPS:YOR149c

A; Map position: 15\_R

C; Keywords: transmembrane protein

F; 9-25/Domain: transmembrane #status predicted &lt;TM1&gt;

F; 89-205/Domain: transmembrane #status predicted &lt;TM2&gt;

F; 215-331/Domain: transmembrane #status predicted &lt;TM3&gt;

F; 271-287/Domain: transmembrane #status predicted &lt;TM4&gt;

F; 344-360/Domain: transmembrane #status predicted &lt;TM5&gt;

Query Match 49.4%; Score 43; DB 2; Length 516;

Best Local Similarity 66.7%; Pred. No. 26; Mismatches 3; Indels 0; Gaps 0;

Qy 6 WSSYMWK 14

Db 204 WKFYRVWK 212

RESULT 14

T08878

superoxinin P205 - bovine

C; Species: Bos primigenius taurus (cattle)

C; Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 16-Jul-1999

C; Accession: T08878

R; Pestorjamas, K.N.; Pope, R.K.; Wulkkuhe, J.D.; Luna, E.J.

J. Cell Biol. 139, 1255-1269, 1997

A; Title: Superoxinein (P205). A novel membrane associated membrane associated F-actin

A; Reference number: Z16509

A; Accession: T08878

A; Status: preliminary; translated from GB/EMBL/DDBJ  
 A; Molecule type: mRNA  
 A; Residues: 1-1792 <PESS>  
 A; Cross-references: EMBL:AF025996; NID:92668622; PID:92668623  
 A; Experimental source: cell line MDBK (Madin Darby Bovine Kidney); ATCC CCL-22  
 C; Superfamily: villin headpiece homology  
 C; Keywords: actin binding; cell adhesion; membrane-associated protein  
 F; 1732-1792/Domain: villin headpiece homology <VHH>

---

Query Match 48.3%; Score 42; DB 2; Length 1792;  
 Best Local Similarity 46.2%; Pred. No. 1.2e+02; Gaps 0;  
 Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 Qy 2 EFHRWSSYMWVK 14  
 :|| :|| |  
 Db 1352 QFHGDAYVVKWK 1364

RESULT 15  
 A75137 hypothetical protein PRB0600 - Pyrococcus abyssi (strain Orsay)  
 C; Species: Pyrococcus abyssi  
 C; Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 20-Aug-1999  
 C; Accession: A75137  
 R; anonymous, Genoscope  
 submitted to the EMBL Data Library, July 1999  
 A; Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru  
 A; Reference number: A75001  
 A; Accession: A75137  
 A; Status: preliminary  
 A; Molecule type: DNA  
 A; Residues: 1-397 <KAW>  
 A; Cross-references: GB:AJ248285; GB:AL096836; NID:95458067; PIDN:CAB49810.1; PID:e151570  
 A; Experimental source: strain Orsay  
 C; Genetics:  
 A; Gene: PAB0600

Query Match 47.1%; Score 41; DB 2; Length 397;  
 Best Local Similarity 40.0%; Pred. No. 40; Gaps 1;  
 Matches 6; Conservative 3; Mismatches 4; Indels 2; Gaps 1;  
 Qy 2 EFH-RWSSYMWVK 14  
 :|| :|| |  
 Db 18 DYHVKRNEQQKLWIK 32

Search completed: September 13, 2000, 02:22:33  
 Job time: 131 sec



Db 555 AEFHRSSYMWK 568

**RESULT 2**

|            |   |      |         |
|------------|---|------|---------|
| ACES_RABIT | STANDARD;   | PRT; | 584 AA. |
| ID         |   |      |         |
| AC         |   |      |         |
| Q29499;    |   |      |         |
| DT         | 01-NOV-1997 (Rel. 35, Created)  |      |         |
| DT         | 01-NOV-1997 (Rel. 35, Last sequence update)   |      |         |
| DT         | 01-NOV-1997 (Rel. 35, Last annotation update)   |      |         |
| DE         | ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7) (FRAGMENT).   |      |         |
| GN         | ACHE.   |      |         |
| OS         | Oryctolagus cuniculus (Rabbit).   |      |         |
| OC         | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;   |      |         |
| OC         | Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.   |      |         |
| RN         | [1]   |      |         |
| RP         | SEQUENCE FROM N.A.  |      |         |
| RC         | TISSUE=MYCROSTE;  |      |         |
| RX         | MEDLINE; 95010096.  |      |         |
| RA         | Jbilo O., Lhermitte Y., Toutant J., Chatonnet A.;   |      |         |
| RT         | "Acetylcholinesterase and butyrylcholinesterase expression in adult rabbit tissues and during development.";  |      |         |
| RL         | Eur. J. Biochem. 225:115-124(1994).   |      |         |
| CC         | -I- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.   |      |         |
| CC         | -I- SUBUNIT: OLIGOMER COMPOSED OF DISULFIDE-LINKED HOMODIMERS.  |      |         |
| CC         | -I- MISCELLANEOUS: SYNAPSES USUALLY CONTAIN ASYMMETRIC MOLECULES OF CHOLINESTERASE, WITH A COLLAGEN-LIKE PART DISULFIDE-BONDED TO THE CATALYTIC PART. A DIFFERENT, GLOBULAR TYPE OF CHOLINESTERASE OCCURS ON THE OUTER SURFACES OF CELL MEMBRANES, INCLUDING THOSE OF ERYTHROCYTES. |      |         |
| CC         | -I- MISCELLANEOUS: THIS IS THE CATALYTIC SUBUNIT OF AN ASYMMETRIC OR SOLUBLE FORM OF ACHE.  |      |         |
| CC         | -I- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.   |      |         |

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EMBL; U05036; AA053235.1; -

DR HSSP; P22303; 2CJU.

DR PF0015; Coesterase; 1.

DR PROSITE; PS00122; CARBOXYLESTERASE\_B; 1.

DR PROSITE; PS00941; CARBOXYLESTERASE\_B2; 1.

KW Serine esterase; Synapse; Membrane; Nerve; Muscle; signal; Neurotransmitter degradation; Glycoprotein.

FT NON\_TER 1 1

FT SIGNAL <1 1

FT CHAIN 2 584

FT ACT\_SITE 204 204

FT ACT\_SITE 335 335

FT ACT\_SITE 448 448

FT DISULFID 70 97

FT DISULFID 258 273

FT DISULFID 410 530

FT DISULFID 581 581

FT CARBOHD 266 266

FT CARBOHD 351 351

FT CARBOHD 465 465

SQ SEQUENCE 584 AA; 64630 MW; 2AE15F303649FE CRC64;

**RESULT 3**

|            |   |      |         |
|------------|---|------|---------|
| ACES_HUMAN | STANDARD;   | PRT; | 614 AA. |
| ID         |   |      |         |
| AC         | P22303;   |      |         |
| DT         | 01-AUG-1991 (Rel. 19, Created)  |      |         |
| DT         | 01-AUG-1991 (Rel. 19, Last sequence update)   |      |         |
| DT         | 15-JUL-1999 (Rel. 38, Last annotation update)   |      |         |
| DE         | ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7).  |      |         |
| GN         | ACHE.   |      |         |
| OS         | Homo sapiens (Human).   |      |         |
| OC         | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.   |      |         |
| RN         | [1]   |      |         |
| RP         | SEQUENCE FROM N.A.  |      |         |
| RX         | MEDLINE; 91083577.  |      |         |
| RA         | Soreq H., Ben Aziz R., Prod'homme C.A., Seidman S., Gnatt A., Neville L., Lieman-Hurwitz J., Lev-Lehman E., Ginzberg D., Lipidot-Lifson Y., Zakut H.;   |      |         |
| RT         | "Molecular cloning and construction of the coding region for human acetylcholinesterase reveals a G + C-rich attenuating structure.";   |      |         |
| RT         | acetylcholinesterase reveals a G + C-rich attenuating structure."   |      |         |
| RL         | Proc. Natl. Acad. Sci. U.S.A. 87:9688-9692(1990).   |      |         |
| RN         | [2]   |      |         |
| RP         | PARTIAL SEQUENCE.   |      |         |
| RC         | TISSUE=ERYTHROCYTE;   |      |         |
| RX         | MEDLINE; 892212136.   |      |         |
| RA         | Chhajlani V., Derr D., Earles B., Schmell E., August T.;  |      |         |
| RT         | "purification and partial amino acid sequence analysis of human erythrocyte acetylcholinesterase.";   |      |         |
| RT         | FEBS Lett. 247:279-282(1989).   |      |         |
| RL         | [3]   |      |         |
| RN         | MUTAGENESIS OF CYS-611.   |      |         |
| RX         | MEDLINE; 92084699.  |      |         |
| RA         | Velin B., Grossfeld H., Kromann C., Leitner M., Gozes Y., Lazar A., Flashner Y., Marcus D., Shafferman A.;  |      |         |
| RT         | "The effect of elimination of intersubunit disulfide bonds on the activity, assembly, and secretion of recombinant human acetylcholinesterase. Expression of acetylcholinesterase Cys-580->Ala mutant"; |      |         |
| RT         | RT  |      |         |
| RL         | J. Biol. Chem. 266:23977-23984(1991).   |      |         |
| RN         | [4]   |      |         |
| RP         | MUTAGENESIS OF ACTIVE SITE RESIDUES AND OF ASP-206 AND ASP-435.   |      |         |
| RX         | MEDLINE; 92388112.  |      |         |
| RA         | Shafferman A., Kromann C., Flashner Y., Leitner M., Grossfeld H., Ordentlich A., Gozes Y., Cohen S., Ariel N., Barak D.;  |      |         |
| RA         | "Mutagenesis of human acetylcholinesterase. Identification of residues involved in catalytic activity and in polypeptide folding.";   |      |         |
| RT         | RT  |      |         |
| RL         | J. Biol. Chem. 267:17640-17648(1992).   |      |         |
| RN         | [5]   |      |         |
| RP         | VARIANT BLOOD GROUP YT(B).  |      |         |
| RX         | MEDLINE; 93256075.  |      |         |
| RA         | Bartels C.F., Zelinski T., Lockridge O.;  |      |         |
| RT         | "Mutation at codon 322 in the human acetylcholinesterase (ACHE) gene accounts for YT blood group polymorphism.";  |      |         |
| RT         | RT  |      |         |
| RL         | Am. J. Hum. Genet. 52:928-936(1993).  |      |         |
| CC         | -I- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.   |      |         |
| CC         | -I- CATALYTIC ACTIVITY: ACETYLCHOLINE + H(2)O = CHOLINE + ACETATE.  |      |         |
| CC         | -I- SUBUNIT: OLIGOMER COMPOSED OF DISULFIDE-LINKED HOMODIMERS.  |      |         |
| CC         | -I- POLYMORPHISM: ACHE IS RESPONSIBLE FOR THE YT BLOOD GROUP SYSTEM.  |      |         |
| CC         | THE MOLECULAR BASIS OF THE YT(A)=YT1/YT2 BLOOD GROUP ANTIGENS IS A SINGLE VARIATION IN POSITION 353; HIS-353 CORRESPONDS TO YT(A) AND THE RARE VARIANT WITH ASN-353 TO YT(B).                           |      |         |
| CC         | -I- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.   |      |         |

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Query Match 100.0%; Score 87; DB 1; Length 584;

Best Local Similarity 100.0%; Pred. No. 6e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRSSYMWK 14  
 ||||| |||||  
 DD 556 AEFHRSSYMWK 569



| RESULT  | 5                                   | SEQUENCE_RAT | STANDARD: | PRT;                        | 614 AA. |
|---|-------------------------------------|--------------|-----------|-----------------------------|---------|
| ACHE  |                                     | ACES_RAT     |           |                             |         |
| P37136  |                                     | ID           |           |                             |         |
| 01-OCT-1994   | (Rel. 30, Created)                  | ACT SITE     |           |                             |         |
| 01-FEB-2000   | (Rel. 39, Last annotation update)   | ACT SITE     |           |                             |         |
| ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7).  |                                     | ACT SITE     |           |                             |         |
| Rattus norvegicus (Rat).  |                                     | ACT SITE     |           |                             |         |
| Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.   |                                     | ACT SITE     |           |                             |         |
| [1]   | SEQUENCE FROM N.A. (T FORM).        | ACT SITE     |           |                             |         |
| MEDLINE: 93107932.  |                                     | ACT SITE     |           |                             |         |
| RA Legay C., Bon S., Vernier P., Coussen F., Massoulie J.; "Cloning and expression of a rat acetylcholinesterase subunit: generation of multiple molecular forms and complementarity with a Torpedo collagenic subunit.", J. Neurochem. 60:337-346(1993).   |                                     | ACT SITE     |           |                             |         |
| [2]   | SEQUENCE FROM N.A. (H AND R FORMS). | ACT SITE     |           |                             |         |
| MEDLINE: 93114454.  |                                     | ACT SITE     |           |                             |         |
| RA Legay C., Bon S., Massoulie J.; "Expression of a cDNA encoding the glycolipid-anchored form of rat acetylcholinesterase.", FEBS Lett. 315:163-166(1993).   |                                     | ACT SITE     |           |                             |         |
| -1- FUNCTION: RAPIDLY HYDROLYZES CHOLINE + H <sub>2</sub> O = CHOLINE + ACETATE.  |                                     | ACT SITE     |           |                             |         |
| -1- CATALYTIC ACTIVITY: ACETYLCHOLINE + H <sub>2</sub> O = CHOLINE + ACETATE.   |                                     | ACT SITE     |           |                             |         |
| -1- SUBUNIT: OLIGOMER COMPOSED OF DISULFIDE-LINED HOMODIMERS.   |                                     | ACT SITE     |           |                             |         |
| -1- CATALYTIC FORMS H (GPI-ANCHOR DIMER) AND T (ASYMMETRIC COLLAGEN-TAILED) WHICH DIFFER IN THEIR C-TERMINUS, ACCOUNT FOR ALL TYPES OF KNOWN ACHE FORMS.  |                                     | ACT SITE     |           |                             |         |
| -1- ALTERNATIVE PRODUCTS: THE DIFFERENT CATALYTIC SUBUNITS ARE ENCODED BY ALTERNATIVELY SPLICED MRNAs THAT ARISE FROM A SINGLE GENE.  |                                     | ACT SITE     |           |                             |         |
| IT IS NOT KNOWN WHETHER THE R FORM REPRESENTS A FUNCTIONAL SPECIES. THE T (ASYMMETRIC) FORM IS SHOWN HERE.  |                                     | ACT SITE     |           |                             |         |
| -1- TISSUE SPECIFICITY: HAS BEEN FOUND IN CENTRAL NERVOUS SYSTEM AND MUSCLE. FOUND IN EMBRYONIC LIVER AND SPLEEN BUT NOT IN ADULT LIVER.  |                                     | ACT SITE     |           |                             |         |
| -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.   |                                     | ACT SITE     |           |                             |         |
| -----   |                                     | ACT SITE     |           |                             |         |
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| EMBL; S50879; AAB4586.1; -.   |                                     | ACT SITE     |           |                             |         |
| EMBL; X70140; CAA49717.1; -.  |                                     | ACT SITE     |           |                             |         |
| EMBL; X70141; CAA49718.1; -.  |                                     | ACT SITE     |           |                             |         |
| PIR; JH0811; P1836; 1MAH.   |                                     | ACT SITE     |           |                             |         |
| HSSP; P00135; Coesterase; 1.  |                                     | ACT SITE     |           |                             |         |
| PFM; P00135; Coesterase; 1.   |                                     | ACT SITE     |           |                             |         |
| PRINTS; PR00878; CHOLINESTERASE.  |                                     | ACT SITE     |           |                             |         |
| DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.   |                                     | ACT SITE     |           |                             |         |
| DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.   |                                     | ACT SITE     |           |                             |         |
| HYDROLASE; Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal; Neurotransmitter degradation; Glycoprotein; Alternative splicing.   |                                     | ACT SITE     |           |                             |         |
| SIGNAL  | 1                                   | ACT SITE     | 31        | POTENTIAL                   | 19      |
| CHAIN   | 32                                  | ACT SITE     | 614       | POTENTIAL                   | 19      |
| ACT SITE  | 234                                 | ACT SITE     | 234       | BY SIMILARITY.              | 1       |
| ACT SITE  | 365                                 | ACT SITE     | 365       | BY SIMILARITY.              | 1       |
| ACT SITE  | 478                                 | ACT SITE     | 478       | BY SIMILARITY.              | 1       |
| DISULFID  | 100                                 | ACT SITE     | 127       | BY SIMILARITY.              | 1       |
| DISULFID  | 288                                 | ACT SITE     | 303       | BY SIMILARITY.              | 1       |
| DISULFID  | 440                                 | ACT SITE     | 560       | BY SIMILARITY.              | 1       |
| DISULFID  | 611                                 | ACT SITE     | 611       | INTERCHAIN (BY SIMILARITY). | 1       |
| CARBOHYD  | 296                                 | ACT SITE     | 296       | POTENTIAL.                  | 1       |
| CARBOHYD  | 381                                 | ACT SITE     | 381       | POTENTIAL.                  | 1       |
| CARBOHYD  | 495                                 | ACT SITE     | 495       | POTENTIAL.                  | 1       |
| CARBOHYD  | 550                                 | ACT SITE     | 650       | POTENTIAL.                  | 1       |
| CARBOHYD  | 725                                 | ACT SITE     | 725       | POTENTIAL.                  | 1       |



|                       |  |                                   |            |  |
|-----------------------|--|-----------------------------------|------------|--|
| FT                    | VARIANT  | 98                                | 98         | D -> G (IN ATYPICAL FORM, DIBUCAINE-RESISTANT).      |
| FT                    | VARIANT  | 271                               | 271        | T -> M (IN FLUORIDE-1).                              |
| FT                    | VARIANT  | 358                               | 358        | L -> I (IN HYPOCHOLINESTERASEMIN).                   |
| FT                    | VARIANT  | 418                               | 418        | G -> V (IN FLUORIDE-2).                              |
| FT                    | VARIANT  | 567                               | 567        | A -> T (IN K VARIANT, WITH REDUCED ENZYME ACTIVITY). |
| FT                    | SEQUENCE   | 602 AA;                           | 68418 MW;  | /FTid=VAR_002364.                                    |
| FT                    | SEQUENCE   |                                   |            | C9836409D9057F27 CRC64;                              |
|                       |  |                                   |            |  |
| Query Match           | Score  | 62;                               | DB 1;      | Length 602;  |
| Best Local Similarity | Score  | 71.3%;                            | DB 1;      | Length 602;  |
| Matches 9;            | Local Similarity   | 64.3%;                            | Pred. No.  | 0.031;   |
|                       | Conservative   | 3;                                | Mismatches | 2;   |
|                       |  |                                   | Indels     | 0;   |
|                       |  |                                   | Gaps       |  |
| Qy                    | 1  | AEFHRWSSSYHWK                     | 14         |  |
|                       |  | :     :                           |            |  |
| Db                    | 573  | AGFHRWNNYMDWK                     | 586        |  |
|                       |  |                                   |            |  |
| RESULT                | 8  | CHLE_RABBIT                       | STANDARD;  | PRT;   |
| ID                    | CHLE_RABBIT  |                                   |            | 581 AA.  |
| AC                    | P21927;  |                                   |            |  |
| DT                    | 01-MAY-1991  | (Rel. 18, Created)                |            |  |
| DT                    | 01-MAY-1991  | (Rel. 18, Last sequence update)   |            |  |
| DT                    | 01-OCT-1996  | (Rel. 34, Last annotation update) |            |  |
| DE                    | CHOLINESTERASE PRECURSOR (EC 3.1.1.8)  | (ACYLCHOLINE ACYLHYDROLASE)       |            |  |
| DE                    | (CHOLINE ESTERASE II)  | (BUTYRYLCHOLINE ESTERASE)         |            |  |
| DE                    | (PSEUDOCHOLINESTERASE).  |                                   |            |  |
| GN                    | BCHE.  |                                   |            |  |
| OS                    | Oryctolagus cuniculus (Rabbit).  |                                   |            |  |
| OC                    | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  |                                   |            |  |
| OC                    | Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  |                                   |            |  |
| RN                    | [1]  | SEQUENCE FROM N.A.                |            |  |
| RP                    | STRAN=LAGOMORHA;   |                                   |            |  |
| RC                    | RCNOMORHA;   |                                   |            |  |
| RX                    | MEDLINE: 90326526.   |                                   |            |  |
| RA                    | Arpagaus M., Chatonnet A., Masson P., Newton M., Vaughan T.A., Bartels C.F., Nogueira C.P., Du B.N., Lockridge O.;   |                                   |            |  |
| RA                    | Use of the polymerase chain reaction for homology probing of butyrylcholinesterase from several vertebrates.; J. Biol. Chem. 266:6966-6974(1991).  |                                   |            |  |
| RT                    | -1- CATALYTIC ACTIVITY: AN ACYLCHOLINE + H2O = CHOLINE + A CARBOXYLIC ACID ANION.  |                                   |            |  |
| RT                    | "Complete" sequence of rabbit butyrylcholinesterase. ; Nucleic Acids Res. 18:3990-3990(1990).  |                                   |            |  |
| RL                    | [2]  | SEQUENCE OF 75-215 FROM N.A.      |            |  |
| RN                    | SEQUENCE OF 75-215 FROM N.A.   |                                   |            |  |
| RP                    | TISSUE-LIVER;  |                                   |            |  |
| RC                    | MEDLINE: 91201348.   |                                   |            |  |
| RX                    | Arpagaus M., Chatonnet A., Masson P., Newton M., Vaughan T.A., Bartels C.F., Nogueira C.P., Du B.N., Lockridge O.;   |                                   |            |  |
| RA                    | Use of the polymerase chain reaction for homology probing of butyrylcholinesterase from several vertebrates.; J. Biol. Chem. 266:6966-6974(1991).  |                                   |            |  |
| RT                    | -1- SUBUNIT: HOMOTRIMER. THE TERRAMER IS COMPOSED OF TWO DIMERS. THE TWO SUBUNITS IN A DIMER ARE LINKED BY A DISULFIDE BOND.   |                                   |            |  |
| CC                    | -1- TISSUE SPECIFICITY: PRESENT IN MOST CELLS EXCEPT ERYTHROCYTES.   |                                   |            |  |
| CC                    | -1- MISCELLANEOUS: CHOLINESTERASE IS HIGHLY REACTIVE WITH ORGANOPHOSPHATE ESTERS.  |                                   |            |  |
| CC                    | -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  |                                   |            |  |
| CC                    |  |                                   |            |  |
| CC                    | This SWISS-PROT entry is copyright. It is produced through a collaborative   |                                   |            |  |
| CC                    | between the Swiss Institute of Bioinformatics and the EMBL Outstation  |                                   |            |  |
| CC                    | the European Bioinformatics Institute. There are no restrictions on  |                                   |            |  |
| CC                    | use by non-profit institutions as long as its content is in no   |                                   |            |  |
| CC                    | modified and this statement is not removed. Usage by and for commercial  |                                   |            |  |
| CC                    | entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce">http://www.isb-sib.ch/announce</a> or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ). |                                   |            |  |
| CC                    | EMBL: X52090; CAA36308; 1; -   |                                   |            |  |
| CC                    | DR   |                                   |            |  |

```

Query Match      70.1%; Score 61; DB 1; Length 581;
Best Local Similarity   64.3%; Pred. No. 0.042;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
PRT: 603 AA.

RESULT 9
HOMO_SAPIENS_HUMAN_MOUSE STANDARD; PRT: 603 AA.
ID Q03311; AC Q03311; DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE CHOLINESTERASE PRECURSOR (EC 3.1.1.8) (ACYLCHOLINE ACYLHYDROLASE)
DE (CHOLINE ESTERASE II) (BUTYRYLCHOLINE ESTERASE)
DE (PSUEDOCHOLINESTERASE).
DE BCHE.
DE Mus musculus (Mouse).
DE Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1] SEQUENCE FROM N.A.
MEDLINE: 90380429.
Rachinsky T.L., Camp S., Li Y., Ekstroem T.J., Newton M., Taylor P.:
"Molecular cloning of mouse acetylcholinesterase: tissue distribution
of alternatively spliced mRNA species.";
Neuron 5:317-327(1990).

[2] SEQUENCE OF 97-237 FROM N.A.
TISSUE-LIVER;
MEDLINE: 91201348.
Arpaoglu M., Chatonnet A., Masson P., Newton M., Vaughan T.A.,
Bartels C.F., Nogueira C.P., la Du B.N., Lockridge O.:
"Use of the polymerase chain reaction for homology probing of
butyrylcholinesterase from several vertebrates.";
J. Biol. Chem. 266:6966-6974(1991).

-1 - CATALYTIC ACTIVITY: AN ACYLCHOLINE + H(2)O = CHOLINE + A
C CARBOXYLIC ACID ANTON.
CC

```

CC -!- SUBUNIT: HOMOTETRAMER. THE TETRAMER IS COMPOSED  
CC OF TWO DIMERS. THE TWO SUBUNITS IN A DIMER ARE LINKED BY A  
CC DISULFIDE BOND.  
CC -!- TISSUE SPECIFICITY: PRESENT IN MOST CELLS (EXCEPT ERYTHROCYTES).  
CC -!- MISCELLANEOUS: CHOLINESTERASE IS HIGHLY REACTIVE WITH  
CC ANGLOPHOSPHATE ESTERS.  
CC -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.

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CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/  
CC or send an email to license@isb-sib.ch).  
CC

DR EMBL; M99492; AAA37328; 1; - .  
DR PIR; A39768; A39768.  
DR HSSP; P21836; IMAH.  
DR MGDB; MGDB:894278; BCHE.  
DR PFAM; PF00335; COOesterase; 1.  
DR PRINTS; PR00878; CHOLINESTERASE.  
DR PROSITE; PS00122; CARBOXYLESTERASE\_B; 1; 1.  
DR PROSITE; PS00941; CARBOXYLESTERASE\_B; 2; 1.  
KW Hydrolase; Serine esterase; Glycoprotein; Signal1.  
SQ SIGNAL 1 29

FT CHAIN 1 30 CHOLINESTERASE.  
FT ACT\_SITE 227 603  
FT ACT\_SITE 354 227 BY SIMILARITY.  
FT ACT\_SITE 467 354 BY SIMILARITY.  
FT DISULFID 94 467 BY SIMILARITY.  
FT DISULFID 281 121 BY SIMILARITY.  
FT DISULFID 429 292 BY SIMILARITY.  
FT DISULFID 600 548 BY SIMILARITY.  
FT CARBOHD 86 600 INTERCHAIN (BY SIMILARITY).  
FT CARBOHD 135 86 POTENTIAL.  
FT CARBOHD 270 135 POTENTIAL.  
FT CARBOHD 370 270 POTENTIAL.  
FT CARBOHD 484 135 POTENTIAL.  
FT CARBOHD 510 510 POTENTIAL.  
FT CARBOHD 515 515 POTENTIAL.  
FT CONFLICT 129 515 R > P (IN REF. 2)  
SQ SEQUENCE 603 AA; 68521 MW; R > P (IN REF. 2) CRC64;

Query Match 70.1%; Score 61; DB 1; Length 603;  
Best Local Similarity 64.3%; Pred. No. 0.043; Indels 0; Gaps 0;  
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AFHRSSYMYHWK 14  
Db 574 AGFHRNSNYMDWQ 587

RESULT 10

NC\_ ARATH STANDARD; PRT; 746 AA.  
AC P56752; CC thaliana.";  
DR 15-FEB-2000 (Rel. 39, Created)  
DR 15-FEB-2000 (Rel. 39, Last sequence update)  
DR 15-FEB-2000 (Rel. 39, Last annotation update)  
DE NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 5, CHLOROPLAST (EC 1.6.5.3).  
GN Arabidopsis thaliana (Mouse-ear cress).  
OS Chloroplast.  
OC Eukaryota; Viriplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Magnoliophyta; eudicotyledons; Rosidae; eurosids II; Brassicales;  
OC Brassicaceae; Arabidopsis.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV\_COLUMNA;  
RA "Complete structure of the chloroplast genome of Arabidopsis

RT thaliana.";  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
CC -!- CATALYTIC ACTIVITY: NADH + PLASTOQUINONE = NAD(+) + PLASTOQUINOL.  
CC

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CC

DR EMBL; AP00423; BAA84434; 1;  
KW Oxidoreductase; NAD; Plastoquinone; Chloroplast.  
SEQUENCE 746 AA; 85238 MW; 1391A787EE729 CRC64;

Query Match 50.6%; Score 44; DB 1; Length 746;  
Best Local Similarity 41.7%; Pred. No. 17;  
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 3 FHRSSYMYHWK 14  
Db 640 FQKWNNSKRHWE 651

RESULT 11

SMP3\_YEAST STANDARD; PRT; 516 AA.  
ID SMP3\_YEAST  
AC Q04174; Q99400;  
DT 01-OCT-1993 (Rel. 27, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)

OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomyces.  
RN [1]  
RP SEQUENCE FROM N.A.  
RN STRAIN=NBWS5;  
RX MEDLINE; 9117215.  
RA Irie K., Araki H., Oshima Y.;  
RA Tarassov I.A., Winsor B., Martin R.P.;  
RT "Mutations in a Saccharomyces cerevisiae host showing increased  
RT holding stability of the heterologous plasmid PSR1.";  
RL Mol. Gen. Genet. 225:257-265 (1991).

RNA SEQUENCE FROM N.A.  
RC STRAIN=S288C / FY1678;  
RA Ayadi A., Bardoune R., Camasses A., Madania A., Poch O.,  
RA Tarassov I.A., Winsor B., Martin R.P.;  
RT Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: ESSENTIAL PROTEIN INVOLVED IN PLASMID MAINTENANCE WITH  
CC SMP2.  
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  
CC -!- SIMILARITY: TO S\_POMBE SPAC4G\_12C.  
CC

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DR EMBL; X58123; CAA41123; 1;  
DR U55020; AAC49635; 1;  
DR 275057; CA99355; 1;  
DR PIR; S13750; S13750.  
DR SGD; L000193; SMP3.  
KW Transmembrane.  
FT TRANSMEM 6 26  
FT TRANSMEM 61 81 POTENTIAL.  
POTENTIAL.  
POTENTIAL.

|                       |  |              |   |            |             |  |          |
|-----------------------|--|--------------|---|------------|-------------|--|----------|
| FT                    | TRANSMEM   | 176          | 196   | POTENTIAL. | DR          | PF01069; Desaturase; 1.  |          |
| FT                    | TRANSMEM   | 211          | 291   | POTENTIAL. | DR          | PF00173; heme_1.   |          |
| FT                    | TRANSMEM   | 271          | 316   | POTENTIAL. | DR          | PRINTS; PS0007; FADDSSATRASE.                                    |          |
| FT                    | TRANSMEM   | 296          | 338   | POTENTIAL. | DR          | PROSITE; PS00476; FATTY_ACID_DESATUR_1; 1.                       |          |
| FT                    | TRANSMEM   | 318          | 369   | POTENTIAL. | KW          | Oxidoreductase; Fatty acid biosynthesis; Multigene family; Iron; |          |
| FT                    | TRANSMEM   | 349          | 123   | POTENTIAL. | KW          | Transmembrane; Endoplasmic reticulum.                            |          |
| FT                    | CONFLICT   | 122          | MQ -> IK (IN REF. 1).   | POTENTIAL. | FT          | TRANSMEM   |          |
| FT                    | CONFLICT   | 163          | E -> G (IN REF. 1).   | POTENTIAL. | FT          | TRANSMEM   |          |
| FT                    | CONFLICT   | 169          | S -> R (IN REF. 1).   | POTENTIAL. | FT          | TRANSMEM   |          |
| FT                    | CONFLICT   | 279          | v -> L (IN REF. 1).   | POTENTIAL. | FT          | TRANSMEM   |          |
| SQ                    | SEQUENCE   | 516 AA;      | 59900 MW;   | 276        | POTENTIAL.  | FT   | TRANSMEM |
| SQ                    | SEQUENCE   | 516 AA;      | 8D8404622CB69534  | CRC64;     | POTENTIAL.  | FT   | TRANSMEM |
| Query Match           |  | 49.4%        | Score 43;   | DB 1;      | Length 516; | L -> M (IN REF. 1).  |          |
| Best Local Similarity |  | 66.7%        | Score 43;   | DB 1;      | Length 516; | 504 MN;  |          |
| Matches               | 6;   | Conservative | Pred. No. 17;   | Indels     | 0;          | AGCC78DD4210ECA CRC64;   |          |
| Qy                    | 6 WSTMVHWK 14  |              |   |            |             |  |          |
| Db                    | 204 WKFYFIRVHWK 212  |              |   |            |             |  |          |
| RESULT 12             |  |              |   |            |             |  |          |
| ACO1_YEAST            | STANDARD;  | PRT;         | 510 AA.   |            |             |  |          |
| ID                    | P21147;  |              |   |            |             |  |          |
| AC                    |  |              |   |            |             |  |          |
| DT                    | 01-MAY-1991 (Rel. 18, Created)   |              |   |            |             |  |          |
| DT                    | 01-OCT-1996 (Rel. 34, Last sequence update)  | YEG24_YEAST  | STANDARD;   | PRT;       | 245 AA.     |  |          |
| DT                    | 15-JUL-1998 (Rel. 36, Last annotation update)  | ID           | YG24-1_YEAST  |            |             |  |          |
| DE                    | ACYL-COA DESATURASE 1 (EC 1.14.99.5) (STEAROYL-COA DESATURASE 1)   | AC           | P53247;   |            |             |  |          |
| DE                    | (FATTY ACID DESATURASE 1).   |              | 01-OCT-1996 (Rel. 34, Created)  |            |             |  |          |
| GN                    | OLE1 OR YGL05W.  |              | 01-OCT-1996 (Rel. 34, Last annotation update)   |            |             |  |          |
| OS                    | Saccharomyces cerevisiae (Baker's yeast).  |              | 15-DEC-1998 (Rel. 37, Last annotation update)   |            |             |  |          |
| OC                    | Saccharomyces cerevisiae (Baker's yeast).  |              | DE HYPOTHETICAL 28.6 KDA PROTEIN IN MUP1-SPR3 INTERGENIC REGION.  |            |             |  |          |
| OC                    | Eukaryota; Ascomycota; Saccharomycetes; Saccharomyctetes; Saccharomyces.   |              | CN YG057C.  |            |             |  |          |
| OC                    | Saccharomyctaceae; Saccharomyces.  |              | OS Saccharomyces cerevisiae (Baker's yeast).  |            |             |  |          |
| OC                    |  |              | RA Entian K. D., Rose M., Koetter P., Roehmer A., Sehrsam I.,   |            |             |  |          |
| RN                    | [1]  |              | RA Hempel S.; Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.  |            |             |  |          |
| RX                    | SEQUENCE FROM N.A.   |              |   |            |             |  |          |
| RP                    | SEQUENCE FROM N.A.   |              |   |            |             |  |          |
| RT                    | Stukey J. E., McDonough V.M., Martin C.E.; "The OLE1 gene of Saccharomyces cerevisiae encodes the delta 9 fatty acid desaturase and can be functionally replaced by the rat stearoyl-CoA desaturase gene." |              | CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -   |            |             |  |          |
| RT                    | J. Biol. Chem. 265:20144-20149(1990).  |              | CC the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch). |            |             |  |          |
| RN                    | [2]  |              | CC  |            |             |  |          |
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| RC                    | STRAIN=S288C;  |              | CC the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch). |            |             |  |          |
| RX                    | MEDLINE: 97377993.   |              | CC  |            |             |  |          |
| RA                    | "Feuermann M., de Montigny J., Potier S., Souciet J.-L.; The characterization of two new clusters of duplicated genes suggests a 'Lego' organization of the yeast Saccharomyces cerevisiae chromosomes."   |              | CC  |            |             |  |          |
| RL                    | Yeast 13:861-869(1997).  |              | CC  |            |             |  |          |
| RN                    | -1 - CATALYTIC ACTIVITY: STEAROYL-COA + AH(2) + O(2) = OLEOYL-COA + A  |              | CC  |            |             |  |          |
| CC                    | + 2 (H(2))O.   |              | CC AND/OR BE INVOLVED IN METAL ION BINDING.   |            |             |  |          |
| CC                    | -1 - COFACTOR: IRON.   |              | CC -1 - SIMILARITY: TO OTHER FATTY ACID DESATURASES.  |            |             |  |          |
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| CC                    | SEQUENCE FROM N.A.   |              | CC  |            |             |  |          |
| CC                    | STRAIN=S288C;  |              | CC  |            |             |  |          |
| CC                    | MEDLINE: 97377993.   |              | CC  |            |             |  |          |
| CC                    | "Feuermann M., de Montigny J., Potier S., Souciet J.-L.; The characterization of two new clusters of duplicated genes suggests a 'Lego' organization of the yeast Saccharomyces cerevisiae chromosomes."   |              | CC  |            |             |  |          |
| CC                    | Yeast 13:861-869(1997).  |              | CC  |            |             |  |          |
| CC                    | -1 - CATALYTIC ACTIVITY: STEAROYL-COA + AH(2) + O(2) = OLEOYL-COA + A  |              | CC  |            |             |  |          |
| CC                    | + 2 (H(2))O.   |              | CC AND/OR BE INVOLVED IN METAL ION BINDING.   |            |             |  |          |
| CC                    | -1 - COFACTOR: IRON.   |              | CC -1 - SIMILARITY: TO OTHER FATTY ACID DESATURASES.  |            |             |  |          |
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| CC                    | -1 - SIMILARITY: TO OTHER FATTY ACID DESATURASES.  |              | CC  |            |             |  |          |
| CC                    | SEQUENCE FROM N.A.   |              | CC  |            |             |  |          |
| CC                    | STRAIN=S288C;  |              | CC  |            |             |  |          |
| CC                    | MEDLINE: 97377993.   |              | CC  |            |             |  |          |
| CC                    | "Feuermann M., de Montigny J., Potier S., Souciet J.-L.; The characterization of two new clusters of duplicated genes suggests a 'Lego' organization of the yeast Saccharomyces cerevisiae chromosomes."   |              | CC  |            |             |  |          |
| CC                    | Yeast 13:861-869(1997).  |              | CC  |            |             |  |          |
| CC                    | -1 - CATALYTIC ACTIVITY: STEAROYL-COA + AH(2) + O(2) = OLEOYL-COA + A  |              | CC  |            |             |  |          |
| CC                    | + 2 (H(2))O.   |              | CC AND/OR BE INVOLVED IN METAL ION BINDING.   |            |             |  |          |
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| CC                    | SEQUENCE FROM N.A.   |              | CC  |            |             |  |          |
| CC                    | STRAIN=S288C;  |              | CC  |            |             |  |          |
| CC                    | MEDLINE: 97377993.   |              | CC  |            |             |  |          |
| CC                    | "Feuermann M., de Montigny J., Potier S., Souciet J.-L.; The characterization of two new clusters of duplicated genes suggests a 'Lego' organization of the yeast Saccharomyces cerevisiae chromosomes."   |              | CC  |            |             |  |          |
| CC                    | Yeast 13:861-869(1997).  |              | CC  |            |             |  |          |
| CC                    | -1 - CATALYTIC ACTIVITY: STEAROYL-COA + AH(2) + O(2) = OLEOYL-COA + A  |              | CC  |            |             |  |          |
| CC                    | + 2 (H(2))O.   |              | CC AND/OR BE INVOLVED IN METAL ION BINDING.   |            |             |  |          |
| CC                    | -1 - COFACTOR: IRON.   |              | CC -1 - SIMILARITY: TO OTHER FATTY ACID DESATURASES.  |            |             |  |          |
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| CC                    | -1 - SIMILARITY: TO OTHER FATTY ACID DESATURASES.  |              | CC  |            |             |  |          |
| CC                    | SEQUENCE FROM N.A.   |              | CC  |            |             |  |          |
| CC                    | STRAIN=S288C;  |              | CC  |            |             |  |          |
| CC                    | MEDLINE: 97377993.   |              | CC  |            |             |  |          |
| CC                    | "Feuermann M., de Montigny J., Potier S., Souciet J.-L.; The characterization of two new clusters of duplicated genes suggests a 'Lego' organization of the yeast Saccharomyces cerevisiae chromosomes."   |              | CC  |            |             |  |          |
| CC                    | Yeast 13:861-869(1997).  |              | CC  |            |             |  |          |
| CC                    | -1 - CATALYTIC ACTIVITY: STEAROYL-COA + AH(2) + O(2) = OLEOYL-COA + A  |              | CC  |            |             |  |          |
| CC                    | + 2 (H(2))O.   |              | CC AND/OR BE INVOLVED IN METAL ION BINDING.   |            |             |  |          |
| CC                    | -1 - COFACTOR: IRON.   |              | CC -1 - SIMILARITY: TO OTHER FATTY ACID DESATURASES.  |            |             |  |          |
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| CC                    | -1 - SIMILARITY: TO OTHER FATTY ACID DESATURASES.  |              | CC  |            |             |  |          |
| CC                    | SEQUENCE FROM N.A.   |              | CC  |            |             |  |          |
| CC                    | STRAIN=S288C;  |              | CC  |            |             |  |          |
| CC                    | MEDLINE: 97377993.   |              | CC  |            |             |  |          |
| CC                    | "Feuermann M., de Montigny J., Potier S., Souciet J.-L.; The characterization of two new clusters of duplicated genes suggests a 'Lego' organization of the yeast Saccharomyces cerevisiae chromosomes."   |              | CC  |            |             |  |          |
| CC                    | Yeast 13:861-869(1997).  |              | CC  |            |             |  |          |
| CC                    | -1 - CATALYTIC ACTIVITY: STEAROYL-COA + AH(2) + O(2) = OLEOYL-COA + A  |              | CC  |            |             |  |          |
| CC                    | + 2 (H(2))O.   |              | CC AND/OR BE INVOLVED IN METAL ION BINDING.   |            |             |  |          |
| CC                    | -1 - COFACTOR: IRON.   |              | CC -1 - SIMILARITY: TO OTHER FATTY ACID DESATURASES.  |            |             |  |          |
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| CC                    | -1 - SIMILARITY: TO OTHER FATTY ACID DESATURASES.  |              | CC  |            |             |  |          |
| CC                    | SEQUENCE FROM N.A.   |              | CC  |            |             |  |          |
| CC                    | STRAIN=S288C;  |              | CC  |            |             |  |          |
| CC                    | MEDLINE: 97377993.   |              | CC  |            |             |  |          |
| CC                    | "Feuermann M., de Montigny J., Potier S., Souciet J.-L.; The characterization of two new clusters of duplicated genes suggests a 'Lego' organization of the yeast Saccharomyces cerevisiae chromosomes."   |              | CC  |            |             |  |          |
| CC                    | Yeast 13:861-869(1997).  |              | CC  |            |             |  |          |
| CC                    | -1 - CATALYTIC ACTIVITY: STEAROYL-COA + AH(2) + O(2) = OLEOYL-COA + A  |              | CC  |            |             |  |          |
| CC                    | + 2 (H(2))O.   |              | CC AND/OR BE INVOLVED IN METAL ION BINDING.   |            |             |  |          |
| CC                    | -1 - COFACTOR: IRON.   |              | CC -1 - SIMILARITY: TO OTHER FATTY ACID DESATURASES.  |            |             |  |          |
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| CC                    | -1 - SIMILARITY: TO OTHER FATTY ACID DESATURASES.  |              | CC  |            |             |  |          |
| CC                    | SEQUENCE FROM N.A.   |              | CC  |            |             |  |          |
| CC                    | STRAIN=S288C;  |              | CC  |            |             |  |          |
| CC                    | MEDLINE: 97377993.   |              | CC  |            |             |  |          |
| CC                    | "Feuermann M., de Montigny J., Potier S., Souciet J.-L.; The characterization of two new clusters of duplicated genes suggests a 'Lego' organization of the yeast Saccharomyces cerevisiae chromosomes."   |              | CC  |            |             |  |          |
| CC                    | Yeast 13:861-869(1997).  |              | CC  |            |             |  |          |
| CC                    | -1 - CATALYTIC ACTIVITY: STEAROYL-COA + AH(2) + O(2) = OLEOYL-COA + A  |              | CC  |            |             |  |          |
| CC                    | + 2 (H(2))O.   |              | CC AND/OR BE INVOLVED IN METAL ION BINDING.   |            |             |  |          |
| CC                    | -1 - COFACTOR: IRON.   |              | CC -1 - SIMILARITY: TO OTHER FATTY ACID DESATURASES.  |            |             |  |          |
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| CC                    | -1 - SIMILARITY: TO OTHER FATTY ACID DESATURASES.  |              | CC  |            |             |  |          |
| CC                    | SEQUENCE FROM N.A.   |              | CC  |            |             |  |          |
| CC                    | STRAIN=S288C;  |              | CC  |            |             |  |          |
| CC                    | MEDLINE: 97377993.   |              | CC  |            |             |  |          |
| CC                    | "Feuermann M., de Montigny J., Potier S., Souciet J.-L.; The characterization of two new clusters of duplicated genes suggests a 'Lego' organization of the yeast Saccharomyces cerevisiae chromosomes."   |              | CC  |            |             |  |          |
| CC                    | Yeast 13:861-869(1997).  |              | CC  |            |             |  |          |
| CC                    | -1 - CATALYTIC ACTIVITY: STEAROYL-COA + AH(2) + O(2) = OLEOYL-COA + A  |              | CC  |            |             |  |          |
| CC                    | + 2 (H(2))O.   |              | CC AND/OR BE INVOLVED IN METAL ION BINDING.   |            |             |  |          |
| CC                    | -1 - COFACTOR: IRON.   |              | CC -1 - SIMILARITY: TO OTHER FATTY ACID DESATURASES.  |            |             |  |          |
| CC                    | -1 - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. ENDOPLASMIC RETICULUM (PROBABLE).  |              | CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -   |            |             |  |          |
| CC                    | -1 - DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE.  |              | CC the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch). |            |             |  |          |
| CC                    | AND/OR BE INVOLVED IN METAL ION BINDING.   |              | CC  |            |             |  |          |
| CC                    | -1 - SIMILARITY: TO OTHER FATTY ACID DESATURASES.  |              | CC  |            |             |  |          |
| CC                    | SEQUENCE FROM N.A.   |              | CC  |            |             |  |          |
| CC                    | STRAIN=S288C;  |              | CC  |            |             |  |          |
| CC                    | MEDLINE: 97377993.   |              | CC  |            |             |  |          |
| CC                    | "Feuermann M., de Montigny J., Potier S., Souciet J.-L.; The characterization of two new clusters of duplicated genes suggests a 'Lego' organization of the yeast Saccharomyces cerevisiae chromosomes."   |              | CC  |            |             |  |          |
| CC                    | Yeast 13:861-869(1997).  |              | CC  |            |             |  |          |
| CC                    | -1 - CATALYTIC ACTIVITY: STEAROYL-COA + AH(2) + O(2) = OLEOYL-COA + A  |              | CC  |            |             |  |          |
| CC                    | + 2 (H(2))O.   |              | CC AND/OR BE INVOLVED IN METAL ION BINDING.   |            |             |  |          |
| CC                    | -1 - COFACTOR: IRON.   |              | CC -1 - SIMILARITY: TO OTHER FATTY ACID DESATURASES.  |            |             |  |          |
| CC                    | -1 - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. ENDOPLASMIC RETICULUM (PROBABLE).  |              | CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -   |            |             |  |          |
| CC                    | -1 - DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE.  |              | CC the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch). |            |             |  |          |
| CC                    | AND/OR BE INVOLVED IN METAL ION BINDING.   |              | CC  |            |             |  |          |
| CC                    | -1 - SIMILARITY: TO OTHER FATTY ACID DESATURASES.  |              | CC  |            |             |  |          |
| CC                    | SEQUENCE FROM N.A.   |              | CC  |            |             |  |          |
| CC                    | STRAIN=S288C;  |              | CC  |            |             |  |          |
| CC                    | MEDLINE: 97377993.   |              | CC  |            |             |  |          |
| CC                    | "Feuermann M., de Montigny J., Potier S., Souciet J.-L.; The characterization of two new clusters of duplicated genes suggests a 'Lego' organization of the yeast Saccharomyces cerevisiae chromosomes."   |              | CC  |            |             |  |          |
| CC                    | Yeast 13:861-869(1997).  |              | CC  |            |             |  |          |
| CC                    | -1 - CATALYTIC ACTIVITY: STEAROYL-COA + AH(2) + O(2) = OLEOYL-COA + A  |              | CC  |            |             |  |          |
| CC                    | + 2 (H(2))O.   |              | CC AND/OR BE INVOLVED IN METAL ION BINDING.   |            |             |  |          |
| CC                    | -1 - COFACTOR: IRON.   |              | CC -1 - SIMILARITY: TO OTHER FATTY ACID DESATURASES.  |            |             |  |          |
| CC                    | -1 - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. ENDOPLASMIC RETICULUM (PROBABLE).</td  |              |   |            |             |  |          |

15-FEB-2000 (Rel. 39, Last annotation update)  
DE RNA-DIRECTED RNA POLYMERASE SUBUNIT P2 (EC 2.7.7.48) (POLYMERASE  
DE ACIDIC PROTEIN) (PA).  
OS Influenza A virus (strain A/Equine/Tennessee/5/86),  
OC viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenza virus A and B group.  
RN SEQUENCE FROM N.A.  
RP MEDLINE: 90021190.  
RA Okazaki K., Kawada Y., Webster R.G.;  
RA "Evolutionary pathways of the PA genes of influenza A viruses.",;  
RJ Virology 172:601-608(1989).  
CC -1- SUBUNIT: INFLUENZA RNA POLYMERASE IS COMPOSED OF THREE SUBUNITS:  
CC P1 (OR PB1), P2 (OR PA), AND P3 (OR PB2).  
CC -1- SIMILARITY: BELONGS TO THE INFLUENZA VIRUS POLYMERASE PA FAMILY.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and thus statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to license@isb-sib.ch).  
CC DR EMBL: M26082; AA043113.1; -.  
CC DR PFAM: PF00603; Flu\_PA\_1.  
RN Transferase; RNA-directed RNA polymerase.  
SQ SEQUENCE 716 AA; 82724 MW; 9922E3E3995B0C96 CRC64;

Query Match Similarity 46.0% Score 40; DB 1; Length 716;  
Best Local Similarity 54.5% Pred. No. 65;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 EPHRWSSYMH 12  
Db 533 EPHKWEKYCVH 543

RESULT 15  
YCX7\_CHLRE ID YCX7\_CHLRE STANDARD; PRTR; 1995 AA.  
AC P36495; Q37303;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE 232.2 KDA PROTEIN (ORF1995) (ORF-S) (ORFA).  
OS Chlamydomonas reinhardtii.  
OG Chloroplast.  
OC Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;  
OC Chlamydomonadae; Chlamydomonas.  
RN [1] Submitted (DEC-1993) to the EMBL/GenBank/DDBJ databases.  
RN [2] SEQUENCE FROM N.A.  
RN [3] SEQUENCE OF 1925-1995 FROM N.A.

RX MEDLINE: 9721803B.  
RA Boudreau E., Turmel M., Goldschmidt-Clermont M., Rochaix J.-D.,  
RA Sivan S., Michaels A., Leu S.;  
RA "A large open reading frame (orf1995) in the chloroplast DNA of  
RR Chlamydomonas reinhardtii encodes an essential protein.",;  
RL Mol. Gen. Genet. 253:649-653(1997).  
RN [2] SEQUENCE OF 1573-1995 FROM N.A.  
RC Sivan S., Michaels A.;  
RN Submitted (DEC-1993) to the EMBL/GenBank/DDBJ databases.  
RN [3] SEQUENCE OF 1925-1995 FROM N.A.  
RX MEDLINE: 87031585.  
RA Woessner J.P., Gilham N.W., Boynton J.B.;  
RT "The sequence of the chloroplast atpB gene and its flanking regions  
RT in Chlamydomonas reinhardtii.",;  
RN Gene 44:17-28(1986).  
RN [4] PARTIAL SEQUENCE FROM N.A.

RX MEDLINE: 94207185.  
RA Boudreau E., Otis C., Turmel M.;  
RA "Conserved gene clusters in the highly rearranged chloroplast genomes  
RR of Chlamydomonas moewusii and Chlamydomonas reinhardtii.",;  
RL Plant Mol. Biol. 24:585-602(1994).  
CC -1- FUNCTION: ESSENTIAL FOR CELL GROWTH. MAY BE INVOLVED IN BINDING  
CC CHLOROPLAST DNA TO EITHER THE CHLOROPLAST ENVELOPE OR THE  
CC THYLAKOID MEMBRANE.  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  
CC -1- SIMILARITY: TO C.vulgaris ORF811.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and thus statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to license@isb-sib.ch).  
CC DR EMBL: X92726; CAA63385.1; -.  
CC DR EMBL: X76936; CA854257.1; -.  
CC DR EMBL: X41289; S41289.  
CC KW Chloroplast; Transmembrane.  
CC FT TRANSMEM 31 51  
CC FT TRANSMEM 53 73  
CC FT TRANSMEM 106 126  
CC FT TRANSMEM 157 177  
CC FT TRANSMEM 212 232  
CC FT TRANSMEM 254 274  
CC FT TRANSMEM 307 327  
CC FT CONFLICT 1588 1588  
SQ SEQUENCE 1995 AA; 232194 MW; E5A3F167EA5FC8A CRC64;  
CC Query Match Similarity 46.0%; Score 40; DB 1; Length 1995;  
CC Best Local Similarity 60.0%; Prod. No. 1.e+02;  
CC Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 RNSSYMMVHK 14  
Db 882 RWRYTMYQHYK 891

Search completed: September 13, 2000, 02:24:31  
Job time: 169 sec



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## OM protein - protein search, using sw model

Run on: September 13, 2000, 02:22:37 ; Search time 14.59 Seconds  
(without alignments)  
14.709 Million cell updates/sec

Title: US-09-155-076-1  
Perfect score: 14  
Sequence: 1 AEFHRWSYMWK 14  
Scoring table: OLIGO Gapext 60.0 , Gapext 60.0  
Searched: 152396 seqs, 15329161 residues  
Word size : 0

Total number of hits satisfying chosen parameters: 152396

Minimum DB seq length: 0  
Maximum DB seq length: 1000000

## Post-processing: Listing first 45 summaries

Database : Issued Patents AA:  
1: /cgns\_6/ptodata/2/iaa/5A.COMB.pep:  
2: /cgns\_6/ptodata/2/iaa/6.COMB.pep:  
3: /cgns\_6/ptodata/2/iaa/6.PCTUS.COMB.pep:  
4: /cgns\_6/ptodata/2/iaa/backfile1.1.pep:  
5: /cgns\_6/ptodata/2/iaa/backfile1.1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query | Match | Length | DB ID              | Description         |
|------------|-------|-------|-------|--------|--------------------|---------------------|
| 1          | 14    | 100.0 | 40    | 2      | US-08-370-156-25   | Sequence 7, Appli   |
| 2          | 14    | 100.0 | 45    | 2      | US-08-370-156-7    | Sequence 8, Appli   |
| 3          | 14    | 100.0 | 45    | 2      | US-08-370-156-8    | Sequence 2, Appli   |
| 4          | 14    | 100.0 | 614   | 1      | US-07-132-922A-2   | Sequence 2, Appli   |
| 5          | 14    | 100.0 | 614   | 2      | US-08-370-156-2    | Sequence 19, Appli  |
| 6          | 14    | 100.0 | 614   | 3      | US-08-346-100-19   | Sequence 21, Appli  |
| 7          | 14    | 100.0 | 614   | 3      | US-08-346-100-20   | Sequence 22, Appli  |
| 8          | 14    | 100.0 | 614   | 3      | US-08-346-100-21   | Sequence 23, Appli  |
| 9          | 14    | 100.0 | 614   | 3      | US-08-346-100-22   | Sequence 24, Appli  |
| 10         | 14    | 100.0 | 614   | 3      | US-08-346-100-23   | Sequence 25, Appli  |
| 11         | 14    | 100.0 | 614   | 3      | US-08-346-100-25   | Sequence 2, Appli   |
| 12         | 14    | 100.0 | 614   | 3      | US-08-314-05-2     | Sequence 66, Appli  |
| 13         | 14    | 100.0 | 614   | 4      | PCT-82-061-06-2    | Sequence 66, Appli  |
| 14         | 9     | 64.3  | 575   | 1      | US-08-348-920-1    | Sequence 1, Appli   |
| 15         | 9     | 64.3  | 575   | 1      | US-08-348-920-2    | Sequence 2, Appli   |
| 16         | 4     | 28.6  | 10    | 2      | US-08-334-222-66   | Sequence 66, Appli  |
| 17         | 4     | 28.6  | 13    | 2      | US-08-933-40-66    | Sequence 66, Appli  |
| 18         | 4     | 28.6  | 13    | 2      | US-09-207-621-66   | Sequence 66, Appli  |
| 19         | 4     | 28.6  | 13    | 2      | US-08-532-818-66   | Sequence 66, Appli  |
| 20         | 4     | 28.6  | 15    | 1      | US-08-551-128A-1   | Sequence 1, Appli   |
| 21         | 4     | 28.6  | 15    | 1      | US-08-551-128A-2   | Sequence 2, Appli   |
| 22         | 4     | 28.6  | 15    | 1      | US-08-133-271-5    | Sequence 145, Appli |
| 23         | 4     | 28.6  | 15    | 1      | US-08-220-788A-179 | Sequence 179, Appli |
| 24         | 4     | 28.6  | 20    | 1      | US-08-844-844A-3   | Sequence 3, Appli   |
| 25         | 4     | 28.6  | 21    | 1      | US-08-384-211-4    | Sequence 4, Appli   |
| 26         | 4     | 28.6  | 27    | 2      | US-08-739-819-4    | Sequence 4, Appli   |
| 27         | 4     | 28.6  | 32    | 3      | US-08-954-915A-18  | Sequence 5, Appli   |

## ALIGNMENTS

RESULT 1  
US-08-370-156-25

; Sequence 25, Application US/08370156  
; Patent No. 5932710

; GENERAL INFORMATION:  
; APPLICANT: Zakut, Haim  
; APPLICANT: Shani, Moshe  
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR  
; ANTIACOHOLINESTERASE SUBSTANCES  
; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Reising, Ethington, Barnard & Perry  
; STREET: P.O. Box 4390  
; CITY: Troy  
; STATE: Michigan  
; COUNTRY: US  
; ZIP: 48099

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/370-156  
; FILING DATE:  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kohn, Kenneth I.  
; REGISTRATION NUMBER: 30,955  
; REFERENCE/DOCKET NUMBER: P-307 (Mulford)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (810) 689-3500  
; TELEFAX: (810) 689-4071  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

Query Match Best Local Similarity Matches 14; Conservativeness 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 AEFHRWSYMWK 14  
Db 12 AEFHRWSYMWK 25

*Search  
Sequence*

RESULT 2  
US-08-370-156-7  
Sequence 7, Application US/08370156  
Patent No. 5932780

GENERAL INFORMATION:  
APPLICANT: Soreq, Hermona  
APPLICANT: Zukut, Haim  
APPLICANT: Shan, Moshe  
TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR  
TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
RESESS: Reising, Ethington, Barnard & Perry  
STREET: P.O. Box 4390  
CITY: TROY  
STATE: Michigan  
COUNTRY: US  
ZIP: 48099

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/370,156  
FILING DATE:  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Kohn, Kenneth I.  
REGISTRATION NUMBER: 30,955  
REFERENCE/DOCKET NUMBER: P-307 (Mulford)

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (810) 689-3500  
TELEFAX: (810) 689-4071  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-370-156-7

Query Match 100.0%; Score 14; DB 2; Length 45;  
Best Local Similarity 100.0%; Pred. No. 7.3e-10;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEPHRWSSYMWHK 14  
Db 17 AEPHRWSSYMWHK 30

RESULT 3  
US-08-370-156-8  
Sequence 8, Application US/08370156  
Patent No. 5932780

GENERAL INFORMATION:  
APPLICANT: Soreq, Hermona  
APPLICANT: Zukut, Haim  
APPLICANT: Shan, Moshe  
TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR  
TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
RESESS: Reising, Ethington, Barnard & Perry  
STREET: P.O. Box 4390  
CITY: TROY  
STATE: Michigan  
COUNTRY: US  
ZIP: 48099

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk



NAME: Hendricks, Glenna  
 REGISTRATION NUMBER: 32,535  
 REFERENCE/DOCKET NUMBER: broomfield  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 425-4250  
 TELEFAX: (703) 425-2767  
 INFORMATION FOR SEQ ID NO: 20:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 614 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: unknown  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: YES  
 ANTI-SENSE: YES  
 FRAGMENT TYPE: N-terminal  
 ORIGINAL SOURCE: human esterases  
 US-08-446-100-20

Query Match 100.0%; Score 14; DB 3; Length 614;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-09;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFRWSSYMHWK 14  
 Db 586 AEFRWSSYMHWK 599

RESULT 9  
 US-08-446-100-22  
 Sequence 22, Application US/08446100  
 Patent No. 6001625  
 GENERAL INFORMATION:  
 APPLICANT: Broomfield, Clarence A.  
 APPLICANT: Millard, Charles B.  
 APPLICANT: Lockridge, Oksana  
 TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases  
 NUMBER OF SEQUENCES: 31  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Hendricks and Assoc.  
 STREET: 9669 A Main Street, P.O. Box 2509  
 CITY: Fairfax  
 STATE: VA  
 COUNTRY: US  
 ZIP: 22031  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/446,100  
 FILING DATE: 19-MAY-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Hendricks, Glenna  
 REGISTRATION NUMBER: 32,535  
 REFERENCE/DOCKET NUMBER: broomfield  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 425-4250  
 TELEFAX: (703) 425-2767  
 INFORMATION FOR SEQ ID NO: 22:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 614 amino acids  
 STRANDEDNESS: single  
 TOPOLOGY: unknown  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: YES  
 ANTI-SENSE: YES  
 FRAGMENT TYPE: N-terminal  
 ORIGINAL SOURCE: human esterases  
 US-08-446-100-22

Query Match 100.0%; Score 14; DB 3; Length 614;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-09;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFRWSSYMHWK 14  
 Db 586 AEFRWSSYMHWK 599

RESULT 10  
 US-08-446-100-23

Sequence 23, Application US/08446100  
 Patent No. 6001625  
 GENERAL INFORMATION:  
 APPLICANT: Broomfield, Clarence A  
 APPLICANT: Millard, Charles B  
 APPLICANT: Lockridge, Oksana  
 TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases  
 NUMBER OF SEQUENCES: 31  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Hendricks and Assoc.  
 STREET: 9669 A Main Street, P.O. Box 2509  
 CITY: Fairfax  
 STATE: VA  
 ZIP: 22031

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/446,100  
 FILING DATE: 19-MAY-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Hendricks, Glenna  
 REGISTRATION NUMBER: 32,535  
 REFERENCE/DOCKET NUMBER: broomfield  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 425-4250  
 TELEFAX: (703) 425-2767  
 INFORMATION FOR SEQ ID NO: 25:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 614 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: unknown  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: YES  
 ANTI-SENSE: YES  
 FRAGMENT TYPE: N-terminal  
 ORIGINAL SOURCE:  
 ORGANISM: human esterases  
 US-08-446-100-25

Query Match Score 14; DB 3; Length 614;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-09;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFRWSSYVHWK 14  
 Db 586 AEFRWSSYVHWK 599

RESULT 12  
 US-08-814-095-2  
 Sequence 2, Application US/08814095  
 Patent No. 6025183  
 GENERAL INFORMATION:  
 APPLICANT: Soreg, Hemona  
 APPLICANT: Zakut, Haim  
 APPLICANT: Shani, Moshe  
 TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR  
 NUMBER OF SEQUENCES: 7  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: KOHN & ASSOCIATES  
 STREET: 30500 No. 6025183thwestern Highway, Suite 410  
 CITY: Farmington Hills  
 STATE: Michigan  
 COUNTRY: U.S.  
 ZIP: 48334

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 FILING DATE:  
 CLASSIFICATION: 800  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Montgomery, Ilene N.  
 REGISTRATION NUMBER: 38,972  
 REFERENCE/DOCKET NUMBER: 2391-00066  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (248) 539-5050  
 TELEFAX: (248) 539-5055

Computer Readable Form:

Sequence 25, Application US/08446100  
 Patent No. 6001625  
 GENERAL INFORMATION:  
 APPLICANT: Broomfield, Clarence A  
 APPLICANT: Millard, Charles B  
 APPLICANT: Lockridge, Oksana  
 TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases  
 NUMBER OF SEQUENCES: 31  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Hendricks and Assoc.  
 STREET: 9669 A Main Street, P.O. Box 2509  
 CITY: Fairfax  
 STATE: VA  
 ZIP: 22031  
 COMPUTER READABLE FORM:

```

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 614 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
JS-08-814-095-2

Query Match 100.0%; Score 14; DB 3; Length 614;
Best Local Similarity 100.0%; Pred. No. 5.5e-09; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0; Number of SEQUENCES: 2

RESULT 13
PCT-US92-06106-2
Sequence 2, Application PC/US9206106
GENERAL INFORMATION:
APPLICANT: Fischer, Meir
TITLE OF INVENTION: ENZYMATICALLY ACTIVE RECOMBINANT HUMAN
TITLE OF INVENTION: ACETYLCHOLINESTERASE AND USES THEREOF
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White, Esq.
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/344,920
FILING DATE: 25-NOV-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glennna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: doc348,920
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-7807
TELEFAX: 301-619-7714
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 575 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-348-920-1

Query Match 64.3%; Score 9; DB 1; Length 575;
Best Local Similarity 100.0%; Pred. No. 0.0022; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Number of SEQUENCES: 2
RESULT 15
US-08-348-920-2
Sequence 2, Application US/08348920
PATENT NO. 5,695,550
GENERAL INFORMATION:
APPLICANT: Doctor, Bhupandra P.
APPLICANT: Maxwell, Donald
APPLICANT: Saxena, Ashima
APPLICANT: Radic, Zoran
APPLICANT: Taylor, Palmer
TITLE OF INVENTION: Compositions for use to Deactivate
TITLE OF INVENTION: Organophosphates
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: John F. Moran
STREET: Off. of Command Judge Adv., HQ USAMRDC, Fort
CITY: Frederick
STATE: MD
COUNTRY: US
ZIP: 21702-5012

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/344,920
FILING DATE: 25-NOV-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glennna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: doc348,920
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-7807
TELEFAX: 301-619-7714
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 575 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-348-920-1

Query Match 64.3%; Score 9; DB 1; Length 575;
Best Local Similarity 100.0%; Pred. No. 0.0022; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Number of SEQUENCES: 2
RESULT 16
US-08-348-920-3
Sequence 2, Application US/08348920
PATENT NO. 5,695,550
GENERAL INFORMATION:
APPLICANT: Doctor, Bhupandra P.
APPLICANT: Maxwell, Donald
APPLICANT: Saxena, Ashima
APPLICANT: Radic, Zoran
APPLICANT: Taylor, Palmer
TITLE OF INVENTION: Compositions for use to Deactivate
TITLE OF INVENTION: Organophosphates
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: John F. Moran
STREET: Off. of Command Judge Adv., HQ USAMRDC, Fort
CITY: Frederick
STATE: MD
COUNTRY: US
ZIP: 21702-5012

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/344,920
FILING DATE: 25-NOV-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glennna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: doc348,920
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-7807
TELEFAX: 301-619-7714
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 575 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-348-920-1

Query Match 100.0%; Score 14; DB 4; Length 614;
Best Local Similarity 100.0%; Pred. No. 5.5e-09; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0; Number of SEQUENCES: 2
RESULT 17
US-08-348-920-4
Sequence 2, Application US/08348920
PATENT NO. 5,695,550
GENERAL INFORMATION:
APPLICANT: Doctor, Bhupandra P.
APPLICANT: Maxwell, Donald
APPLICANT: Saxena, Ashima
APPLICANT: Radic, Zoran
APPLICANT: Taylor, Palmer
TITLE OF INVENTION: Compositions for use to Deactivate
TITLE OF INVENTION: Organophosphates
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: John F. Moran
STREET: Off. of Command Judge Adv., HQ USAMRDC, Fort
CITY: Frederick
STATE: MD
COUNTRY: US
ZIP: 21702-5012

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/344,920
FILING DATE: 25-NOV-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glennna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: doc348,920
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-7807
TELEFAX: 301-619-7714
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 575 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-348-920-1

Query Match 100.0%; Score 14; DB 4; Length 614;
Best Local Similarity 100.0%; Pred. No. 5.5e-09; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0; Number of SEQUENCES: 2
RESULT 18
US-08-348-920-5
Sequence 2, Application US/08348920
PATENT NO. 5,695,550
GENERAL INFORMATION:
APPLICANT: Doctor, Bhupandra P.
APPLICANT: Maxwell, Donald
APPLICANT: Saxena, Ashima
APPLICANT: Radic, Zoran
APPLICANT: Taylor, Palmer
TITLE OF INVENTION: Compositions for use to Deactivate
TITLE OF INVENTION: Organophosphates
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: John F. Moran
STREET: Off. of Command Judge Adv., HQ USAMRDC, Fort
CITY: Frederick
STATE: MD
COUNTRY: US
ZIP: 21702-5012

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/344,920
FILING DATE: 25-NOV-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glennna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: doc348,920
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-7807
TELEFAX: 301-619-7714
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 575 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-348-920-1

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; STREET: Detrick
; ; CITY: Frederick
; STATE: MD
; COUNTRY: US
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/348,920
; FILING DATE: 25-NOV-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: doc348,920
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-7807
; TELEFAX: 301-619-7714
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 575 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; US-08-348-920-2

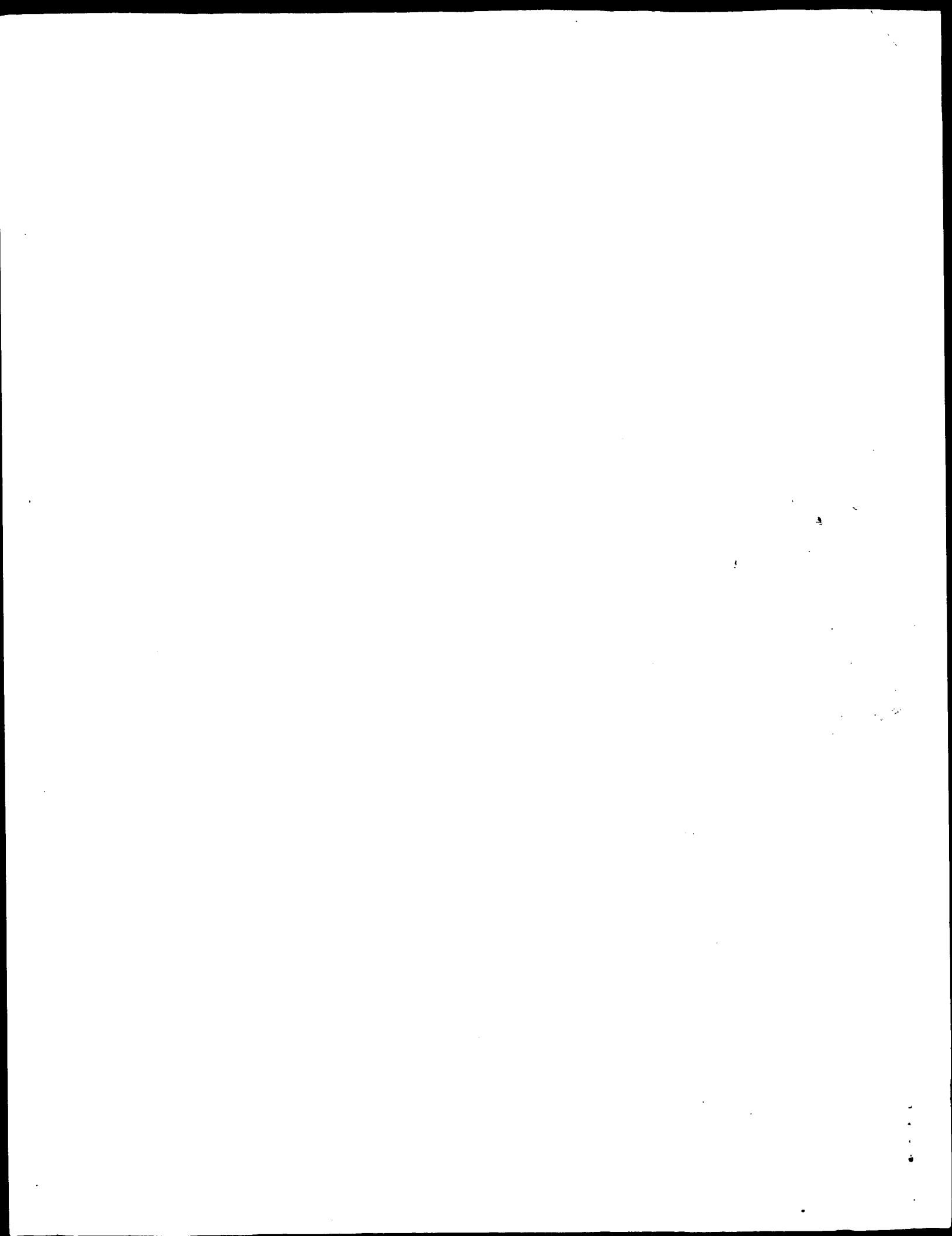
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Query Match Score 9; DB 1; Length 575;
Best Local Similarity 100.0%; Pred. No. 0.002%;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 EFHRWSSYM 10
Db 548 EFHRWSSYM 556

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Search completed: September 13, 2000, 02:25:26  
 Job time: 169 sec



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OM protein - protein search, using sw model

Run on: September 13, 2000, 02:23:37 ; Search time 17.58 Seconds  
 (without alignments)  
 49.283 Million cell updates/sec

Title: US-09-155-076-1  
 Perfect score: 14  
 Sequence: 1 AEFHRWSSIMVHWK 14

Scoring table: OLIGO  
 Gapext 60.0 , Gapext 60.0

Searched: 178050 seqs, 61884766 residues

Word size : 0

Total number of hits satisfying chosen parameters: 178050

Minimum DB seq length: 0  
 Maximum DB seq length: 1000000

Post-processing: Listing first 45 summaries

Database : PIR\_64;\*

- 1: Pir1;\*
- 2: pir2;\*
- 3: pir3;\*
- 4: Pir4;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID       | Description                         |
|------------|-------|-------------|--------|----------|-------------------------------------|
| 1          | 14    | 100.0       | 583    | S10712   | acetylcholinesterase                |
| 2          | 14    | 100.0       | 584    | S48724   | acetylcholinesterase                |
| 3          | 14    | 100.0       | 614    | JH0811   | acetylcholinesterase                |
| 4          | 14    | 100.0       | 614    | A39256   | acetylcholinesterase                |
| 5          | 14    | 100.0       | 614    | JH0314   | acetylcholinesterase                |
| 6          | 9     | 64.3        | 596    | 1 ACRIE  | acetylcholinesterase                |
| 7          | 9     | 64.3        | 599    | 1 A38868 | acetylcholinesterase                |
| 8          | 9     | 64.3        | 767    | S47639   | acetylcholinesterase                |
| 9          | 6     | 42.9        | 330    | 2 S53990 | DNA methyltransferase               |
| 10         | 6     | 42.9        | 469    | 2 S74825 | probable Rieske iron-sulfur protein |
| 11         | 5     | 35.7        | 222    | F81124   | hypothetical protease               |
| 12         | 5     | 35.7        | 236    | 1 S09256 | conserved hypothetical protein      |
| 13         | 5     | 35.7        | 236    | 1 A36170 | homoeotic protein H                 |
| 14         | 5     | 35.7        | 250    | 1 WJHU4B | homoeotic protein H                 |
| 15         | 5     | 35.7        | 255    | 2 T24405 | hypothetical protease               |
| 16         | 5     | 35.7        | 255    | 2 H70078 | conserved hypothetical protein      |
| 17         | 5     | 35.7        | 282    | 2 T05569 | hypothetical protein                |
| 18         | 5     | 35.7        | 318    | 2 B69349 | conserved hypothetical protein      |
| 19         | 5     | 35.7        | 335    | 1 B75576 | oxido-reductase - D                 |
| 20         | 5     | 35.7        | 338    | 2 B70024 | hypothetical protease               |
| 21         | 5     | 35.7        | 339    | 2 D71262 | probable hemolysin                  |
| 22         | 5     | 35.7        | 357    | 2 T12040 | cysteine proteases                  |
| 23         | 5     | 35.7        | 365    | 2 G65038 | hypothetical protease               |
| 24         | 5     | 35.7        | 408    | 2 D75616 | probable acyl-CoA                   |
| 25         | 5     | 35.7        | 415    | 2 T14419 | S-locus-specific g-                 |
| 26         | 5     | 35.7        | 428    | 2 T07809 | S-receptor kinase                   |
| 27         | 5     | 35.7        | 429    | 2 T14418 | S-locus-specific g-                 |
| 28         | 5     | 35.7        | 431    | 2 T22699 | hypothetical protease               |
| 29         | 5     | 35.7        | 440    | 2        |                                     |

ALIGMENTS

RESULT 1

S10712 acetylcholinesterase (EC 3.1.1.7) - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 21-Nov-1993 #sequence-revision 23-Mar-1995 #text\_change 12-May-1995

C;Accession: S10712; A39734; B39734; B25650

R;Doctor, B.P.; Chapman, T.C.; Christner, C.E.; Deal, C.D.; de la Hozz, D.M.; Gentry, FEBS Lett. 266, 133-132, 1990

A;Title: Complete amino acid sequence of fetal bovine serum acetylcholinesterase and

A;Reference number: S10712; MUID:9030335

A;Accession: S10712

A;Molecule type: protein

A;Residues: 1-583 <DOC>

A;Experimental source: fetal serum

R;Robertson, W.L.; Doctor, B.P.; Foster, J.D.; Rosenberry, T.L.

J. Biol. Chem. 266, 7481-7487, 1991

A;Title: Bovine brain acetylcholinesterase primary sequence involved in intersubunit

A;Reference number: A39734; MUID:91212055

A;Accession: A39734

A;Molecule type: protein

A;Residues: 1-15, R', 1'-38; 225-235, 'X', 237-244; 248-264, 'X', 266-273; 365-380; 396-404, 'X'

A;Accession: B39734

A;Molecule type: protein

A;Residues: 1-38 <R02>

A;Experimental source: fetal serum

R;Bon, S.; Chang, J.Y.; Strasbourg, A.D.

FEBS Lett. 209, 206-212, 1986

A;Title: Identical N-terminal peptide sequences of asymmetric forms and of low-salt-s

esterase.

A;Reference number: A91370; MUID:87080761

A;Accession: B25650

A;Molecule type: protein

A;Residues: 'X\$, 3-12 <BON>

A;Experimental source: caudate nucleus

C;Keywords: cholinesterase; cholinesterase homology

F;32.58/Domain: cholinesterase homology <CHE>

F;61,265,350,464,41/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;203/Active site: Ser #status predicted

Query Match 100.0% ; Score 14; DB 2; Length 583;  
 Best local Similarity 100.0%; Pred. No. 8.9e-10;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSIMVHWK 14

Db 555 AEFHRWSSIMVHWK 568

RESULT 2

A; Molecule type: mRNA; DNA  
 A; Residues: 1-614 <S0R>  
 A; Cross-references: GB:N55040; PID:g177974; RID:AAA68151\_1; PID:g177975  
 C; Species: *Oryctolagus cuniculus* (domestic rabbit)  
 C; Date: 07-May-1995 #text\_change 14-Nov-1997  
 C; Accession: S48724  
 R; Jbilo, O.; L Hermite, Y.; Talesa, V.; Toutant, J.P.; Chatonnet, A.  
 Eur. J. Biochem. 225, 115-124, 1994  
 A; Title: Acetylcholinesterase and butyrylcholinesterase expression in adult rabbit tissue  
 A; Reference number: S48724; MUID:95010096  
 A; Accession: S48724  
 A; Status: preliminary  
 A; Molecule type: mRNA  
 A; Residues: 1-584 <JB1>  
 C; Superfamily: cholinesterase; cholinesterase homology <CHE>  
 C; Keywords: glycoprotein; cholinesterase homology <CHE>  
 F; 32-539/Domain: cholinesterase homology <CHE>

Query Match 100.0%; Score 14; DB 2; Length 584;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-10;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFRWSSYMWK 14  
 Db 556 AEFRWSSYMWK 569

RESULT 3  
 JH0811 acetylcholinesterase (EC 3.1.1.7) catalytic chain precursor - rat  
 C; Species: *Rattus norvegicus* (Norway rat)  
 C; Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 18-Jun-1999  
 C; Accession: JH0811  
 R; Legay, C.; Bon, S.; Vernier, P.; Couussen, F.; Massoulie, J.  
 J. Neurochem. 60, 337-346, 1993  
 A; Title: Cloning and expression of a rat acetylcholinesterase subunit: generation of mu...  
 A; Reference number: JH0811; MUID:93107932  
 A; Molecule type: mRNA  
 A; Residues: 1-614 <LBG>  
 A; Cross-references: GB:50879; NID:g262092; PID:9262093  
 A; Experimental source: striatum  
 C; Comment: This protein is responsible for hydrolysis of acetylcholine at cholinergic synapses  
 C; Keywords: carboxylic ester hydrolase; glycoprotein; membrane protein; muscle; nerve; muscle  
 F; 1-31/Domain: signal sequence #status predicted <SIG>  
 F; 32-614/Domain: acetylcholinesterase catalytic chain #status predicted <CAT>  
 F; 63-569/Domain: cholinesterase homology <CHE>  
 F; 100-127, 288-303, 440-560/Disulfide bonds #status predicted  
 F; 234-365, 478/Active site: Ser, Glu, His #status predicted  
 F; 296, 381, 493/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 14; DB 2; Length 614;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-10;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4  
 A39256 acetylcholinesterase (EC 3.1.1.7) precursor, brain splice form - human  
 C; Species:  *Homo sapiens* (man)  
 C; Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 18-Jun-1999  
 R; Soeq, H.; Ben Aziz, R.; Prod'Y, C.A.; Seidman, S.; Gnatt, A.; Neville, L.; Lieman-Hurwitz, R.; Schmeil, E.; August, T.  
 FEBS Lett. 247, 279-282, 1989  
 A; Title: Purification and partial amino acid sequence analysis of human erythrocyte a...  
 A; Reference number: S03959; MUID:89232136  
 A; Accession: S03959  
 A; Molecule type: protein  
 A; Residues: 256-266, 'Y', 268-273, 306-308, 'X', 310-313, 'X', 315-316, 'D', 318-323, 'D'  
 A; Experimental source: erythrocytes  
 A; Note: this form was a disulfide-linked homodimer  
 C; Genetics:  
 A; Gene: GDB:ACHE; YT  
 A; Cross-references: GDB:118746; OMIM:100740  
 A; Map Position: 7q22.7/q22  
 C; Superfamily: cholinesterase; cholinesterase homology <CHE>  
 F; 63-569/Domain: cholinesterase homology <CHE>

Query Match 100.0%; Score 14; DB 2; Length 614;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-10;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5  
 Qy 1 AEFRWSSYMWK 14  
 Db 586 AEFRWSSYMWK 599

Query Match 100.0%; Score 14; DB 2; Length 614;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-10;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6  
 Qy 1 AEFRWSSYMWK 14  
 Db 586 AEFRWSSYMWK 599

Query Match 100.0%; Score 14; DB 2; Length 614;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-10;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

C;Comment: Synapses usually contain this 11S (asymmetric) form of cholinesterase with holinesterase occurs on the outer surfaces of cell membranes, including those of eryt complex: 11S form is disulfide linked homodimer; 18S form is homotetramer, a dimer

A;Function: C;Function: hydrolyzes acetylcholine to choline and acetate

A;Pathway: C;Pathway: neurotransmitter degradation

C;Superfamily: cholinesterase; cholinesterase homology

C;Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; membrane

F;1-27/Domain: signal sequence #status predicted <SIG>

F;22-596/Product: acetylcholinesterase, 11S form #status experimental <CHB>

F;51-554/Domain: cholinesterase homology <CHB>

F;80-478/554/Binding site: carboxyhydrate (Asn) (covalent) #status predicted

F;88-115/275-286/423-542/Disulfide bonds: #status experimental

F;105/Binding site: substrate (Trp) #status experimental

F;221/Active site: Ser #status experimental

F;348-461/Active site: Glu His #status predicted

F;437/Binding site: carboxyhydrate (Asn) (covalent) #status experimental

F;593/Disulfide bonds: interchain #status experimental

A;Residues: <NS>; 11-596 <SC2>

A;Cross-references: GB:X03439; NID:964389

A;Experimental source: electric organ

A;Note: Parts of this sequence, including the amino and carboxyl ends of the mature protein

R;Schumacher, M.; Camp, S.; Mault, Y.; Newton, M.; MacPhee-Quiigley, K.; Taylor, S.S.; Fed. Proc., 45, 2976-2981, 1986

A;Title: Primary structure of acetylcholinesterase: implications for regulation and function

A;Reference number: A60820; MUID:87054662

A;Accession: A60820

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 22-596 <SC2>

R;Schumacher, M.; Mault, Y.; Camp, S.; Taylor, P.

J. Biol. Chem. 263, 18979-18987, 1988

A;Title: Multiple messenger RNA species give rise to the structural diversity in acetylcholinesterase

A;Reference number: A92701; MUID:89066655

A;Accession: A31962

A;Molecule type: mRNA

A;Cross-references: EMBL:X03439; NID:964389

A;Experimental source: clones AChE-11 and ACHE-18

A;Note: Revision to sequence A0773

A;Accession: B1962

A;Molecule type: DNA: mRNA

A;Residues: 499-565 <SC4>

A;Cross-references: GB:X03439; NID:964389

A;Experimental source: clone AChE-1

R;MacPhee-Quiigley, K.; Taylor, P.

J. Biol. Chem. 260, 12185-12189, 1985

A;Title: Primary structures of the catalytic subunits from two molecular forms of acetylcholinesterase

A;Reference number: A23902; MUID:8608285

A;Accession: A23902

A;Molecule type: protein

A;Residues: 22-B-24-45-214-237 <MAC>

A;Note: active site Ser identification

R;Kreienkamp, H.J.; Weise, C.; Raba, R.; Aaviksaar, A.; Hucho, F.

R;Mault, Y.; Camp, S.; Gibney, G.; Rachinsky, T.L.; Ekstroem, T.J.; Taylor, P.

A;Title: Anionic subites of the catalytic center of acetylcholinesterase from Torpedo a

A;Reference number: A41117; MUID:91296772

A;Accession: B4117

A;Molecule type: protein

A;Residues: 100-108 <KRE>

A;Note: substrate binding site

R;Mault, Y.; Camp, S.; Gibney, G.; Rachinsky, T.L.; Ekstroem, T.J.; Taylor, P.

A;Title: Single gene encodes glycophospholipid-anchored and asymmetric acetylcholinesterase

A;Reference number: PS0113; MUID:90166618

A;Accession: S15677

A;Status: Preliminary

A;Molecule type: DNA

A;Residues: 557-596 <MAU>

A;Cross-references: EMBL:X56516

R;MacPhee-Quiigley, K.; Vedyck, T.S.; Taylor, P.

A;Reference number: A50061; PDB:1ACE

A;Title: profile of the disulfide bonds in acetylcholinesterase.

A;Reference number: A43039; MUID:87008586

A;Contents: annotation; disulfide bonds

R;Sussman, J.L.; Harrel, M.; Silman, I.

A;Submitted to the Brookhaven Protein Data Bank, October 1991

J. Biol. Chem. 261, 13565-13570, 1986

A;Reference number: A43039; MUID:87008586

A;Annotation: X-ray crystallography, 2.8 angstroms, residues 26-481, 511-555 of

R;Sussman, J.L.; Harrel, M.; Frolow, F.; Oefner, C.; Goldman, A.; Toker, I.; Silman, I.

Science 253, 872-879, 1991

A;Reference number: A43038; MUID:91343938

A;Contents: annotation; X-ray crystallography, 2.8 angstroms, residues 26-481, 511-555 of



Db 20 AEFHR 24

RESULT 12

F81124 conserved hypothetical protein NMB1075 [imported] - *Neisseria meningitidis* (group B strain) C;Species: *Neisseria meningitidis*

C;Accession: F81124

C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 31-Mar-2000

Hickey, E.K.; Rettelin, H.; Saunders, N.J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Qin, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masiognani, V.; Piazza, M.; Science 287, 1809-1815, 2000

A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ye, A.;Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.

A;Reference number: A81000; MUID:20115755

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-222 <TET>

A;Cross-references: GB:AE002458; GB:AE00098; NID:97226311; PID:AAF41470.1; PID:g722631

A;Experimental source: serogroup B, strain MC58

C;Genetics:

A;Gene: NMB1075

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Best Local Similarity 100.0%; Pred. No. 33;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHR 5

Db 75 AEFHR 79

RESULT 13

S09256 homeotic protein Hox D4 - chicken

N;Alternate names: homeotic protein Chox-4.2; homeotic protein Chox-a

C;Species: Gallus gallus (chicken)

C;Date: 29-Jan-1993 #sequence\_revision 29-Jan-1993 #text\_change 24-Jul-1997

A;Accession: S09256

R;Sasaki, H.; Yokono, E.; Kuroiwa, A.

Nucleic Acids Res. 18, 1739-1747, 1990

A;Title: Specific DNA binding of the two chicken deformed family homeodomain proteins, C

A;Reference number: S09256; MUID:90245562

A;Accession: S09256

A;Molecule type: mRNA

A;Residues: 1-236 <SSA>

A;Cross-references: EMBL:X52671; EMBL:X52672

C;Genetics:

A;Gene: hoxD4

C;Function:

A;Description: control of embryonic development by tissue- and stage-specific regulation

C;Superfamily: homeotic protein Hox D4; homeobox homology <Hox>

F;146-202/Domain: homeobox homology <Hox>

Query Match 35.7%; Score 5; DB 1; Length 236;

Best Local Similarity 100.0%; Pred. No. 35;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SSYMV 11

Db 4 SSYMV 8

RESULT 14

A36170 homeotic protein Hox D4 - mouse

N;Alternate names: homeotic protein Hox 4.2; homeotic protein Hox 5.1

C;Species: Mus musculus (house mouse)

C;Date: 14-Dec-1990 #sequence\_revision 14-Dec-1990 #text\_change 24-Jul-1997

R;Featherstone, M.S.; Baron, A.; Gaunt, S.J.; Mattei, M.G.; Duboule, D.

Proc. Natl. Acad. Sci. U.S.A. 85, 4760-4764, 1988

A;Title: Hox-5.1 defines a homeobox-containing gene locus on mouse chromosome 2.

A;Reference number: A36170; MUID:88263027

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-250 <FEA>

A;Cross-references: GB:J03770

C;Genetics:

A;Gene: Hoxd-4

A;NAP position: 2

A;Function:

A;Description: control of embryonic development by tissue- and stage-specific regulation

C;Superfamily: homeotic protein Hox D4; homeobox homology <Hox>

C;Keywords: DNA binding; embryo; homeobox; nucleus; transcription regulation

F;153-209/Domain: homeobox homology <Hox>

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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 4 SSYMV 8

RESULT 15

WJH4B homeotic protein Hox D4 - human

N;Alternate names: homeotic protein c13; homeotic protein Hox 4B; homeotic protein Hox 4B

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 22-Jun-1999

C;Accession: S10955; A38787; A5238; S15546

R;Clanetti, L.; di Cristofaro, A.; Zapavigna, V.; Bottero, L.; Boccoli, G.; Testa, U

Nucleic Acids Res. 18, 4361-4368, 1990

A;Title: Molecular mechanisms underlying the expression of the human HOX-5.1 gene.

A;Reference number: S10955; MUID:90356367

A;Accession: S10955

A;Molecule type: DNA

A;Residues: 1-255 <CTA>

A;Cross-references: EMBL:X173360; NID:g32394; PIDN:CAA35237.1; PID:g236652

A;Accession: A38787

A;Molecule type: mRNA

A;Residues: 1-122, 'S', 124-255 <CTA2>

R;Navillo, F.; Samone, A.; Giampaolo, A.; Faiella, A.; Zapavigna, V.; Acampora, D.;

Nature 324, 664-668, 1986

A;Title: Differential and stage-related expression in embryonic tissues of a new huma

A;Accession: A25238

A;Molecule type: mRNA

A;Residues: 1-122, 'S', 124-141, 'A', 143-255 <MAV>

R;Boncinelli, E.; Acampora, D.; Pannese, M.; d'Esposito, M.; Somma, R.; Gaudino, G.;

Genome 31, 75-756, 1999

A;Title: Organization of human class I homeobox genes.

A;Accession: S15036; MUID:90215256

A;Molecule type: DNA

A;Residues: 154-219 <BON>

C;Genetics: ♀

A;Gene: GDB:HoxD4

A;Cross-references: GDB:120677; OMIM:142981

A;Map position: 2q31-2q31

A;Introns: 145/1

C;Function:

A;Description: control of embryonic development by tissue- and stage-specific regulation

C;Superfamily: homeotic protein Hox D4; homeobox homology <Hox>

C;Keywords: DNA binding; embryo; homeobox; nucleus; transcription regulation

Wed Sep 13 08:11:28 2000

us-09-155-076-1.rpr

Page 6

F;155-211/Domain: homeobox homology <HOX>

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Db 4 SSIMV 8

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Date: Sep 13, 2000 3:47 AM

About: Results were produced by the GenCore software, version 4.5,
Copyright (C) 1993-2000 CompuGen Ltd.

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gb_om:OCU05036 + 14.00    287.51     6.4e-08    1947     Orcytolagus cuniculus acetylcholinesterase
gb_om:SD0879 + 14.00    287.11     6.8e-08    2086     Sorex coronatus acetylcholinesterase mRNA
gb_pr:AMMABE + 14.00    287.04     6.8e-08    2089     Mouse mRNA for acetylesterase
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REFERENCE 1 (bases 1 to 140)
AUTHORS Mendelson,I., Kronman,C., Ariel,N., Shafferman,A. and Velan,B.
TITLE Bovine acetylcholinesterase: cloning, expression and
characterization
JOURNAL Biochem. J. 334 (Pt 1), 251-259 (1998)
MEDLINE 98359754
REFERENCE 2 (bases 1 to 140)
AUTHORS Mendelson,I., Kronman,C., Ariel,N., Shafferman,A. and Velan,B.
TITLE Direct Submission
JOURNAL Submitted (28-APR-1998) Biochemistry and Molecular Genetics, Israel
Institute for Biological Research, PO Box 19, Ness Ziona 70450, Israel
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 Reference Legay,C., Bon,S., Vernier,P., Coussen,F. and Massoulie,J.  
 Authors Cloning and expression of a rat acetylcholinesterase subunit: generation of multiple molecular forms and complementarity with a Torpedo collagenic subunit  
 Title J. Neurochem. 60 (1), 337-346 (1993)  
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 AUTHORS Taylor, P.  
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 AUTHORS Rachinsky, T.L., Camp, S., Li, Y., Ekstrom, T.J., Newton, M. and Taylor, P.  
 TITLE Molecular cloning of mouse acetylcholinesterase: tissue distribution of alternatively spliced mRNA species  
 JOURNAL Neuron 5 (3), 317-327 (1990)  
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 Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 2118)  
 AUTHORS Soreq,H.E., Ben-Aziz,R., Prody,C.A., Seidman,S., Gnatt,A.,

Neville,L., Lieman-Hurwitz,J., Lev-Lehman,E., Ginzberg,D., Lapidot-Lifson,Y. and Zukut,H.

**TITLE** Molecular cloning and construction of the coding region for human acetylcholinesterase reveals a G + C-rich attenuating structure

**JOURNAL** Proc. Natl. Acad. Sci. U.S.A. 87 (24), 9688-9692 (1990)

**MEDLINE** 91088577

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  - /note="GO0-118-746; does not fit consensus"
  - 310. . 1998
- mat\_peptide
  - /gene="ACHE"
  - /EC\_number="3.1.1.7"
  - /note="GO0-118-746"

**BASE COUNT** 355 a 755 c 680 g 428 t

**ORIGIN**

**alignment\_scores:**

| Quality             | Length  | Length:           | 14      |
|---------------------|---------|-------------------|---------|
| 14.00               | 0       | Ratio:            | 1.000   |
| Percent Similarity: | 100.000 | Percent Identity: | 100.000 |

**alignment\_block:** US-09-155-076-1 x HORACHE ..

Align seg 1/1 to: HORACHE from: 1 to: 2218

1 AlagluPheHisArgTrpSerTyrMetValHistRplys 14  
1912 GCGAGTTCAACGGCTGGAGCTCTATGGTCACTGGAAAG 1953

**seq\_name:** gb\_pat:AR070205

**seq\_documentation\_block:** AR070205 2256 bp DNA

**LOCUS** Sequence 5 from patent US 5891725.

**DEFINITION** AR070205 AR070205.1 GI:7221093

**VERSION**

**KEYWORDS**

**SOURCE** Unknown.

**ORGANISM** Unknown

**REFERENCE** 1 (bases 1 to 2256)

**AUTHORS** Soreq,H., Zukut,H. and Eckstein,F.

**TITLE** Synthetic antisense oligodeoxynucleotides and pharmaceutical compositions containing them

**JOURNAL** Patent: US 5891725-A 5 06 APR-1999;

**FEATURES** Location/Qualifiers

- source 1. . 2256
- BASE COUNT 390 a 757 c 680 g 429 t

**alignment\_scores:**

| Quality             | Length  | Length:           | 14      |
|---------------------|---------|-------------------|---------|
| 14.00               | 0       | Ratio:            | 1.000   |
| Percent Similarity: | 100.000 | Percent Identity: | 100.000 |

**alignment\_block:** US-09-155-076-1 x AR070205 ..

Align seg 1/1 to: AR070205 from: 1 to: 2256

1 AlagluPheHisArgTrpSerTyrMetValHistRplys 14  
1915 GCGAGTTCCACCGCTGGAGTCCTACATGGTCACTGGAAAG 1956

**seq\_name:** gb\_pat:AR070207

**seq\_documentation\_block:** AR070207 3016 bp DNA

**LOCUS** AR070207 Sequence 7 from patent US 5891725.

**DEFINITION** AR070207

**VERSION** AR070207.1 GI:7221095

**KEYWORDS**

**SOURCE**

**ORGANISM** Unknown

**UNCLASSIFIED**

**REFERENCE** 1 (bases 1 to 3016)

**AUTHORS** Soreq,H., Zukut,H. and Eckstein,F.

**TITLE** Synthetic antisense oligodeoxynucleotides and pharmaceutical compositions containing them

**JOURNAL** Patent: US 5891725-A 7 06 APR-1999;

**FEATURES** Location/Qualifiers

- source 1. . 3016
- BASE COUNT 497 a 1065 c 840 g 614 t

**alignment\_scores:**

| Quality             | Length  | Length:           | 14      |
|---------------------|---------|-------------------|---------|
| 14.00               | 0       | Ratio:            | 1.000   |
| Percent Similarity: | 100.000 | Percent Identity: | 100.000 |

**alignment\_block:** US-09-155-076-1 x AR070207 ..

Align seg 1/1 to: AR070207 from: 1 to: 3016

1 AlagluPheHisArgTrpSerTyrMetValHistRplys 14  
1915 GCGAGTTCCACCGCTGGAGTCCTACATGGTCACTGGAAAG 2716

**seq\_name:** gb\_pat:AR070206

**seq\_documentation\_block:** AR070206 3096 bp DNA

**LOCUS** AR070206 Sequence 6 from patent US 5891725.

**DEFINITION** AR070206

**VERSION** AR070206.1 GI:7221094

**KEYWORDS**

SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 3096)  
 AUTHORS Soreq, H., and Eckstein, F.  
 TITLE Synthetic antisense oligodeoxynucleotides and pharmaceutical compositions containing them  
 Patent: US 5891723 A 06-AKR-1999;  
 FEATURES Location/Qualifiers 1..3096 /organism="unknown"  
 source 509 a 1089 c 872 g 626 t  
 BASE COUNT ORIGIN CDS  
 JOIN (92..1150,1517..2001,2768..2937,3785..3906)

alignment\_scores:  
 Quality: 14.00 Length: 14  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Identity: 100.000

alignment\_block:  
 US-09-155-076-1 x AR070206 ..

Align seg 1/1 to: AR070206 from: 1 to: 3096

1 AlaGluPheHisArgTrpSerSerTyrMetValHisTrpLys 14  
 2755 GCGAGTTCACGGCTTCCACATGGACTGGAG 2796

seq\_name: qb\_on:AF053485

seq\_documentation\_block:  
 LOCUS Felis catus acetylcholinesterase glycoprophospholipid-anchored form  
 DEFINITION Felis catus acetylcholinesterase glycoprophospholipid-anchored form  
 precursor (ACHE) and acetylcholinesterase collagen-tailed or  
 globular form precursor (ACHE) genes, complete cds.  
 ACCESSION AF053485  
 VERSION AF053485.1  
 KEYWORDS GI:3003019  
 SOURCE cat.  
 ORGANISM Felis catus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Carnivora; Fissipedia; Felidae; Felis.

REFERENCE Bartels, C.F., Xie, W.-H., Miller-Lindholm, A.K. and Lockridge, O.  
 AUTHORS 1 (bases 1 to 3958)  
 TITLE Sequence and characterization of domestic cat acetylcholinesterase  
 and butyrylcholinesterase  
 Unpublished  
 2 (bases 1 to 3958)  
 Bartels, C.F., Xie, W.-H., Miller-Lindholm, A.K. and Lockridge, O.  
 Direct Submission  
 Submitted (12-MAR-1998) Epiley Institute, University of Nebraska  
 Medical Center, 600 S. 42nd St., Omaha, NE 68198-6805, USA  
 JOURNAL  
 FEATURES Location/Qualifiers 1..3958  
 source /organism="Felis catus"  
 /db\_xref="taxon:9655"  
 mRNA  
 JOIN (<92..1150,1517..2001,2768..2937,3785..3906)  
 /gene="ACHE"  
 /product="acetylcholinesterase collagen-tailed or globular  
 form precursor"  
 JOIN (<92..1150,1517..2001,2768..2937,3051..>3178)  
 /gene="ACHE"  
 /product="acetylcholinesterase glycophospholipid-anchored  
 form precursor"  
 <92..>306  
 gene  
 /gene="ACHE"  
 CDS  
 JOIN (92..1150,1517..2001,2768..2937,3051..3178)  
 /note="ACHE b-form; encoded by exon 4 spliced to exon 5"  
 /codon\_start=1  
 /product="acetylcholinesterase glycophospholipid-anchored  
 form precursor"

/protein\_id="AAC08996.1"  
 /db\_xref="GI:3003021"  
 /translation="MRRPPCPLYPTPSLAAPILLIPLGGAAEADPELLTVRGQQ  
 LRGYRLLAAGGPYSALGLIPADFPVGRPFLEPEKRPWGTLDATAFQSICQYD  
 TLYPGECDEMNPNEELSEDCLYLWNTYPAPASPPVWYGGCFYGSASSLWD  
 YDGRFLAAEGTIVLSNNYRVGAGFALPGSREAPANGLLDORLAQWQDNVATE  
 GGDDMSVTLFGESAGAASVGMLHSPPRLFRALVAGSAPNGPATVYGEARRA  
 FLSDTPPEALINACDEFHGLQVLYKGDSYELVYGAEGFSKNESTISRAQFLAGVR  
 VGFOQASDIAAEAVWVLTIDWLPEDPARLREAMSVDWVHNVCPVQLAGLARQ  
 ARVYATIFPDKVPPWYQFRLPSLNTAENIFQAOLMRWV  
 ANFARTGPDNDPDPKVPWYQFRLPSLNTAENIFQAOLMRWV  
 LLSATASKAPSICSGPAGCAGEARPRPQLSPLLPLLFLLSRLRL"  
 JOIN (92..1150,1517..2001,2768..2937,3785..3906)

/note="ACHE t-form; encoded by exon 4 spliced to exon 5"  
 /codon\_start=1  
 /product="acetylcholinesterase collagen-tailed or globular  
 form precursor"  
 /protein\_id="AAC08995.1"  
 /db\_xref="GI:3003020"  
 /translation="MRRPPCPLYPTPSLAAPILLIPLGGAAEADPELLTVRGQQ  
 LRGYRLLAAGGPYSALGLIPADFPVGRPFLEPEKRPWGTLDATAFQSICQYD  
 TLYPGECDEMNPNEELSEDCLYLWNTYPAPASPPVWYGGCFYGSASSLWD  
 YDGRFLAAEGTIVLSNNYRVGAGFALPGSREAPANGLLDORLAQWQDNVATE  
 GGDDMSVTLFGESAGAASVGMLHSPPRLFRALVAGSAPNGPATVYGEARRA  
 FLSDTPPEALINACDEFHGLQVLYKGDSYELVYGAEGFSKNESTISRAQFLAGVR  
 VGFOQASDIAAEAVWVLTIDWLPEDPARLREAMSVDWVHNVCPVQLAGLARQ  
 ARVYATIFPDKVPPWYQFRLPSLNTAENIFQAOLMRWV  
 ANFARTGPDNDPDPKVPWYQFRLPSLNTAENIFQAOLMRWV  
 LLSATATDDEAEROWKAHFHRNSYMMHWKNQDHSHQDR-SDL"

BASE COUNT 723 a 1256 c 1205 g 772 t 2 others  
 ORIGIN

alignment\_scores:  
 Quality: 14.00 Length: 14  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
 alignment\_block: US-09-155-076-1 x AF053485 ..  
 Align seg 1/1 to: AF053485 from: 1 to: 3958

1 AlagluPhHeHisArgTrpSerSerTyrMetValHisTrpLys 14  
 3817 GCAGACTTCACCGTGCTCCATACGTGCACTGGAG 3858

seq\_name: qb\_pr3:HEADACHEB

seq\_documentation\_block:  
 LOCUS HEADACHEB 4185 bp DNA PRI 23-JUN-1995  
 DEFINITION Homo sapiens acetylcholinesterase (ACHE) gene, exons 2-6.  
 ACCESSION I42812  
 VERSION I42812.1 GI:854582  
 KEYWORDS acetylcholinesterase.  
 SOURCE Homo sapiens DNA.  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (sites)  
 REFERENCES Bartels, C.F., Zelinski, T. and Lockridge, O.  
 TITLE Mutation at codon 322 in the human acetylcholinesterase (ACHE) gene  
 accounts for Y7 blood group polymorphism  
 An. J. Hum. Genet. 52 (5), 928-936 (1993)  
 JOURNAL 93256075  
 REFERENCE 2 (bases 1 to 4185)  
 AUTHORS Bartels, C.F., Moriarity, P.L., Becker, R.E., Robbs, R.S.,  
 Sorenson, R.C., Mountjoy, C.P. and Lockridge, O.  
 TITLE Polymorphic sites in the acetylcholinesterase gene of patients with  
 Alzheimer's disease



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<note>"M2EF, score = 100%"</note>
<note>"not_experimental"</note>
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<note>"Region: CPG island"</note>
<note>"not_experimental"</note>
intron
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intron
<note>"not_experimental"</note>
2497 . 2596
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<note>"not_experimental"</note>
2597 . 2675
<note>"Xpound exon prediction, score = 98% (0%)"</note>
exon
<note>"not_experimental"</note>
2597 . 2675
<note>"Alignment: EST, | Intron"</note>
<note>"not_experimental"</note>
2676 . 2980
<note>"Alignment: EST, | Intron"</note>
<note>"not_experimental"</note>
3170 . 3528
<note>"Alignment: EST, | Intron"</note>
<note>"not_experimental"</note>
3529 . 3585
<note>"M2EF, score = 100%"</note>
<note>"not_experimental"</note>
3539 . 3764
<note>"CpG island score = 0.82, GC = 62.80%, CpGs = 18%"</note>
<note>"Region: CPG island"</note>
<note>"not_experimental"</note>
3548 . 3702
<note>"Xpound exon prediction, score = 98% (0%)"</note>
intron
<note>"not_experimental"</note>
3637 . 3702
<note>"Alignment: CDS, |CG415001|87.9|46|111"</note>
<note>"not_experimental"</note>
3703 . 3780
<note>"Alignment: CDS, | Intron"</note>
<note>"not_experimental"</note>
3781 . 3934
<note>"M2EF, score = 97.3%"</note>
<note>"not_experimental"</note>
3781 . 3934
<note>"Xpound exon prediction, score = 99% (0%)"</note>
intron
<note>"not_experimental"</note>
3781 . 3927
<note>"Alignment: CDS, |CG415001|85.7|112|258"</note>
<note>"not_experimental"</note>
3812 . 3960
<note>"BLASTN (EMBL), 110. .258 of emb|U41500|CG41500<br/>Cricetulus griseus arsenite-resistance protein (ars2)"</note>
mRNA
<note>"Region: Data base match"</note>
<note>"not_experimental"</note>
4054 . 4281
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<note>"not_experimental"</note>
4054 . 4247
<note>"Xpound exon prediction, score = 98% (0%)"</note>
exon
<note>"BLASTX (GENPEPT), 58. .87 of gbl|U41500|CGU41500_1<br/>Cricetulus griseus arsenite-resistance protein (ars2)"</note>
<note>"not_experimental"</note>
4191 . 4220
<note>"BLASTN (GENPEPT), 87. .139 of gbl|U41500|CGU41500_1<br/>Cricetulus griseus arsenite-resistance protein (ars2)"</note>
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4437 . 4593
<note>"M2EF, score = 97%"</note>
<note>"not_experimental"</note>
4437 . 4593
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4437 . 4593
alignment_scores: Quality: 14.00 Length: 14
Ratio: 1.000 Gaps: 0

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Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
US-09-155-076-1 x HSAF002993/rev ..

Align seg 1/1 to reverse of: HSAF002993 from: 1 to: 34921

1 AlaGluPheHisArgTrpSerSerTyMetValHisTrpLys 14  
6375 GCGAGATCCACGCCGGAGCTCATGGCAGCTGGAG 6934

seq\_name: gb\_htg29:Ac011895

seq\_documentation\_block:

LOCUS Ac011895 175155 bp DNA HTG 21-APR-2000

DEFINITION Homo sapiens chromosome 7 clone RP11-126L15, WORKING DRAFT  
SEQUENCE, 3 unordered pieces.

ACCESSION AC011895

VERSION AC011895.3 GI:76310854

KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.

KWOSI human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Waterston,R.H.

TITLE The sequence of Homo sapiens cDNA

JOURNAL Unpublished

2 (bases 1 to 175155)

AUTHORS Waterston,R.H.

TITLE Direct Submission

JOURNAL Submitted (15-OCT-1999) Genome Sequencing Center, Washington

University School of Medicine, 4444 Forest Park Parkway, St. Louis,

MO 63108, USA

On Apr 21, 2000 this sequence version replaced gi:6136444.

----- Genome Center -----

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: http://genome.wustl.edu/gsc/index.shtml

Center project name: H\_NH0126L15

----- Summary Statistics -----

Sequencing vector: M13: 74%

Sequencing vector: plasmid; 268

Chemistry: Dye-primer ET; 67% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 173580 bases at least Q40

Consensus quality: 17920 bases at least Q30

Consensus quality: 174136 bases at least Q20

Insert size: 184000; agarose-fp

Insert size: 174955; sum-of-contigs

Quality coverage: 7.01 in Q20 bases; agarose-fp

Quality coverage: 7.40 in Q20 bases; sum-of-contigs

\* NOTE: This is a 'working draft' sequence. It currently

\* consists of 3 contigs. The true order of the pieces

\* is not known and their order in this sequence record is

\* arbitrary. Gaps between the contigs are represented as

\* runs of N, but the exact sizes of the gaps are unknown.

\* This record will be updated with the finished sequence

\* as soon as it is available and the accession number will

\* be preserved.

1 28804: contig of 28804 bp in length

\* 28805 28904: gap of unknown length

\* 28905 28940: contig of 64436 bp in length

\* 93341 93440: gap of unknown length

\* 93441 175155: contig of 81715 bp in length.

FEATURES

Source 1 .175155

/organism="Homo sapiens"

/db\_xref="taxon:9606"

mRNA

seq\_documentation\_block:

LOCUS AF030422 4472 bp DNA VRT 20-NOV-1997

DEFINITION Electrophorus electricus acetylcholinesterase catalytic subunit

ACCESSION AF030422

VERSION AF030422.1 GI:2613035

KEYWORDS electric eel.

ORGANISM Electrophorus electricus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;

Neopterigii; Teleostei; Euteleostei; Ostariophysi; Gymnotiformes;

Gymnotodei; Gymnotorhidae; Electrophorus.

REFERENCE 1 (bases 1 to 4472)

AUTHORS Simon,S. and Massoulié,J.

TITLE Cloning and expression of acetylcholinesterase from Electrophorus

REFERENCE 2 (bases 1 to 4472)

AUTHORS Simon,S. and Massoulié,J.

TITLE Direct submission

JOURNAL Submitted (15-OCT-1997) Neurobiology, Ecole Normale Supérieure, 46 Rue d'Ulm, Paris 75005, France

FEATURES Location/Qualifiers

source 1 . 4472

/organism="Electrophorus electricus"

/db\_xref="taxon:8005"

sig\_peptide 118 . 186

CDS join(118 .. 1525..1694 .. 1886,2052 .. 2230..3582 .. 3703)

/EC\_number="3.1.1.7"

/note="Type T catalytic subunit"

/codon\_start=1

/product="acetylcholinesterase catalytic subunit precursor"

/protein\_id="AAB6606\_1"

/db\_xref="GI:2613036"

/translation="MKLIDALIFEPVIMFFIHLSTAQTDPETLMTRLGQVQGTQLPV

VPRSHYTAFLGIPFAFPPLGMRFPEPKWNPDKWYDPRYQYQVDTSPYGF

SGTEMMWPNMSEDCLYKNTWNPAPRPHNLTAVWYGGFYSGSSSLDVYDRYL

AHSBKVYVSMNRSVAFLLQRLQWQDAPNGVLLDQRNLQWQDAPNGVLL

VTFGESESAGASVGMHLLSPDRKPTFLILQSGVPNGPRTVSDEARRAIKGRL

VGGPDGNDTDLDICLRSKPSQDPLIDENWLPESGLFRFSEFVPUVDGVVPPDTPAMLI

NSENFKDQILQJLUGVNQNEGSPFLYIAGPSKDNBLITREDFLQGVKMSPHANEIG

LEAVILOYTDWDEDNPIKRNREADDVQDLYQVCPLOAKMVOYSIQLQGOTATAS

OGHNWGNSGSANSNSOVSYLYWANPARGNPINVDGSLDSRRKPVTSTEKHVGNTD

RNLYTLEDEKLSRMMLWANRELPLNTENTDAERWKAFHRNSYMMWKNQDFHY

SXKVKHGKQSFCALWNRRELPLNTENTDAERWKAFHRNSYMMWKNQDFHY

SKOERCINL"

join(<18 .. 1525..1694 .. 1886,2052 .. 2230..3582 .. 3703)

/product="acetylcholinesterase catalytic subunit precursor"

join(18 .. 1525..1694 .. 1886,2052 .. 2230..3582 .. 3700)

/note="acetylcholinesterase catalytic subunit"

BASE COUNT 1234 a 904 c 983 g 1351 t 2 GluPheHisArgTrpSerSerTyrMet 10  
ORIGIN 139 GACTTTCTCGTGAGTCACATG 165

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alignment\_scores:  
 Quality: 10.00 Length: 10  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Identity: 100.000

alignment\_block:  
 US-09-155-076-1 x AF030422 ..

Align seg 1/1 to: AF030422 from: 1 to: 4472

1 AlaGluPheHisArgTrpSerSerTyrMet 10  
 3614 GCAGAGTCCACCGATGGAGTCTACATG 3643

seq\_name: gb\_ov:TMACHE2

seq\_documentation block:

LOCUS TMACHE2 605 bp mRNA VRT 14-JUL-1995  
 DEFINITION Torpedo marmorata mRNA fragment for acetylcholinesterase C-term.  
 (PACHE2).

ACCESSION X13172

VERSION X13172.1 GI:64416

KEYWORDS acetylcholinesterase; alternative splicing.

SOURCE marbled electric ray.  
 Organism Torpedo marmorata

ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Chondrichtyes;  
 Elasmobrachii; Rajiformes; Torpedinoidei; Torpedinidae; Torpedo.

REFERENCE Sikorav,J.L., Duval,N., Anselmet,A., Bon,S., Krejci,E., Legry,C.,  
 Osterlund,M., Reimund,B. and Massoulie,J.

AUTHORS

TITLE Complex alternative splicing of acetylcholinesterase transcripts in  
 Torpedo electric organ; primary structure of the precursor of the  
 glycolipid anchored dimeric form

JOURNAL EMBO J. 7 (10), 2983-2993 (1988)

COMMENT See also X13173, X13174 and X05497  
 Data kindly reviewed (24-May-1989) by Massoulie J.

FEATURES Location/Qualifiers

source L .605  
 /organism="Torpedo marmorata"  
 /db\_xref="taxon:788"  
 /tissue\_type="electric organ."  
 /clone="PACHE2"  
 /note="common mRNA sequence"

misc\_feature <1..103  
 /codon\_start\_1  
 /product="acetylcholinesterase (74 AA)"  
 /protein\_id="CAA31570.1"  
 /db\_xref="GI:64417"  
 /db\_xref="SWISS-PROT:P07692"  
 /translation="FIDINTEPKVQIRYOMCVWNQFLPKLNNATEIDEAERQW  
 RTEFHRSYMMHWKNDQSRHENQEL"

misc\_feature 104 ..>605  
 /note="unique mRNA sequence of PACHE2"

BASE COUNT 127 a 228 c 117 g 133 t 9 Length: 9  
 ORIGIN 139 Gaps: 0  
 Percent Similarity: 100.000 Identity: 100.000

alignment\_scores:  
 Quality: 9.00 Length: 9  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
 US-09-155-076-1 x TMACHE2 ..

Align seg 1/1 to: TMACHE2 from: 1 to: 605



OM of: US-09-155-076-1 to: N\_Geneseq\_36:\* out\_format : pfs  
 Date: Sep 13, 2000 3:50 AM  
 About: Results were produced by the Gencore software, version 4.5.  
 Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:  
 -MODEL=frame+p2n,model -DEV=xlp  
 -O=/cgn2.1/usPf0\_spool/US09155076/runat\_29082000\_092339\_16943/app\_query.fasta\_1.144  
 -DB=N\_Geneseq\_36 -QFORMAT=fastap -GAPEXT=4 -LOOPEXT=4 -500  
 -MINMATCH=0.100 -MINPAIR=0.050 -MINPAIREXT=0.000  
 -QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=60.000 -XGAPEXT=60.000  
 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=60.000 -YGAPEXT=60.000  
 -DELOP=6.000 -DELET=7.000 -START=1 -MATRIX=oligo  
 -THR\_MIN=1 ALIGN=15 -MODE=LOCAL -OUTFILE=pfs -NORM=ext -MINLEN=0  
 -MAXLEN=1000000 -USR=US09155076 -CGN1\_1\_75 -NCPU=6 -ICPU=3  
 -LONGLOG -NO\_XLUPXY -WAIT -THREADS=1

Search information block:  
 Query: US-09-155-076-1  
 Query length: 14  
 Database: N\_Geneseq\_36:  
 Database sequences: 311585  
 Database length: 1209602  
 Search time (sec): 75.910000

WARN: YGAPOP and YGAPEXT must be equal. Assuming YGAPOP=60.000  
 WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.000

| score_list:  |
|--|
| Sequence N_Geneseq_36:Q059999 Strd Orig zscore Len ! Documentation   |
| N_Geneseq_36:Q059999 + 14.00 275.66 9.4e-08 1800 1 Sequence encoding foetal human acetylcholinesterase (AC)  |
| N_Geneseq_36:Q05998 + 14.00 274.15 1.1e-07 2253 1 Sequence encoding human acetylcholinesterase (AC)          |
| N_Geneseq_36:Q99002 + 14.00 274.14 1.1e-07 2256 1 Human acetylcholinesterase (AC)                            |
| N_Geneseq_36:T74084 - 6.00 2116.61 67.94 1237 1 Feline immunodeficiency virus CC                             |
| N_Geneseq_36:T47239 - 6.00 2116.01 73.38 1353 1 FIV gag gene. Recombinant racco CC                           |
| N_Geneseq_36:T9076 - 6.00 2116.01 73.38 1353 1 Feline immunodeficiency virus CC                              |
| N_Geneseq_36:085885 - 6.00 2115.69 76.38 1418 1 gag gene of NCSU1 strain of feline immunodeficiency virus CC |
| N_Geneseq_36:W8400 - 6.00 2114.45 89.61 1707 1 Human secreted protein gene 19 CC                             |
| N_Geneseq_36:T84154 - 6.00 2109.06 178.86 3815 1 DNA encoding one known and fou CC                           |
| N_Geneseq_36:V53496 - 6.00 2108.81 515.01 13059 1 Staphylococcus aureus contig CC                            |
| N_Geneseq_36:V74531 + 6.00 2108.53 86.53 3.2e+03 110000 1 Continuation (5 of 6) of V3 CC                     |
| N_Geneseq_36:V30459_4 - 6.00 2108.53 86.53 3.2e+03 110000 1 Continuation (5 of 6) of V3 CC                   |
| N_Geneseq_36:Q57988 + 5.00 124.05 26.15 20 1 Sequence of PCR primer for HBV S                                |
| N_Geneseq_36:T5042 + 5.00 122.83 30.39 24 1 Rat hexokinase I gene PCR primer CC                              |
| N_Geneseq_36:T00113 + 5.00 122.83 30.59 24 1 Hexokinase PCR primer SEQ ID NO: CC                             |
| N_Geneseq_36:V00151 + 5.00 122.83 30.59 24 1 Hexokinase PCR primer SEQ ID NO: CC                             |
| N_Geneseq_36:T75202 + 5.00 122.83 30.59 24 1 Primer used in an assay for ta CC                               |
| N_Geneseq_36:T1232 - 5.00 121.12 38.11 31 1 Cellular apoptosis susceptibility gene CC                        |
| N_Geneseq_36:T11589 + 5.00 118.62 52.50 45 1 Oligonucleotide L4 for monellin CC                              |
| N_Geneseq_36:T11581 - 5.00 118.62 52.50 45 1 Oligonucleotide U3 for monellin CC                              |
| N_Geneseq_36:T72037 + 5.00 116.36 52.50 63 1 Human CPG2 PCR primer CME 00399 CC                              |
| N_Geneseq_36:T65258 - 5.00 113.54 100.68 96 1 Platelet derived growth factor A CC                            |
| N_Geneseq_36:T89719 - 5.00 111.99 122.84 121 1 Friedreich's ataxia STM gene CC                               |
| N_Geneseq_36:T89401 - 5.00 107.77 210.95 227 1 EST clone Cr771. New polynucleotid CC                         |
| N_Geneseq_36:T25215 + 5.00 106.94 234.70 257 1 Methods for diagnosing Friedreich CC                          |
| N_Geneseq_36:T226052 - 5.00 106.46 249.54 276 1 Human gene signature HUNG0376 CC                             |
| N_Geneseq_36:Q60632 + 5.00 106.44 250.31 277 1 Human brain Expressed Sequence CC                             |
| N_Geneseq_36:N70902 - 5.00 106.32 254.19 282 1 EST clone EN271. New polynucleotid CC                         |
| N_Geneseq_36:T87692 + 5.00 106.32 254.19 282 1 Methods for diagnosing Friedreich CC                          |
| N_Geneseq_36:N93187 - 5.00 106.25 256.51 285 1 Human gene signature HUNG0388 CC                              |
| N_Geneseq_36:Q50695 - 5.00 106.25 256.51 285 1 Human gene signature HUNG0376 CC                              |
| N_Geneseq_36:T09154 - 5.00 106.25 256.51 285 1 Monellin single-chain analogue CC                             |
| N_Geneseq_36:T11578 - 5.00 106.25 256.51 285 1 Single chain form monellin anal CC                            |
| N_Geneseq_36:N789719 - 5.00 106.25 256.51 285 1 Single-chain monellin synthetic CC                           |
| N_Geneseq_36:T893527 - 5.00 106.25 256.51 285 1 DNA encoding single-chain form CC                            |
| N_Geneseq_36:T89115 - 5.00 106.25 256.51 285 1 Synthetic gene encoding single CC                             |
| N_Geneseq_36:Y17095 - 5.00 106.25 256.51 285 1 Single chain monellin protein a CC                            |
| N_Geneseq_36:Q48036 - 5.00 106.09 261.92 292 1 "Fused monellin" gene. New recd CC                            |

! Sequence of a synthetic non-c  
 ! Staphylococcus aureus contic  
 ! Human brain Expressed Secon  
 ! Streptococcus pneumoniae sp  
 ! Staphylococcus aureus contic  
 ! Probe (184) for microbial qn  
 seq\_name: N\_Geneseq\_36:Q05999  
 seq\_documentation\_block:  
 ID Q05999 standard; DNA; 1800 BP.  
 AC Q05999;  
 DT 16-JAN-1991 (first entry)  
 DE Sequence encoding foetal human acetylcholinesterase (h2ChE).  
 KW Organophosphorous poisoning; OP; cancer; leukaemia;  
 KW metakaryocytopesis; ovarian cancer; ds.  
 OS Homo sapiens.  
 FH Key  
 FT Location/Qualifiers  
 FT 1..1500  
 FT 3' utr /\*tag= a  
 FT 1501..1800 /\*tag= b  
 FT EP-388906-A.  
 PN PD 26-SEP-1990.  
 PR PF 20-MAR-1990..105274.  
 PA (TISS ) YISSUM RES DEV CO.  
 PI Soreq H, Zukut H;  
 WP; 90-29165/39.  
 DR P-PSDB; R06390.  
 PT Human acetylcholinesterase DNA and prodn. of recombinant hACHE -  
 PT for treatment of organo-phosphorous poisioning and diagnosis of haemo -  
 PT cytropetic disorders and ovarian carcinomas.  
 PS Disclosure: Fig 1C: 47pp; English.  
 CC hACHE is useful as an active pharmaceutical component for the  
 CC prophylaxis and treatment of organophosphorous poisoning, and  
 CC post-surgical apnea due to succinylcholine administration.  
 CC DNA probe to the sequence may be used in diagnosis of various  
 CC leukaemias, abnormal megakarytopoiesis and ovarian carcinomas.  
 CC Bases given as N are obscured in the patent specification.  
 SQ Sequence 1800 BP; 330 A; 602 C; 326 T;  
 alignment\_scores:  
 Quality: 14.00  
 Ratio: 1.000  
 Gaps: 0  
 Percent Similarity: 100.000  
 Percent Identity: 100.000  
 alignment\_block:  
 US-09-155-076-1 x Q05999 ..  
 Align seg 1/1 to: Q05999 from: 1 to: 1800  
 Align seg 1/1 to: Q05999 from: 1 to: 1800  
 1 AlaGluPhHeHsArgTrPSeSerTyMetylHistPlys 14  
 1414 GCGAGTTCCACCGCTTGTGACTGTGGAG 1455  
 seq\_name: N\_Geneseq\_36:Q05998  
 seq\_documentation\_block:  
 ID Q05998 standard; DNA;  
 AC Q05998;  
 DT 16-JAN-1991 (first entry)  
 DE Sequence encoding human acetylcholinesterase (h2ChE).  
 KW Organophosphorous poisoning; OP; cancer; leukaemia;  
 KW metakaryocytopesis; ovarian cancer; ds.  
 OS Homo sapiens.  
 PN EP-388906-A.  
 PD 26-SEP-1990.  
 PR PF 20-MAR-1989..105274.  
 PA (TISS ) YISSUM RES DEV CO.  
 PI Soreq H, Zukut H;



FT 1513. .1535  
 FT /\*tag= b  
 FT /note= "3, primer binding region"  
 PN W09640266-A1.  
 PD 19-DEC-1996.  
 PF 03-JUN-1996; U08508.  
 PR 07-JUN-1995; US-162090.  
 PA (AMHP ) AMERICAN HOME PROD CORP.  
 PI Chavez LG, Chu H, Wasmoen T;  
 DR WPI; 97-051908/05.  
 DR P-PSDB; W07847.  
 PT Recombinant raccoon poxvirus - with at least 1 internal gene  
 encoding feline immunodeficiency virus env or gag protein, useful in  
 vaccine for prophylaxis of disease  
 PS Claim 11: Fig 5A-C; 50pp; English.  
 CC The FIV gag gene (T47239) encoding the FIV gag protein (W07847) can  
 be included in recombinant raccoon poxviruses (RRPV) to provide  
 recombinant vaccines that protect felines from FIV infection. The  
 gag gene was obtld by PCR amplification (see also T47246-47) and  
 cloned into pSL1190. Vero cells were infected with wild-type RRV  
 (ATCC VR-838) and then transfected with PSCII-FIV gag to obtain  
 the RRPV. Other RRPVs may include DNA sequences encoding FIV  
 env (see also T47238), envAB or immunogenic fragments of FIV env  
 CC sequence 1353 BP; 480 A; 230 C; 325 G; 318 T;

alignment\_scores:  
 Quality: 6.00 Length: 6  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000

seq\_name: N\_Geneseq\_36:Q85885

seq\_documentation\_block:  
 ID Q85885 standard; cdNA; 1418 BP.  
 AC Q85885;  
 DT 24-OCT-1995 (first entry)  
 DE gag gene of NCSU1 strain of feline immunodeficiency virus.  
 KW Feline immunodeficiency virus; FIV; CD4; CD8; antigen; vaccine;  
 KW diagnosis; primer; probe; acquired immune deficiency syndrome; AIDS;  
 KW model system; screening; long terminal repeat; LTR; ss.  
 OS Feline immunodeficiency virus (NCSU1 strain).  
 FH Key Location/Qualifiers  
 FT 23 .1375 /\*tag= a  
 FT /product= NCSU1 FIV gag gene product.

FT FT  
 PN W09505460-A.  
 PD 23-FEB-1995.  
 PF 25-JUL-1994; U08364.  
 PR 03-SEP-1991; US-752424.  
 PR 12-AUG-1993; US-105710.  
 PA (UNIV ) UNIV NORTH CAROLINA STATE.  
 PI Tompkins MB, Tompkins WAF;  
 DR WPI; 95-09876/013.  
 DR P-PSDB; R71479.  
 PT New isolate of feline immunodeficiency virus - and infected host  
 PT cells, DNA, vectors and infected cats, useful in vaccines and as  
 PT models for human AIDS  
 PS Example 12: Page 38-40; 50pp; English.  
 CC The NCSU1 strain (ATCC VR233) of the feline immunodeficiency virus  
 CC (FIV) is highly infectious in vivo and causes a rapid inversion of  
 CC the CD4+:CD8+ ratio in infected animals. Antigenic fragments of the  
 CC virus can be used in vaccines. Fragments of the DNA can also be used  
 CC diagnostically as probes and primers and for expressing viral  
 CC antigens. Cats infected with the virus are useful as model systems  
 CC for studying AIDS and for screening therapeutic drugs. Two primers  
 CC (Q85883, Q85884) were used to amplify the gag gene of the NCSU1  
 CC strain of FIV for its subcloning and subsequent sequencing.  
 SQ Sequence 1418 BP; 506 A; 239 G; 341 C; 332 T;

alignment\_scores:  
 Quality: 6.00 Length: 6  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000

seq\_name: N\_Geneseq\_36:T49076

seq\_documentation\_block:  
 ID T49076 standard; DNA; 1353 BP.  
 AC T49076;  
 DT 24-SEP-1997 (first entry)  
 DE Feline immunodeficiency virus gag gene encoding DNA.  
 KW FIV p10; nucleocapsid; virion; vaccine; cat; ss.  
 OS Feline immunodeficiency virus.  
 FH Key Location/Qualifiers  
 FT 1. .1353 /\*tag= a  
 FT /product= FIV\_gag  
 FT misc\_feature  
 FT 1126..1241 /\*tag= b  
 FT /note= "can delete this segment of nucleotides  
 FT encoding the nucleocapsid (p10) protein"  
 PN W09640953-A1.  
 PD 19-DEC-1996.  
 PF 03-JUN-1996; U08639.  
 PR 07-JUN-1995; US-479703.  
 PA (AMHP ) AMERICAN HOME PROD CORP.  
 PI Chavez LG, Huang C, Wasmoen T;  
 DR WPI; 97-065191/06.  
 DR P-PSDB; W08435.  
 PT Plasmid encoding feline immunodeficiency virus with incomplete  
 PT nucleo: capsid p10 protein - for production of virion(s) lacking  
 PT packaged RNA useful in FIV vaccines  
 PS Claim 2; Fig 2; 36pp; English.  
 CC The present sequence encodes the feline immunodeficiency virus  
 CC (FIV) gag gene, which contains the nucleotides encoding the whole  
 CC nucleocapsid (p10) protein. In a preferred example of the FIV

3 PheHisArgTrpSerSer 8  
 ||||||| |||||  
 388 TTCTAGATGGTGTAGT 371

seq\_name: N\_Geneseq\_36.v84600

## seq\_documentation.block:

ID: V84600 standard; DNA: 1707 BP.

AC: V84600;

DT: 01-NAR-1999 (first entry)

DE: Human secreted protein gene 190 clone HIASB53.  
 KW: Human; secreted protein; fusion protein; gene therapy; protein therapy;  
 KW: diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;  
 KW: developmental abnormality; blood; allergy; renal; ds;  
 KW: foetal deficiency; brain; hepatic; lymphoma;  
 KW: immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;  
 KW: inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;  
 KW: cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;  
 KW: osteoporosis; arthritis; testis; lung; thyroiditis; thyroditis; digestion;  
 KW: endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.  
 OS: Homo sapiens.

PN: W09854963-A2.

PD: 10-DEC-1998.

PF: 04-JUN-1998; 0114:22.

PR: 18-DEC-1997; US-070523.

PR: 06-JUN-1997; US-048877.

PR: 06-JUN-1997; US-048881.

PR: 06-JUN-1997; US-048884.

PR: 06-JUN-1997; US-048893.

PR: 06-JUN-1997; US-048896.

PR: 06-JUN-1997; US-048899.

PR: 06-JUN-1997; US-048915.

PR: 06-JUN-1997; US-048949.

PR: 06-JUN-1997; US-048964.

PR: 06-JUN-1997; US-048972.

PR: 06-JUN-1997; US-049010.

PR: 06-JUN-1997; US-049315.

PR: 05-SEP-1997; US-057628.

PR: 05-SEP-1997; US-057635.

PR: 05-SEP-1997; US-057647.

PR: 05-SEP-1997; US-057650.

PR: 05-SEP-1997; US-057651.

PR: 05-SEP-1997; US-057661.

PR: 05-SEP-1997; US-057761.

PR: 05-SEP-1997; US-057764.

PR: 05-SEP-1997; US-057770.

PR: 05-SEP-1997; US-057775.

PR: 05-SEP-1997; US-057778.

PR: 06-JUN-1997; US-048875.

PR: 06-JUN-1997; US-048900.

PR: 06-JUN-1997; US-048916.

PR: 06-JUN-1997; US-048962.

PR: 06-JUN-1997; US-048894.

PR: 06-JUN-1997; US-048897.

PR: 06-JUN-1997; US-048970.

PR: 06-JUN-1997; US-048974.

PR: 06-JUN-1997; US-049373.

PR: 05-SEP-1997; US-057584.

PR: 05-SEP-1997; US-057629.

PR: 05-SEP-1997; US-057642.

PR: 05-SEP-1997; US-057645.

PR: 05-SEP-1997; US-057648.

PR: 05-SEP-1997; US-057651.

PR: 05-SEP-1997; US-057662.

PR: 05-SEP-1997; US-057666.

PR: 05-SEP-1997; US-057760.

PR: 05-SEP-1997; US-057763.

PR: 05-SEP-1997; US-057769.

PR: 05-SEP-1997; US-057774.

PR: 05-SEP-1997; US-057777.

PR: 05-SEP-1997; US-057778.

PR: 05-SEP-1997; US-057779.

PR: 05-SEP-1997; US-057780.

PR: 05-SEP-1997; US-057781.

PR: 05-SEP-1997; US-057782.

PR: 05-SEP-1997; US-057783.

PR: 05-SEP-1997; US-057784.

PR: 05-SEP-1997; US-057785.

PR: 05-SEP-1997; US-057786.

PR: 05-SEP-1997; US-057787.

PR: 05-SEP-1997; US-057788.

PR: 05-SEP-1997; US-057789.

PR: 05-SEP-1997; US-057790.

PR: 05-SEP-1997; US-057791.

PR: 05-SEP-1997; US-057792.

PR: 05-SEP-1997; US-057793.

PR: 05-SEP-1997; US-057794.

PR: 05-SEP-1997; US-057795.

PR: 05-SEP-1997; US-057796.

PR: 05-SEP-1997; US-057797.

PR: 05-SEP-1997; US-057798.

PR: 05-SEP-1997; US-057799.

PR: 05-SEP-1997; US-057800.

PR: 05-SEP-1997; US-057801.

PR: 05-SEP-1997; US-057802.

PR: 05-SEP-1997; US-057803.

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PR: 05-SEP-1997; US-057817.

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PR: 05-SEP-1997; US-057821.

PR: 05-SEP-1997; US-057822.

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PR: 05-SEP-1997; US-057824.

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PR: 05-SEP-1997; US-057827.

PR: 05-SEP-1997; US-057828.

PR: 05-SEP-1997; US-057829.

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PR: 05-SEP-1997; US-057831.

PR: 05-SEP-1997; US-057832.

PR: 05-SEP-1997; US-057833.

PR: 05-SEP-1997; US-057834.

PR: 05-SEP-1997; US-057835.

PR: 05-SEP-1997; US-057836.

PR: 05-SEP-1997; US-057837.

PR: 05-SEP-1997; US-057838.

PR: 05-SEP-1997; US-057839.

PR: 05-SEP-1997; US-057840.

PR: 05-SEP-1997; US-057841.

PR: 05-SEP-1997; US-057842.

PR: 05-SEP-1997; US-057843.

PR: 05-SEP-1997; US-057844.

PR: 05-SEP-1997; US-057845.

PR: 05-SEP-1997; US-057846.

PR: 05-SEP-1997; US-057847.

PR: 05-SEP-1997; US-057848.

PR: 05-SEP-1997; US-057849.

PR: 05-SEP-1997; US-057850.

PR: 05-SEP-1997; US-057851.

PR: 05-SEP-1997; US-057852.

PR: 05-SEP-1997; US-057853.

PR: 05-SEP-1997; US-057854.

PR: 05-SEP-1997; US-057855.

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PR: 05-SEP-1997; US-057859.

PR: 05-SEP-1997; US-057860.

PR: 05-SEP-1997; US-057861.

PR: 05-SEP-1997; US-057862.

PR: 05-SEP-1997; US-057863.

PR: 05-SEP-1997; US-057864.

PR: 05-SEP-1997; US-057865.

PR: 05-SEP-1997; US-057866.

PR: 05-SEP-1997; US-057867.

PR: 05-SEP-1997; US-057868.

PR: 05-SEP-1997; US-057869.

PR: 05-SEP-1997; US-057870.

PR: 05-SEP-1997; US-057871.

PR: 05-SEP-1997; US-057872.

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PR: 05-SEP-1997; US-057874.

PR: 05-SEP-1997; US-057875.

PR: 05-SEP-1997; US-057876.

PR: 05-SEP-1997; US-057877.

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PR: 05-SEP-1997; US-057881.

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PR: 05-SEP-1997; US-057890.

PR: 05-SEP-1997; US-057891.

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PR: 05-SEP-1997; US-057893.

PR: 05-SEP-1997; US-057894.

PR: 05-SEP-1997; US-057895.

PR: 05-SEP-1997; US-057896.

PR: 05-SEP-1997; US-057897.

PR: 05-SEP-1997; US-057898.

PR: 05-SEP-1997; US-057899.

PR: 05-SEP-1997; US-057900.

PR: 05-SEP-1997; US-057901.

PR: 05-SEP-1997; US-057902.

PR: 05-SEP-1997; US-057903.

PR: 05-SEP-1997; US-057904.

PR: 05-SEP-1997; US-057905.

PR: 05-SEP-1997; US-057906.

PR: 05-SEP-1997; US-057907.

PR: 05-SEP-1997; US-057908.

PR: 05-SEP-1997; US-057909.

PR: 05-SEP-1997; US-057910.

PR: 05-SEP-1997; US-057911.

PR: 05-SEP-1997; US-057912.

PR: 05-SEP-1997; US-057913.

PR: 05-SEP-1997; US-057914.

PR: 05-SEP-1997; US-057915.

PR: 05-SEP-1997; US-057916.

PR: 05-SEP-1997; US-057917.

PR: 05-SEP-1997; US-057918.

PR: 05-SEP-1997; US-057919.

PR: 05-SEP-1997; US-057920.

PR: 05-SEP-1997; US-057921.

PR: 05-SEP-1997; US-057922.

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PR: 05-SEP-1997; US-057925.

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PR: 05-SEP-1997; US-057931.

PR: 05-SEP-1997; US-057932.

PR: 05-SEP-1997; US-057933.

PR: 05-SEP-1997; US-057934.

PR: 05-SEP-1997; US-057935.

PR: 05-SEP-1997; US-057936.

PR: 05-SEP-1997; US-

Align seg 1/1 to reverse of: T84600 from: 1 to: 1707

6 TrpSerTyrMetVal 11  
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 750 TGGTCCTATGGTT 733

seq\_name: N\_Geneseq\_36:T84154

seq\_documentation\_block:  
 ID T84154 standard; DNA: 3815 BP.

AC V53496; (first entry)  
 DT 07-SEP-1998 DE DNA encoding one known and four unknown staphylococcus aureus proteins.  
 DE Staphylococcus aureus protein; antisense sequence; control;  
 KW Staphylococcal gene; regulatory element; bacterial gene expression;  
 KW vaccine; Staphylococcal infection; food poisoning; scaled skin syndrome;  
 KW toxic shock syndrome; ss.  
 KW Staphylococcus aureus;  
 FH Location/Qualifiers  
 FT 257 . 934  
 FT /product= "Preprotein translocase SECY subunit"  
 FT 945 . 1280  
 FT /\*\*tag= b  
 FT /product= "Encodes protein W28243"  
 FT 1610 . 2362  
 FT /\*\*tag= C  
 FT /product= "Encodes protein W28244"  
 FT 3364  
 FT /\*\*tag= d  
 FT /product= "Encodes protein W28245"  
 FT 3380 . 3559  
 FT /\*\*tag= e  
 FT /product= "Encodes protein W28246"  
 PN W09730070-A1.  
 PD 21-AUG-1997.  
 PF 19-FEB-1997; U02318.  
 PR PA (SMITHKLINE BEPHAM CORP.  
 PI Black MT, Burnham MK, Hodgson JE, Knowles DJC, Nicholas RO,  
 PR Pratt JM, Reichard RW, Rosenberg M, Ward JM;  
 DR WPI: 97-424569/39.  
 P-PSDB: W28242, W28243, W28244, W28245, W28246.  
 Novel polypeptides from staphylococcus aureus strain WCUH29 - used  
 PR to isolate antimicrobial compounds, and in vaccines against S.  
 PR aureus infection  
 PS Claim 9; Pages 915-916; 980pp; English.

The present sequence encodes four Staphylococcus aureus proteins of  
 unknown function. The sequence also encodes a Staphylococcus aureus  
 protein, that, based on homology with a Bacillus subtilis protein,  
 is believed to be a preprotein translocase SECY subunit. The present  
 sequence was obtained from a library of clones of S. aureus WCUH 29  
 in Escherichia coli. The DNA sequence can be used in the construction  
 of ribozymes and antisense sequences to control the expression of  
 Staphylococcal genes. The DNA sequence is also useful as a source of  
 regulatory elements for the control of bacterial gene expression. The  
 encoded protein may be used to produce vaccines to enable a host to  
 produce specific antibodies with antibacterial action. These vaccines  
 and antibodies would protect a host against invasion by S. aureus, and  
 conditions relating to Staphylococcal infection, e.g. Staphylococcal  
 food poisoning, scaled skin syndrome, and toxic shock syndrome.  
 Sequence 3815 BP; 1267 A; 562 C; 750 G; 1199 T;

alignment\_scores:  
 Quality: 6.00 Length: 6  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
 US-09-155-076-1 x T84154/rev ..  
 Align seg 1/1 to reverse of: T84154 from: 1 to: 3815

4 HisArgTrpSerSerTyr 9  
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 985 CATCGTGTGTCATCGTAC 968

seq\_name: N\_Geneseq\_36:V53496

seq\_documentation\_block:  
 ID V53496 standard; DNA: 3815 BP.

AC V53496; (first entry)  
 DT 13-MAY-1998 DE DNA encoding a Staphylococcus aureus protein of unknown function.  
 DE Staphylococcus aureus Protein; immune response induction; eye infection;  
 KW T-cell immune response; gastrointestinal infection;  
 KW respiratory infection; inhibitor; bacterial; gastrointestinal infection;  
 KW central nervous system; kidney infection; urinary tract infection;  
 KW antimicrobial compound identification; broad spectrum antibiotic;  
 KW therapy; ss.  
 OS Staphylococcus aureus.  
 PN EP 841394-AZ.  
 PD 13-MAY-1998.  
 PF 24-SEP-1997; 307485.  
 DR 24-SEP-1996; US-027032.  
 PA (SMIK ) SMITHKLINE BEPHAM CORP.  
 PA (SMIK ) SMITHKLINE BEPHAM PLC.  
 PA Black MT, Burnham MKR, Hodgson JE, Knowles DJC, Reichard RW, Rosenberg M,  
 PI Loretto MA, Nicholas RO, Pratt JM, Reichard RW, Rosenberg M,  
 PI Ward JM; Page 160-162; 390pp; English.  
 PI WPI; 98-252940/23.  
 DR P-PSDB; W7704.  
 PT New nucleic acid sequences from Staphylococcus aureus WCUH29 -  
 PT useful in vaccines and for treatment of bacterial infections of, e.g.  
 PT respiratory tract and central nervous system  
 PS Claim 1; Page 160-162; 390pp; English.  
 CC This sequence encodes a Staphylococcus aureus protein of unknown  
 CC function, and represents a DNA sequence of the invention.  
 CC The DNA sequences were isolated from Staphylococcus aureus WCUH29  
 CC (NCIMB 40771). Host cells containing the DNA sequences are used to  
 CC produce polypeptides or fragments. The proteins are used in the treatment  
 CC of disease, for inducing an immune response by administering them, to  
 CC produce antibody and/or T-cell immune response. Antagonists of the  
 CC proteins are used for the inhibition of bacterial polypeptides.  
 CC Conditions which may be treated include bacterial infections, especially  
 CC respiratory, cardiac, gastrointestinal, central nervous, eye, kidney,  
 CC urinary tract, skin, bones and joints. The proteins can also be used to  
 CC identify antimicrobial compounds which are broad spectrum antibiotics,  
 CC especially useful in the treatment of H. pylori infection.  
 SQ Sequence 3815 BP; 1267 A; 562 C; 750 G; 1199 T;

alignment\_scores:  
 Quality: 6.00 Length: 6  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
 US-09-155-076-1 x V53496/rev ..

Align seg 1/1 to reverse of: V53496 from: 1 to: 3815

4 HisArgTrpSerSerTyr 9  
 ||||| ||||| |||||  
 985 CATCGTGTGTCATCGTAC 968

seq\_name: N\_Geneseq\_36:V74531

seq\_documentation\_block:  
 ID V74531 standard; DNA: 13059 BP.  
 AC V74531; ●  
 DT 16-MAR-1999 (first entry)  
 DE Staphylococcus aureus Contig SEQ ID #220.  
 KW Computer readable medium; vaccine; S. aureus infection; immunodetection;  
 KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;

KW skin infection; surgical wound infection; scalded skin syndrome;  
 KW toxic shock syndrome; ds.  
 OS Staphylococcus aureus.  
 Location/Qualifiers  
 FT 301 .360  
 misc\_feature  
 FT /\*tag= "these bases represent a line of missing text in  
 FT the sequence listing in the specification. They  
 FT are included to maintain the nucleotide numbering  
 FT given in the specification for this DNA sequence"  
 misc\_feature 2101 .2160  
 FT /\*tag= "these bases represent a line of missing text in  
 FT the sequence listing in the specification. They  
 FT are included to maintain the nucleotide numbering  
 FT given in the specification for this DNA sequence"  
 misc\_feature 3901 .3960  
 FT /\*tag= "these bases represent a line of missing text in  
 FT the sequence listing in the specification. They  
 FT are included to maintain the nucleotide numbering  
 FT given in the specification for this DNA sequence"  
 misc\_feature 5701 .5760  
 FT /\*tag= "these bases represent a line of missing text in  
 FT the sequence listing in the specification. They  
 FT are included to maintain the nucleotide numbering  
 FT given in the specification for this DNA sequence"  
 misc\_feature 7501 .7500  
 FT /\*tag= "these bases represent a line of missing text in  
 FT the sequence listing in the specification. They  
 FT are included to maintain the nucleotide numbering  
 FT given in the specification for this DNA sequence"  
 misc\_feature 9301 .9360  
 FT /\*tag= "these bases represent a line of missing text in  
 FT the sequence listing in the specification. They  
 FT are included to maintain the nucleotide numbering  
 FT given in the specification for this DNA sequence"  
 misc\_feature 11101 .11160  
 FT /\*tag= "these bases represent a line of missing text in  
 FT the sequence listing in the specification. They  
 FT are included to maintain the nucleotide numbering  
 FT given in the specification for this DNA sequence"  
 misc\_feature 12901 .12960  
 FT /\*tag= "these bases represent a line of missing text in  
 FT the sequence listing in the specification. They  
 FT are included to maintain the nucleotide numbering  
 FT given in the specification for this DNA sequence"  
 PN EP-786519-A2.  
 PD 30-JUL-1997.  
 PR 07-JAN-1997; 100117.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PI Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA,  
 PI Rosen CA,  
 DR 97-374922/35.  
 PT Polynucleotide(s) and proteins derived from *Staphylococcus aureus*  
 PT stored on computer readable medium and used in the production of  
 PT anti-*S. aureus* vaccines  
 PS Claim 1: Page 972-980; 3211PP; English.  
 CC This sequence represents one of 5191 *Staphylococcus aureus* DNA sequences  
 CC of the invention. The DNA sequences are recorded on a computer readable  
 CC medium, preferably selected from a floppy or hard disk, random access  
 CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using  
 CC the *S. aureus* DNA sequences allows putative functions to be assigned so  
 CC that protein-encoding or regulatory regions of commercial, therapeutic or  
 CC industrial importance can be obtained. Specifically, sequences which are  
 CC likely to encode antigens can be identified and these polypeptides can  
 CC be used in a vaccine composition against *S. aureus* infection. The

CC polypeptides can also be used in a kit for the immunodetection of  
 CC *S. aureus* in a sample. *S. aureus* is implicated in numerous human diseases,  
 CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,  
 CC skin and surgical wound infections, scalded skin syndrome, toxic shock  
 CC syndrome, etc. organisms transformed with the DNA sequences can be used  
 CC for recombinant production of the polypeptides. The new DNA sequences  
 CC (and their fragments) are useful as primers or probes for isolating  
 CC homologues of any of the *S. aureus* DNA sequences contained on the  
 CC computer readable medium.  
 Sequence 13059 BP; 3881 A; 2438 C; 1860 G; 4390 T;

alignment\_scores:  
 Quality: 6.00 Length: 6  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Identity: 100.000

alignment\_block:  
 US-09-155-076-1 x V74531 ..

Align seg 1/1 to: V74531 from: 1 to: 13059

4 His Arg Trp Ser Ser Tyr 9  
 10149 CATCGTGGTCATCGTAC 10166

seq\_name: N\_Geneseq\_36:v30458\_4

seq\_documentation\_block:  
 Continuation (5 of 6) of V30458 from base 400001 (Rhizobium species plasmid pNGR234a.  
 WP Sequence split into 6 fragments Locus v30458 Accession v30458  
 WP Fragment Name Begin End  
 V30458-0 1 110000  
 V30458-1 100001 210000  
 V30458-2 200001 310000  
 V30458-3 300001 410000  
 V30458-4 400001 510000  
 V30458-5 500001 534720

alignment\_scores:  
 Quality: 6.00 Length: 6  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Identity: 100.000

alignment\_block:  
 US-09-155-076-1 x V30458\_4/rev ..

Align seg 1/1 to reverse of: V30458\_4 from: 1 to: 110000

3 Phe His Arg Trp Ser Ser 8  
 73348 TTTCACAGGTGTCCTCT 73331

seq\_name: N\_Geneseq\_36:v30459\_4

seq\_documentation\_block:  
 Continuation (5 of 6) of V30459 from base 400001 (Rhizobium species symbiotic plasmid  
 WP Sequence split into 6 fragments Locus v30459 Accession v30459  
 WP Fragment Name Begin End  
 V30459-0 1 110000  
 V30459-1 100001 210000  
 V30459-2 200001 310000  
 V30459-3 300001 410000  
 V30459-4 400001 510000  
 V30459-5 500001 536165

alignment\_scores:  
 Quality: 6.00 Length: 6  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Identity: 100.000

alignment\_block:  
US-09-155-076-1 x V30459\_4/rev  
Align seg 1/1 to reverse of: V30459\_4 from: 1 to: 1100000

3 PheHisArgGtpSerSer 8  
||||||| 73348 TTTCACAGGTTCCCTCT 73331

seq\_name: N\_Geneseq\_36:067988

seq\_documentation\_block:  
ID Q67988 standard; DNA; 20 BP.

AC DT 02-JAN-1995 (first entry)  
DE Sequence of PCR primer for HBV S-region.  
Core antigen; recombinant replicable vaccinia virus; hepatitis;  
KW prevention; therapy; epitope; hepatitis B virus; PCR primer; ss.  
OS Synthetic.  
PN WO912617A.  
PD 09-JUN-1994.  
PF 24-NOV-1993; U11474.

PR 25-NOV-1992; US-982211.  
PA (ITBI-) INT BIOTECHNOLOGY LAB INC.  
PI Bernstein EG, Lewis T, Okeefe RN, Souw PTS;  
WPI: 94-200247/24.  
PT Prevention and treatment of hepatitis - using recombinant  
replicable vaccinia viruses contg. hepatitis B virus surface and  
core antigen nucleotide sequences.

Example: Page 76; 252pp; English.  
A construct was made consisting from the amino terminus of  
the S antigen, and a 7 AA tail (NSGQIYK). This fusion  
polypeptide is referred to as core-S\* because only a small  
portion of the S antigen is present. A 197 bp piece of the S  
region containing the immunogenic regions was generated by PCR  
of pLEH-Q4 using primer Q67987 which hybridises from bases  
+304 to +323 of the S region and is designed to introduce  
a BAP1 site. A second primer was Q67988 which hybridises to the  
opposite strand from bps +500 to +481 of the S region and is designed to  
create an EcoRI site upon amplification. The sequences of the  
core-S\* fusion in the resulting plasmid, pHL28, are given in  
Q67971 and R55588.  
Sequence 20 BP; 5 A; 4 C; 6 G; 5 T;

alignment\_scores:  
Quality: 5.00 Length: 5  
Ratio: 1.00 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
US-09-155-076-1 x Q67988 ..  
Align seg 1/1 to: Q67988 from: 1 to: 20

1 AlaGluPheHisArg 5  
||||||| 5 GCGGATTCCATAGG 19

seq\_name: N\_Geneseq\_36:T75042

seq\_documentation\_block:  
ID T75042 standard; DNA; 24 BP.  
AC DT 02-FEB-1998 (first entry)  
DE Rat hexokinase I gene PCR primer.  
KW recombinant protein; expression; secretory cell line; RIN;  
KW insulinoma; hexokinase I; insulin; diabetes; gene therapy; primer;  
KW PCR; Polymerase chain reaction; rat; ss.  
OS Synthetic.  
OS Rattus sp.  
PN WO9726321-A2.

PD 24-JUL-1997; U00761.  
PF 17-JAN-1997; U00761.  
PR 15-OCT-1996; US-038427.  
PR 19-JAN-1996; US-589028.  
(BETA-) BETAGENE INC.  
PA (TEXA) UNIV TEXAS SYSTEM.  
PI Clark SA, Halban PA, Kruse F, McGarry D, Newgard CB;  
PI Normington KD, Quade C, Thigpen AE;  
WPI: 97-1385326/35.  
DR Recombinant cell engineered to provide amylin to a mammal - useful  
PT to treat e.g. angiogenesis, anoxia, obesity, hypertension,  
osteooporosis etc.  
PT Example 1; Page 132; 33pp; English.

This primer is located in the rat hexokinase I (HKI) gene  
downstream of a putative recombination site. It was used with a  
primer (see T75041) located upstream of the recombination site  
in a control PCR to detect homologous and random integrants of a  
HKI gene replacement vector following electroporation of rat RIN  
insulinoma cells. Interference with HKI function reduces the  
growth rate of cells and may allow the development of engineered  
cells that exhibit glucose-regulatable insulin secretion. The  
invention provides methods for production of heterologous  
polypeptides, e.g. amylin, using recombinantly engineered cell  
lines. Also described are methods of engineering cells for high  
level expression, methods of large-scale heterologous protein  
production, methods for treatment of disease in vivo using viral  
delivery systems and recombinant cell lines, and methods for  
isolating novel amylin receptors.  
Sequence 24 BP; 4 A; 6 C; 6 G; 8 T;

alignment\_scores:  
Quality: 5.00 Length: 5  
Ratio: 1.00 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
US-09-155-076-1 x T75042 ..  
Align seg 1/1 to: T75042 from: 1 to: 24

7 SerSerTyrMetVal 11  
||||||| 5 AGCTCTTACATGGTG 19



OM of: US-09-155-076-1 to: Issued\_Patents\_NA:\* out\_format : pfs  
 Date: Sep 13, 2000 3:48 AM  
 About: Results were produced by the GenCore software, version 4.5,  
 Copyright (c) 1993-2000 Compugen Ltd.

## Command line parameters:

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-Q-/cgn2_1/podata/spool1/us09155076/runat_29082000_092539_16923/app_query.fasta_1.144
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -GAPOP=4.500
-GAPEXT=0.050 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QGAPOP=4.500 -QGPEXT=0.050 -XGAPOP=60.000 -XGPEXT=60.000
-XGAPOP=6.000 -DEFLEXT=7.000 -STRRT=1 -MATRIX=OLIGO
-TRANS=human40.cdi -LIST=15 -DOCALIGN=200 -THR_SCOREB=quality
-MAXLEN=1000000 -ALIGN=15 -MODE=N -OUTFILE=Pfs -NORMEXT -MINLEN=0
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## Search information block:

Query: US-09-155-076-1
 Query Length: 14
 Database: Issued\_Patents\_NA:\*
 Database sequences: 243080
 Database length: 68771915
 Search time (sec): 60.430000
 WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP=60.000
 WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.000

## score list:

| Sequence   | Stnd  | Orig   | ZScore  | Escore | Len | Documentation | Length: | Quality: | Length: |
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| /cgn2_6/podata/2/ina/5D_COMB.seq;US-08-310-156-24 +    | 14.00 | 87.63  | 1.5e-08 | 374    | 1   |               | 14      | 0.00     | 14.00   |
| /cgn2_6/podata/2/ina/5D_COMB.seq;US-08-310-156-26 +    | 14.00 | 279.16 | 4.3e-08 | 1215   | 1   |               | 14      | 0.00     | 14.00   |
| /cgn2_6/podata/2/ina/5A_COMB.seq;US-07-72-962A-01 +    | 14.00 | 276.97 | 6.2e-08 | 1845   | 1   |               | 14      | 0.00     | 14.00   |
| /cgn2_6/podata/2/ina/5C_PCTUS.COMB.seq;US-06-106-1 +   | 14.00 | 276.97 | 6.2e-08 | 1845   | 1   |               | 14      | 0.00     | 14.00   |
| /cgn2_6/podata/2/ina/5C_COMB.seq;US-08-318-826A-5 +    | 14.00 | 275.63 | 7.3e-08 | 2256   | 1   |               | 14      | 0.00     | 14.00   |
| /cgn2_6/podata/2/ina/5D_COMB.seq;US-08-315-156-1 +     | 14.00 | 275.63 | 7.3e-08 | 2256   | 1   |               | 14      | 0.00     | 14.00   |
| /cgn2_6/podata/2/ina/5C_COMB.seq;US-08-314-095-1 +     | 14.00 | 275.63 | 7.3e-08 | 2256   | 1   |               | 14      | 0.00     | 14.00   |
| /cgn2_6/podata/2/ina/5C_COMB.seq;US-08-318-826A-7 +    | 14.00 | 273.69 | 9.4e-08 | 3016   | 1   |               | 14      | 0.00     | 14.00   |
| /cgn2_6/podata/2/ina/5D_COMB.seq;US-08-316-156-5 +     | 14.00 | 273.69 | 9.4e-08 | 3016   | 1   |               | 14      | 0.00     | 14.00   |
| /cgn2_6/podata/2/ina/5C_COMB.seq;US-08-314-095-5 +     | 14.00 | 273.69 | 9.4e-08 | 3016   | 1   |               | 14      | 0.00     | 14.00   |
| /cgn2_6/podata/2/ina/5C_COMB.seq;US-08-318-826A-6 +    | 14.00 | 273.31 | 9.6e-08 | 3096   | 1   |               | 14      | 0.00     | 14.00   |
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| /cgn2_6/podata/2/ina/5C_COMB.seq;US-08-314-095-7 +     | 14.00 | 25.30  | 7.7e-07 | 3500   | 1   |               | 14      | 0.00     | 14.00   |
| /cgn2_6/podata/2/ina/5B_COMB.seq;US-08-442-090-7 -     | 6.00  | 115.99 | 57.13   | 1353   | 1   |               | 14      | 0.00     | 14.00   |
| /cgn2_6/podata/2/ina/5C_COMB.seq;US-09-383-13 -        | 6.00  | 115.99 | 57.13   | 1353   | 1   |               | 14      | 0.00     | 14.00   |
| /cgn2_6/podata/2/ina/5D_COMB.seq;US-08-107-383-13 -    | 6.00  | 115.68 | 59.13   | 1353   | 1   |               | 14      | 0.00     | 14.00   |
| /cgn2_6/podata/2/ina/5A_COMB.seq;US-08-105-710-6 -     | 6.00  | 115.68 | 59.48   | 1418   | 1   |               | 14      | 0.00     | 14.00   |
| /cgn2_6/podata/2/ina/5A_COMB.seq;US-08-363-901-6 -     | 6.00  | 115.68 | 59.48   | 1418   | 1   |               | 14      | 0.00     | 14.00   |
| /cgn2_6/podata/2/ina/5C_COMB.seq;US-08-776-251-24 -    | 5.00  | 123.43 | 22.01   | 21     | 1   | Se            | 14      | 0.00     | 14.00   |
| /cgn2_6/podata/2/ina/5C_COMB.seq;US-08-776-251-35 +    | 5.00  | 123.43 | 22.01   | 21     | 1   | Se            | 14      | 0.00     | 14.00   |
| /cgn2_6/podata/2/ina/5C_COMB.seq;US-08-483-415-30 +    | 5.00  | 118.34 | 42.28   | 45     | 1   | Se            | 14      | 0.00     | 14.00   |
| /cgn2_6/podata/2/ina/5C_COMB.seq;US-08-483-415-30 +    | 5.00  | 118.34 | 42.28   | 45     | 1   | Se            | 14      | 0.00     | 14.00   |
| /cgn2_6/podata/2/ina/5A_COMB.seq;US-08-458-976-41 -    | 5.00  | 118.34 | 42.28   | 45     | 1   | Se            | 14      | 0.00     | 14.00   |
| /cgn2_6/podata/2/ina/5A_COMB.seq;US-08-293-81E-14 +    | 5.00  | 122.26 | 25.56   | 25     | 1   | Se            | 14      | 0.00     | 14.00   |
| /cgn2_6/podata/2/ina/5A_COMB.seq;US-08-293-81E-30 +    | 5.00  | 122.26 | 25.56   | 25     | 1   | Se            | 14      | 0.00     | 14.00   |
| /cgn2_6/podata/2/ina/5D_COMB.seq;US-09-116-607-6 +     | 5.00  | 122.26 | 25.56   | 25     | 1   | Se            | 14      | 0.00     | 14.00   |
| /cgn2_6/podata/2/ina/5A_COMB.seq;US-05-092-11 -        | 5.00  | 120.83 | 30.73   | 31     | 1   | Se            | 14      | 0.00     | 14.00   |
| /cgn2_6/podata/2/ina/5C_PCTUS.COMB.seq;US-05-092-11 -  | 5.00  | 120.83 | 30.73   | 31     | 1   | Se            | 14      | 0.00     | 14.00   |
| /cgn2_6/podata/2/ina/5A_COMB.seq;US-08-479-783-45 -    | 5.00  | 118.34 | 42.28   | 45     | 1   | Se            | 14      | 0.00     | 14.00   |
| /cgn2_6/podata/2/ina/5A_COMB.seq;US-08-479-725-45 -    | 5.00  | 118.34 | 42.28   | 45     | 1   | Se            | 14      | 0.00     | 14.00   |
| /cgn2_6/podata/2/ina/5B_COMB.seq;US-08-618-693-45 -    | 5.00  | 113.28 | 80.91   | 96     | 1   | Se            | 14      | 0.00     | 14.00   |
| /cgn2_6/podata/2/ina/5B_COMB.seq;US-08-618-693-45 -    | 5.00  | 113.28 | 80.91   | 96     | 1   | Se            | 14      | 0.00     | 14.00   |
| /cgn2_6/podata/2/ina/5C_PCTUS.COMB.seq;US-08-080-134 - | 5.00  | 113.28 | 80.91   | 96     | 1   | Se            | 14      | 0.00     | 14.00   |
| /cgn2_6/podata/2/ina/5C_COMB.seq;US-08-454-557C-25 -   | 5.00  | 107.89 | 161.40  | 215    | 1   | Se            | 14      | 0.00     | 14.00   |
| /cgn2_6/podata/2/ina/5D_COMB.seq;US-08-340-426D-25 -   | 5.00  | 107.89 | 161.40  | 215    | 1   | Se            | 14      | 0.00     | 14.00   |
| /cgn2_6/podata/2/ina/5D_COMB.seq;US-08-450-675C-25 -   | 5.00  | 107.89 | 161.40  | 215    | 1   | Se            | 14      | 0.00     | 14.00   |
| /cgn2_6/podata/2/ina/5B_COMB.seq;US-08-459-5711A-25 -  | 5.00  | 107.89 | 161.40  | 215    | 1   | Se            | 14      | 0.00     | 14.00   |
| /cgn2_6/podata/2/ina/5B_COMB.seq;US-08-483-415-3 -     | 5.00  | 106.01 | 205.47  | 285    | 1   | Se            | 14      | 0.00     | 14.00   |

seq\_name: /cgn2\_6/podata/2/ina/5D\_COMB.seq;US-08-370-156-24
 seq\_documentation\_block:
 Sequence 24, Application US-08370156
 Patent No. 5932780
 GENERAL INFORMATION:
 APPLICANT: Soled, Hermona
 APPLICANT: Zakut, Haim
 APPLICANT: Shani, Moshe
 TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Reising, Ethington, Barnard & Perry
 STREET: P.O. Box 4390
 CITY: Troy
 STATE: Michigan
 COUNTRY: US
 ZIP: 48099
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US-08/370,156
 FILING DATE:
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Kohn, Kenneth I.
 REFERENCE/DOCKET NUMBER: P-307 (Mulford)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (810) 689-3500
 TELEFAX: (810) 689-4071
 INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 374 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 alignment\_scores:
 Quality: 14.00
 Ratio: 1.000
 Percent Similarity: 100.000
 Percent Identity: 100.000
 alignment\_block:
 US-09-155-076-1 x US-08-370-156-24
 Align seg 1/1 to: US-08-370-156-24 from: 1 to: 374
 1 AlagliupheHisargTrpSerTyrMetValHistPlys 14
 33 GCCAGATTCACCGCTCATGGTCAGCTTGAAAG 74
 seq\_name: /cgn2\_6/podata/2/ina/5D\_COMB.seq;US-08-370-156-24
 Sequence 26, Application US-08370156
 Patent No. 5932780
 GENERAL INFORMATION:
 APPLICANT: Soled, Hermona
 APPLICANT: Zakut, Haim

APPLICANT: Shani, Moshe  
 TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR NUMBER OF SEQUENCES: 27  
 CORRESPONDENCE ADDRESS:  
 ADDRESSSE: Reising, Ethlington, Barnard & Perry  
 STREET: P.O. Box 4390  
 CITY: Troy  
 STATE: Michigan  
 COUNTRY: US  
 ZIP: 48099  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/370.156  
 FILING DATE:  
 CLASSIFICATION: 536  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Kohn, Kenneth I.  
 REGISTRATION NUMBER: 30,955  
 REFERENCE/DOCKET NUMBER: P-307 (Mulford)  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (810) 689-3500  
 TELEFAX: (810) 689-4071  
 INFORMATION FOR SEQ ID NO: 26:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1215 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1..78  
 ;US-08-370-156-26

alignment\_scores:  
 Quality: 14.00 Length: 14  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Identity: 100.000

alignment\_block:  
 US-09-155-076-1 x US-08-370-156-26 ..  
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1 AlaGluPheHisArgTrpSerSerTyrMetValHistRplys 14  
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seq\_name: /cgn2\_6/ptodata/2/ina/5A\_COMBO.seq:US-07-732-962A-1

seq\_documentation\_block:  
 ; Sequence 1, Application US/07732962A  
 ; Patent No. 5248604  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fischer, Meir  
 ; TITLE OF INVENTION: EXPRESSION OF ENZYMATIICALLY ACTIVE  
 ; TITLE OF INVENTION: RECOMBINANT HUMAN ACETYLCHOLINESTERASE  
 ; NUMBER OF SEQUENCES: 2  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: John P. White, Esq.  
 ; STREET: 30 Rockefeller Plaza  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10112  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US92/06106  
 ; FILING DATE: 15920722  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: White, John P.  
 ; REGISTRATION NUMBER: 28,678  
 ; TELECOMMUNICATION INFORMATION:  
 ; REFERENCE/DOCKET NUMBER: 39304-B-PCT/JPW/EAB  
 ; TELEPHONE: (212) 977-9550  
 ; TELEFAX: (212) 664-0525

TELEX: 422523 COOP UI  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1845 base pairs  
 TYPE: NUCLEIC ACID  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 FEATURE:  
 NAME/KEY CDS  
 LOCATION: 1..1842  
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 alignment\_scores:  
 Quality: 14.00 Length: 14  
 Ratio: 1.000 Gaps: 0  
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 1 AlaglutarheHisArgtrpSerSerTrpSerSerTrpSerMetValHistrpLys 14  
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 seq\_documentation\_block:  
 Sequence 1, Application US/08370156  
 Patent No. 5932780  
 GENERAL INFORMATION:  
 APPLICANT: Soreq, Hermona  
 APPLICANT: Zakut, Haim  
 APPLICANT: Shani, Moshe  
 TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR  
 NUMBER OF SEQUENCES: 27  
 CURRENT APPLICATION ADDRESS:  
 ADDRESSEE: Reissig, Ethlington, Barnard & Perry  
 STREET: P.O. Box 4390  
 CITY: TROY  
 STATE: Michigan  
 COUNTRY: US  
 ZIP: 48099  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/370/156  
 FILING DATE:  
 CLASSIFICATION: 536  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Kohn, Kenneth I.  
 REGISTRATION NUMBER: 30,955  
 REFERENCE/DOCKET NUMBER: P-307 (Mulford)  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (810) 689-3500  
 TELEFAX: (810) 689-4071  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2256 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-370-156-1  
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 Quality: 14.00 Length: 14  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000  
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seq\_name: /cgn2\_6/podata/2/ina/6\_COMB.seq.US-08-814-095-1

seq\_documentation\_block:  
 ; Sequence 1, Application US/08814095  
 ; Patent No. 6025183  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Soreq, Hermona  
 ; APPLICANT: Zukut, Haim  
 ; APPLICANT: Eckstein, Fritz  
 ; TITLE OF INVENTION: Synthetic Antisense  
 ; TITLE OF INVENTION: Oligodeoxynucleotides and Pharmaceutical Compositions  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Kohn & Associates  
 ; STREET: 30500 No. 58911-25thwestern Hwy., Suite 410  
 ; CITY: Farmington Hills  
 ; STATE: Michigan  
 ; COUNTRY: US  
 ; ZIP: 48334  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/318,826A  
 ; FILING DATE:  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Kohn, Kenneth I.  
 ; REGISTRATION NUMBER: 30,955  
 ; REFERENCE/DOCKET NUMBER: 2391.00001  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (248) 539-5050  
 ; TELEFAX: (248) 539-5055  
 ; INFORMATION FOR SEQ ID NO: 7:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 3016 base pairs  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA to mRNA  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 160..2010  
 ; OTHER INFORMATION: /note= "Splice Variant: Exons 1, 2,  
 ; OTHER INFORMATION: 3, 4, 5 and 6."  
 ; US-08-318-826A-7

alignment\_scores:  
 Quality: 14.00 Length: 14  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
 US-09-155-076-1 x US-08-814-095-1 ..

Align seg 1/1 to: US-08-814-095-1 from: 1 to: 2256  
 1 AlagliuPheHisArgTrpSerSerrtyNetvalHistplys 14  
 1915 GCGAGTTCACCCGCTGGACTCATGGTCACTGAAG 1956

seq\_name: /cgn2\_6/podata/2/ina/5C\_COMB.seq.US-08-318-826A-7

seq\_documentation\_block:  
 ; Sequence 5, Application US/08370156  
 ; Patent No. 5932780

**GENERAL INFORMATION:**

APPLICANT: Soreq, Hermona  
 APPLICANT: Zakut, Haim  
 APPLICANT: Shani, Moshe

TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR NUMBER OF SEQUENCES: 27

TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTANCES

CORRESPONDENCE ADDRESS:

ADDRESSEE: Reising, Ethlington, Barnard & Perry

STREET: P.O. Box 4390

CITY: Troy

STATE: Michigan

Country: US

ZIP: 48099

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/370,156

FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Kohn, Kenneth I.

REGISTRATION NUMBER: 30,955

REFERENCE/DOCKET NUMBER: P-307 (Mulford)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (810) 689-3500

TELEFAX: (810) 689-4071

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 3016 base Pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY: CDS

LOCATION: 160..2010

US-08-370-156-5

**alignment\_scores:**

| Quality             | Length:   |
|---------------------|-----------|
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| Ratio:              | Gaps:     |
| 1.000               | 0         |
| Percent Similarity: | Identity: |
| 100.000             | 100.00    |

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Align seg 1/1 to: US-09-155-076-1 x US-08-370-156-5 ..

**alignment\_block:**

US-09-155-076-1 x US-08-370-156-5

**seq\_name:** /cgn2\_6/ptodata/2/ina/6\_COMB.seq

**seq\_documentation\_block:**

Sequence 5, Application US/08814095  
 Patent No. 602183

**GENERAL INFORMATION:**

APPLICANT: Soreq, Hermona  
 APPLICANT: Zakut, Haim  
 APPLICANT: Shani, Moshe

TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR NUMBER OF SEQUENCES: 7

TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTANCES

CORRESPONDENCE ADDRESS:

ADDRESSEE: KORN & ASSOCIATES

STREET: 30500 No. 6025183thwestern Highway, Suite 41

CITY: Farmington Hills

STATE: Michigan

```

COUNTRY: U.S.
ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/814,095
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Montgomery, Irene N.
REGISTRATION NUMBER: 38,972
REFERENCE/DOCKET NUMBER: 2391-00066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (248) 539-5050
TELEFAX: (248) 539-5055
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3016 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Alternatively spliced AC
DESCRIPTION: comprising exons 2, 3, 4, 5 and 6
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 160...2010
US-08-814-095-5

alignment_scores:
Quality: 14.00 Length: 1
Percent Similarity: 100.000 Gaps: 0
Identity: 100.0

Align seg 1/1 to: US-08-814-095-5 from: 1 to: 3016
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1 GCGGAATTCACGGCTGGAGGTCCCACTATGGCTCTGGAG 27
2675

seq_name: /cgn2_6/ptodata/2/ina/5C_COMB.seq; US-08-318

seg_documentation_block:
; Sequence 6, Application US/08318826A
; Patent No. 5891725
; GENERAL INFORMATION:
; APPLICANT: Soreg, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Lickstein, Fritz
; TITLE OF INVENTION: Synthetic Antisense Oligodeoxynucleotides and Their Containing Them
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kohn & Associates
; STREET: 3050 No. 5891725thwestern Hwy., Suite 100
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: US
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/318,826A  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 CLASSIFICATION: 514  
 NAME: Kohn, Kenneth I.  
 REFERENCE/DOCKET NUMBER: 30,955  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (810) 689-3500  
 TELEFAX: (810) 689-4071  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3096 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 160..1959  
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 US-08-370-156-3

alignment\_scores:  
 Quality: 14.00  
 Length: 14  
 Ratio: 1.00  
 Gaps: 0  
 Percent Similarity: 100.000  
 Percent Identity: 100.000

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 OTHER INFORMATION: /note- "Splice variant: Exons 1, 2,  
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 US-08-318-826A-6

align seg 1/1 to: US-08-318-826A-6 from: 1 to: 3096  
 Quality: 14.00  
 Length: 14  
 Ratio: 1.00  
 Gaps: 0  
 Percent Similarity: 100.000  
 Percent Identity: 100.000

align\_block:  
 US-09-155-076-1 x US-08-318-826A-6 ..

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 1 AlagliupheHisArgTrpSerSerTyrMetValHistRplys 14  
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 2755 GCCGAGTTCCACCGCTGGAGCTCTACATGGACTGAAAG 2796

seq\_name: /cgn2\_6/podata/2/ina/6\_COMB.seq;US-08-814-095-3

seq\_documentation\_block:  
 ; Sequence 3, Application US/08814095  
 ; GENERAL INFORMATION:  
 ; Patent No. 6025153  
 ; COMPUTER READABLE FORM:  
 ; REFERENCE/DOCKET NUMBER: 30,955  
 ; TELECOMMUNICATION INFORMATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Kohn & ASSOCIATES  
 ; ADDRESS: KOHN & ASSOCIATES  
 ; STREET: 30500 No. 6025183thwestern Highway, Suite 410  
 ; CITY: Farmington Hills  
 ; STATE: Michigan  
 ; COUNTRY: U.S.  
 ; ZIP: 48334  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/814,095  
 ; FILING DATE:  
 ; CLASSIFICATION: 800  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Montgomery, Irene N.  
 ; REGISTRATION NUMBER: 38,972  
 ; REFERENCE/DOCKET NUMBER: 2391.00066  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (248) 539-5050  
 ; TELEFAX: (248) 539-5055  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 3096 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single

align seg 1/1 to: US-08-370-156-3 from: 1 to: 3096  
 1 AlagliupheHisArgTrpSerSerTyrMetValHistRplys 14  
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 2755 GCCGAGTTCCACCGCTGGAGCTCTACATGGACTGAAAG 2796

seq\_name: /cgn2\_6/podata/2/ina/6\_COMB.seq;US-08-814-095-3

seq\_documentation\_block:  
 ; Sequence 3, Application US/08814095  
 ; GENERAL INFORMATION:  
 ; Patent No. 5932780  
 ; COMPUTER READABLE FORM:  
 ; REFERENCE/DOCKET NUMBER: 30,955  
 ; TELECOMMUNICATION INFORMATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Kohn & ASSOCIATES  
 ; ADDRESS: KOHN & ASSOCIATES  
 ; STREET: 30500 No. 6025183thwestern Highway, Suite 410  
 ; CITY: Farmington Hills  
 ; STATE: Michigan  
 ; COUNTRY: U.S.  
 ; ZIP: 48334  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/814,095  
 ; FILING DATE:  
 ; CLASSIFICATION: 800  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Montgomery, Irene N.  
 ; REGISTRATION NUMBER: 38,972  
 ; REFERENCE/DOCKET NUMBER: 2391.00066  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (248) 539-5050  
 ; TELEFAX: (248) 539-5055  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 3096 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single

TOPOLOGY: linear  
 MOLECULE TYPE: other nucleic acid  
 /desc = "Alternatively spliced AChE  
 DESCRIPTION: comprising exons 2, 3, 4 and 5 as well as the translated portion  
 DESCRIPTION: of Intron 4 (readthrough)"  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 160 . 1959  
 US-08-814-095-3

alignment\_scores:  
 Quality: 14.00 Length: 14  
 Percent Similarity: 100.000 Gaps: 0  
 Ratio: 1.000 Percent Identity: 100.000

alignment\_block:  
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Align seg 1/1 to: US-08-814-095-3 from: 1 to: 3096

1 AlagluPheHisArgTrpSerSerTyrMetVaHistRPLys 14  
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seq\_name: /cgn2\_6/ptodata/2/1na/6\_COMB.seq;us-08-814-095-7

seq\_documentation\_block:  
 Sequence 7, Application US/08814095

GENERAL INFORMATION:  
 Patent No. 6025183

APPLICANT: Sored, Hermona  
 APPLICANT: Zukut, Haim  
 APPLICANT: Shani, Moshe

TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR  
 TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTANCES

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: KOHN & ASSOCIATES  
 STREET: 30500 No. 6025183thwestern Highway, Suite 410  
 CITY: Farmington Hills  
 STATE: Michigan  
 COUNTY: U.S.  
 ZIP: 48334

COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/814,095  
 FILING DATE:  
 CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:  
 NAME: Montgomery, Ilene N.  
 REGISTRATION NUMBER: 38 972  
 REFERENCE/DOCKET NUMBER: 2391.00066

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (248) 539-5050  
 TELEFAX: (248) 539-5055

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 35060 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid  
 DESCRIPTION: /desc = "Cosmid including AChE gene and ARS gene"  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO

OTHER INFORMATION: /gene= "AR"  
 OTHER INFORMATION: /number= 3  
 FEATURE:  
 NAME/KEY: exon  
 LOCATION: complement (33493..33591)  
 OTHER INFORMATION: /gene= "AR"  
 OTHER INFORMATION: /number= 4  
 FEATURE:  
 NAME/KEY: exon  
 LOCATION: complement (33297..33408)  
 OTHER INFORMATION: /gene= "AR"  
 OTHER INFORMATION: /number= 5  
 FEATURE:  
 NAME/KEY: exon  
 LOCATION: complement (32959..33094)  
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 LOCATION: complement (32569..32628)  
 OTHER INFORMATION: /gene= "AR"  
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 LOCATION: complement (32386..32468)  
 OTHER INFORMATION: /gene= "AR"  
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 LOCATION: complement (31894..32080)  
 OTHER INFORMATION: /gene= "AR"  
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 NAME/KEY: exon  
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 FEATURE:  
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 LOCATION: complement (30187..30274)  
 OTHER INFORMATION: /gene= "AR"  
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 FEATURE:  
 NAME/KEY: exon  
 LOCATION: complement (29945..30073)  
 OTHER INFORMATION: /gene= "AR"  
 OTHER INFORMATION: /number= 15  
 FEATURE:  
 NAME/KEY: exon  
 LOCATION: complement (29664..29856)  
 OTHER INFORMATION: /gene= "ARS"  
 OTHER INFORMATION: /number= 16  
 US-08-814-095-7

Percent Similarity: 100.000 Percent Identity: 100.000  
 alignment\_block:  
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 1 AlaGluPheHisArgTrpSerSerMetValHistDproS 14  
 28039 GCGAGTCCACGGCTTACATGGACTGAAG 28080  
 seq\_name: /cgn2\_6/ptodata/2/1na/5B\_CONB.seq:US-08-482-090-13

seq\_documentation\_block:  
 ; Sequence 13. Application US/08482090  
 ; Patent No. 5820869  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wasmoen, Terri  
 ; APPLICANT: Chu, Hsien-Tue  
 ; APPLICANT: Chavez, Lloyd  
 ; TITLE OF INVENTION: Recombinant Raccoon Pox Viruses and  
 ; TITLE OF INVENTION: Their Use as an Effective Vaccine Against Feline  
 ; TITLE OF INVENTION: Immunodeficiency Virus Infection  
 ; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Darby & Darby  
 ; STREET: 805 Third Avenue  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: U.S.A.  
 ; ZIP: 10022  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC Compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATE:  
 ; APPLICATION NUMBER: US/08/482,090  
 ; FILING DATE: 07-JUN-1995  
 ; CLASSIFICATION: 424  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Schaffer, Robert  
 ; REGISTRATION NUMBER: 31,194  
 ; REFERENCE/DOCKET NUMBER: 0632/0B170  
 ; TELECOMMUNICATION INFORMATION:  
 ; LENGTH: 1353 base Pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: Single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; ORIGINAL SOURCE: ORGANISM: feline immunodeficiency virus  
 ; INDIVIDUAL ISOLATE: NCSU-1  
 ; POSITION IN GENOME:  
 ; MAP POSITION: 1-1353  
 ; UNITS: bp  
 ; US-08-482-090-13

alignment\_scores:  
 ; Quality: 6.00 Length: 6  
 ; Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000  
 alignment\_block:  
 US-09-155-076-1 x US-08-482-090-13/rev ..  
 Align seg 1/1 to reverse of: US-08-482-090-13 from: 1 to: 1353

alignment\_scores:  
 ; Quality: 14.00 Length: 14  
 ; Ratio: 1.000 Gaps: 0

3 pheHisArgTrpSerSer 8  
|||||||  
366 TTCAAGATGCTAGT 349



| Result No. | Score | Query       | Match | Length | DB ID  | Description                          |
|------------|-------|-------------|-------|--------|--------|--------------------------------------|
| 1          | 14    | ACES_BOVIN  | 583   | 1      | P23795 | bos taurus                           |
| 2          | 14    | ACES_RABBIT | 584   | 1      | Q29439 | oryctolagus                          |
| 3          | 14    | ACES_HUMAN  | 614   | 1      | P22303 | homo sapien                          |
| 4          | 14    | ACES_MOUSE  | 614   | 1      | P18136 | mus musculus                         |
| 5          | 14    | ACES_RAT    | 614   | 1      | P37136 | rattus norvegicus                    |
| 6          | 9     | ACES_CHICK  | 643   | 1      | P36196 | gallus gallus                        |
| 7          | 6     | PMT1_SCHPO  | 429   | 1      | P40999 | schizosaccharomyces pombe            |
| 8          | 5     | HXD4_CHICK  | 330   | 1      | P17278 | gallus gallus                        |
| 9          | 5     | HXD4_BRARE  | 357   | 1      | O57314 | brachdanio rerio                     |
| 10         | 5     | HXD4_MOUSE  | 250   | 1      | P10628 | mus musculus                         |
| 11         | 5     | HXD4_HUMAN  | 357   | 1      | P09016 | homo sapien                          |
| 12         | 5     | YX4B_BACSU  | 357   | 1      | P42313 | bacillus subtilis                    |
| 13         | 5     | YFIN_ECOLI  | 282   | 1      | P46139 | escherichia coli                     |
| 14         | 5     | HXL1_ECOLI  | 408   | 1      | P37095 | escherichia coli                     |
| 15         | 5     | NU4M_LOCMI  | 357   | 1      | Q36124 | locusta migratoria                   |
| 16         | 5     | YDT_BACSU   | 444   | 1      | O34662 | bacillus subtilis                    |
| 17         | 5     | PHOQ_ECOLI  | 357   | 1      | P23837 | escherichia coli                     |
| 18         | 5     | TPP1_MOUSE  | 538   | 1      | O89023 | mus musculus                         |
| 19         | 5     | CHLE_MOUSE  | 357   | 1      | Q03311 | mus musculus                         |
| 20         | 5     | YA16_CHLPN  | 603   | 1      | Q9z6p3 | chlamydia pneumoniae                 |
| 21         | 5     | AMY_STRLI   | 357   | 1      | Q05884 | streptomyces                         |
| 22         | 5     | YK26_CAEEL  | 1018  | 1      | P34333 | candida beldhamiae                   |
| 23         | 5     | GP21_RAT    | 357   | 1      | P11634 | rattus norvegicus                    |
| 24         | 4     | RL5_HALME   | 286   | 1      | P50557 | halobacter halophilus                |
| 25         | 4     | RL30_HAEIN  | 286   | 1      | P46366 | haemophilus acrythrophilus           |
| 26         | 4     | RL30_ACYS   | 286   | 1      | P46184 | acrythrophilus anabaena cyanoformans |
| 27         | 4     | YHYD_ANACY  | 286   | 1      | P16420 | carbonylase                          |
| 28         | 4     | FER1_DUNSA  | 286   | 1      | P00239 | halobacter halophilus                |
| 29         | 4     | NHP1_BABBO  | 286   | 1      | P40632 | babesia bovis                        |
| 30         | 4     | CYAY_HAEIN  | 286   | 1      | P71388 | haemophilus suis                     |
| 31         | 4     | Y53_BTBT3   | 286   | 1      | P28732 | bacteriophaga                        |
| 32         | 4     | CYAY_ECOLI  | 286   | 1      | P27338 | escherichia coli                     |
| 33         | 4     | FER_MYCSM   | 286   | 1      | P00215 | mycobacterium avium subsp. parvum    |

## ALIGNMENTS

|  |                               |
|--|-------------------------------|
| Scoring table:                                     | OLIGO                         |
| Gapop:   | 60.0 , Gapext: 60.0           |
| Searched:  | 85661 seqs, 30989116 residues |
| Word size :  | 0                             |
| Total number of hits satisfying chosen parameters: | 85661                         |
| Minimum DB seq length: 0                           |                               |
| Maximum DB seq length: 1000000                     |                               |

Post-processing: Listing first 45 summaries  
Database : SwissProt\_38:\*

## SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## RESULTS

| RESULT | 1  | ACES_BOVIN | STANDARD; | PRP; | 583 AA. |
|--------|--|------------|-----------|------|---------|
| ID     | ACES_BOVIN   |            |           |      |         |
| AC     | P23795;  |            |           |      |         |
| AC     | P23795;  |            |           |      |         |
| DT     | 01-Nov-1991 (Rel. 20, Created)   |            |           |      |         |
| DT     | 01-Nov-1991 (Rel. 20, Last sequence update)  |            |           |      |         |
| DT     | 01-Oct-1996 (Rel. 34, Last annotation update)  |            |           |      |         |
| DE     | ACETYLCHOLINESTERASE (EC 3.1.1.7).   |            |           |      |         |
| GN     | ACHE.  |            |           |      |         |
| OS     | Bos taurus (Bovine).   |            |           |      |         |
| OC     | Bukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Peccora; Bovoidea; Bovidae; Bovinae; Bos. |            |           |      |         |
| RN     | [1]  |            |           |      |         |
| RP     | SEQUENCE;  |            |           |      |         |
| RC     | TISSUE=FETAL SERUM;  |            |           |      |         |
| RD     | MEDLINE: 90306335.   |            |           |      |         |
| RA     | Doctor B.P., Chapman T.C., Christner C.E., Deal C.D., de la Hoz D.M., Gentry M.K., Ogert R.A., Rush R.S., Smyth M.K., Wolfe A.D.;                            |            |           |      |         |
| RT     | "Complete amino acid sequence of fetal bovine serum acetylcholinesterase and its comparison in various regions with other cholinesterases.";                 |            |           |      |         |
| RT     | FEBS Lett. 266:123-127(1990).  |            |           |      |         |
| CC     | -1 FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.   |            |           |      |         |
| CC     | -1 CATALYTIC ACTIVITY: ACETYLCHOLINE + H(+)O = CHOLINE + ACETATE.  |            |           |      |         |
| CC     | -1 SUBUNIT: OLIGOMER COMPOSED OF DISULFIDE-LINKED HOMODIMERS.  |            |           |      |         |
| CC     | -1 SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.   |            |           |      |         |
| DR     | PIR: S10712; S10712.   |            |           |      |         |
| DR     | HSPB: P22303; 2CLJ.  |            |           |      |         |
| DR     | PFAM: PF00135; Coesterase; 1.  |            |           |      |         |
| DR     | PRINTS: PR00878; COLENSTRASE.  |            |           |      |         |
| DR     | PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.   |            |           |      |         |
| DR     | PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.   |            |           |      |         |
| KW     | Hydrolase; Serine esterase; Synapse; Membrane; Nerve; Muscle;  |            |           |      |         |
| KW     | Neurotransmitter degradation; Glycoprotein   |            |           |      |         |
| FT     | ACT_SITE 203 BY SIMILARITY.  |            |           |      |         |
| FT     | ACT_SITE 334 BY SIMILARITY.  |            |           |      |         |
| FT     | ACT_SITE 447 BY SIMILARITY.  |            |           |      |         |
| FT     | DISULFID 69 BY SIMILARITY.   |            |           |      |         |
| FT     | DISULFID 257 BY SIMILARITY.  |            |           |      |         |
| FT     | DISULFID 403 BY SIMILARITY.  |            |           |      |         |
| FT     | DISULFID 580 BY SIMILARITY.  |            |           |      |         |
| FT     | CARBOHYD 61 BY SIMILARITY.   |            |           |      |         |
| FT     | CARBOHYD 265 BY POTENTIAL.   |            |           |      |         |
| FT     | CARBOHYD 350 BY POTENTIAL.   |            |           |      |         |
| FT     | CARBOHYD 464 BY POTENTIAL.   |            |           |      |         |
| FT     | CARBOHYD 541 BY POTENTIAL.   |            |           |      |         |
| SQ     | SEQUENCE 64238 MW; 78655017E494279F CRC64;   |            |           |      |         |

Query Match 1 AEFRWSSTMVHVK 14  
Best Local Similarity 14; Score 14; DB 1; Length 583;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFRWSSTMVHVK 14

Db 555 AEFHRWSSYMWK 568

| RESULT   | 2         | 3            |
|--|-----------|--------------|
| ACES_RABBIT  | STANDARD; | PRT; 584 AA. |
| ID   |           |              |
| AC Q29495;   |           |              |
| AC ID NOV-1997 (Rel. 35, Created)  |           |              |
| DT 01-NOV-1997 (Rel. 35, Last sequence update)   |           |              |
| DT 01-NOV-1997 (Rel. 35, Last annotation update)   |           |              |
| DT 01-NOV-1997 (Rel. 35, Last annotation update)   |           |              |
| DE ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7) (FRAGMENT).   |           |              |
| GN ACHE.   |           |              |
| OS Oryctolagus cuniculus (Rabbit).   |           |              |
| OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  |           |              |
| OC [1]   |           |              |
| RN RN  |           |              |
| RP SEQUENCE FROM N.A.  |           |              |
| RC TISSUE= MUSCLE;   |           |              |
| RM MEDLINE; 95010096.  |           |              |
| RA Jbilo O., Lhermitte Y., Toutant J., Chatonnet A.;   |           |              |
| BT "Acetylcholinesterase and butyrylcholinesterase expression in adult rabbit tissues and during development.";  |           |              |
| RT Proc. J. Biochem. 225:115-124(1994).  |           |              |
| CC -I- FUNCTION: RAPIDLY HYDROLYZES CHOLINE + H(2)O = CHOLINE + ACETATE.   |           |              |
| CC -I- CATALYTIC ACTIVITY: ACETYLCHOLINE + H(2)O = CHOLINE + ACETATE.  |           |              |
| CC -I- OLIGOMER COMPOSED OF DISULFIDE-LINKED HOMODIMERS.   |           |              |
| CC -I- MISCELLANEOUS: SYNAPSES USUALLY CONTAIN ASYMMETRIC MOLECULES OF CHOLINESTERASE, WITH A COLLAGEN-LIKE PART DISULFIDE-BONDED TO THE CATALYTIC PART. A DIFFERENT, GLOBULAR TYPE OF CHOLINESTERASE OCCURS ON THE OUTER SURFACES OF CELL MEMBRANES, INCLUDING THOSE OF ERYTHROCYTES.   |           |              |
| CC -I- MISCELLANEOUS: THIS IS THE CATALYTIC SUBUNIT OF AN ASYMMETRIC OR SOLUBLE FORM OF ACHE.  |           |              |
| CC -I- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.   |           |              |
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| CC DR EMBL: U05036; AAA5235.1; -.  |           |              |
| CC DR HSSP: P22303; 2CLJ.  |           |              |
| DR PFAM: PF00135; Coesterase; 1.   |           |              |
| DR PROSITE: PS00122; CARBOXYLESTERASE_B-1; 1.  |           |              |
| DR PROSITE: PS00941; CARBOXYLESTERASE_B-2; 1.  |           |              |
| KW Hydrolase; Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal; Neurotransmitter degradation; Glycoprotein.   |           |              |
| FT NON-TER 1   |           |              |
| FT SIGNAL <1 1   |           |              |
| FT CHAIN 2 584   |           |              |
| FT ACT_SITE 204 204  |           |              |
| FT ACT_SITE 335 335  |           |              |
| FT ACT_SITE 448 448  |           |              |
| FT DISULFID 70 97  |           |              |
| FT DISULFID 258 273  |           |              |
| FT DISULFID 410 530  |           |              |
| FT DISULFID 581 581  |           |              |
| FT CARBOHYD 266 266  |           |              |
| FT CARBOHYD 351 351  |           |              |
| FT CARBOHYD 465 465  |           |              |
| SQ SEQUENCE 584 AA; 64630 MW; 2AE157F3063649FE CRC64;  |           |              |
| Query Match 100.0%; Score 14; DB 1; Length 584;  |           |              |
| Best Local Similarity 100.0%; Pred. No. 9e-10; Mismatches 0; Indels 0; Gaps 0;   |           |              |
| Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  |           |              |
| Qy 1 AEFHRWSSYMWK 14   |           |              |
| Db 556 AEFHRWSSYMWK 569  |           |              |

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CC -----

|   |  |    |   |
|---|--|----|---|
| DR  | EMBL; M55040; AAA68151.1; -.   | RA | Bourne Y., Taylor P.; Marchot P.; "Acetylcholinesterase inhibition by fasciculin: crystal structure of the complex." ; RT   |
| DR  | PTR; S03959; S03959.   | RT | Cell. 83:503-512(1995).   |
| DR  | PTR; A39256; A39256.   | RL | RN [3]  |
| DR  | PDE; 2CJL; 04-MAR-98.  | RP | X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  |
| DR  | CARBANK; CCSD; 29374; -.   | RX | MEDLINE; 99115643.  |
| DR  | CARBANK; CCSD; 32958; -.   | RA | Bourne Y., Taylor P.; Bougis P.E.; Marchot P.; "Crystal structure of mouse acetylcholinesterase. A peripheral site occluding loop in a tetrameric assembly." ; RT   |
| DR  | CARBANK; CCSD; 35085; -.   | RL | J. Biol. Chem. 274:2983-2970(1999).   |
| DR  | S07SS-2DPAGE; P22303; HUMAN.   | CC | -I- FUNCTION: RAPIDLY HYDROLYSES CHOLINE RELEASED INTO THE SYNAPSE.   |
| DR  | MM: 110740; -.   | CC | -I- CATALYTIC ACTIVITY: ACETYLCHOLINE + H(2)O = CHOLINE + ACETATE.  |
| DR  | MIM; 112100; -.  | CC | -I- SUBUNIT: OLIGOMER COMPOSED OF DISULFIDE-LINKED HOMODIMERS.  |
| DR  | PFAM; PF00135; Coesterase; 1.  | CC | -I- ALTERNATIVE PRODUCTS: THE DIFFERENT CATALYTIC SUBUNITS ARE ENCODED BY ALTERNATIVELY SPLICED mRNAs THAT ARISE FROM A SINGLE GENE.  |
| DR  | PRINTS; PRO0087; CHOLINESTERASE.   | CC | -I- THE T (ASYMMETRIC) FORM IS SHOWN HERE.  |
| DR  | PROSITE; PS00122; CARBOXYLESTERASE_B-1; 1.                               | CC | -I- TISSUE SPECIFICITY: PREDOMINATES IN MOST EXPRESSING TISSUES EXCEPT ERYTHROCYTES WHERE A GLYCOPHOSPHOLIPID-ATTACHED FORM OF ACHE PREDOMINATES.   |
| DR  | PROSITE; PS00941; CARBOXYLESTERASE_B-2; 1.                               | CC | -I- MISCELLANEOUS: SYNAPSES USUALLY CONTAIN ASYMMETRIC MOLECULES OF CHOLINESTERASE, WITH A COLLAGEN-LIKE PART DISULFIDE-BONDED TO THE CATALYTIC PART. A DIFFERENT, GLOBULAR TYPE OF CHOLINESTERASE OCCURS ON THE OUTER SURFACES OF CELL MEMBRANES, INCLUDING THOSE OF ERYTHROCYTES.                     |
| KN  | Hydrolase; Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;    | CC | -I- MISCELLANEOUS: THIS IS THE CATALYTIC SUBUNIT OF AN ASYMMETRIC OR SOLUBLE FORM OF ACHE.  |
| KN  | Neurotransmitter degradation; Glycoprotein; Polymorphism.                | CC | -I- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.   |
| KN  | Blood group antigen; Alternative splicing; 3D-structure.                 | CC | This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - FTId=VAR00359. This statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ |
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| FT  | CHAIN 32   | CC | or send an email to license@isb-sib.ch).  |
| FT  | ACT_SITE 611 614   | CC | EMBL; X56518; CAA39867.1; -.  |
| FT  | DISULFID 234 234   | CC | DR PIR; JH0314; JH0314.   |
| FT  | CARBOHYD 296 296   | CC | DR PDB; 1IMAH; 03-APR-96.   |
| FT  | CARBOHYD 381 381   | CC | DR PDB; 1MAA; 20-APR-99.  |
| FT  | CARBOHYD 495 495   | CC | DR MGN; MG1:87876; ACHE.  |
| FT  | VARIANT 353 353  | CC | DR PRAM; PF00115; Coesterase; 1.  |
| FT  | MUTAGEN 234 234  | CC | DR PROSITE; PS00122; CARBOXYLESTERASE_B-1; 1.   |
| FT  | MUTAGEN 365 365  | CC | DR PROSITE; PS00941; CARBOXYLESTERASE_B-2; 1.   |
| FT  | MUTAGEN 478 478  | CC | DR HYDROLASE; Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;  |
| FT  | MUTAGEN 206 206  | CC | DR Neurotransmitter degradation; Glycoprotein; Alternative splicing;  |
| FT  | MUTAGEN 435 435  | CC | DR 3D-structure.  |
| FT  | MUTAGEN 611 611  | CC | FT SIGNAL 1 31  |
| FT  | DISULFID 611 611   | CC | FT CHAIN 32 614 ACETYLCHOLINESTERASE.   |
| FT  | BRIDGE FORMATION   | CC | FT ACT_SITE 234 234   |
| FT  | FT PIR; JH0314; JH0314.  | CC | FT ACT_SITE 365 365   |
| FT  | FT PDB; 1MAA; 20-APR-99.   | CC | FT ACT_SITE 478 478   |
| FT  | FT MGN; MG1:87876; ACHE.   | CC | FT DISULFID 100 127   |
| FT  | FT PRAM; PF00115; Coesterase; 1.   | CC | FT DISULFID 288 303   |
| FT  | FT PROSITE; PS00122; CARBOXYLESTERASE_B-1; 1.                            | CC | FT DISULFID 440 560   |
| FT  | FT PROSITE; PS00941; CARBOXYLESTERASE_B-2; 1.                            | CC | FT DISULFID 611 611 INTERCHAIN (BY SIMILARITY).   |
| FT  | FT HYDROLASE; Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal; | CC | FT CARBOHYD 296 296 POTENTIAL.  |
| FT  | FT Neurotransmitter degradation; Glycoprotein; Alternative splicing;     | CC | FT CARBOHYD 381 381   |
| FT  | FT 3D-structure.   | CC | FT CARBOHYD 495 495 POTENTIAL.  |
| SQ  | SEQUENCE 614 AA: 67796 MW: B9AA84C77831C302 CRC64;                       | CC | SQ SEQUENCE 614 AA: 68168 MW: 66E2512463C21172 CRC64;   |
| Query Match   | Score 14; DB 1; Length 614;  |    | Query Match Score 14; DB 1; Length 614;   |
| Best Local Similarity   | 100.0%   |    | Best Local Similarity 100.0%;   |
| Matches   | 100.0%   |    | Pred. No. 9.4e-10;  |
| 14; Conservative  | 0; Mismatches 0;   |    | Matches 14; Conservative 0; Mismatches 0;   |
| Oy  | 0; Indels 0; Gaps 0;   |    | Indels 0; Gaps 0;   |
| 1   | 1  |    | Indels 0; Gaps 0;   |
| AEPHRWSSYMWK 14   |  |    | Indels 0; Gaps 0;   |
| Db  | 586 AEPHRWSSYMWK 599   |    | Indels 0; Gaps 0;   |
| RESULT 4  |  |    | Indels 0; Gaps 0;   |
| ID ACES_MOUSE   | STANDARD; PRT; 614 AA.   |    | Indels 0; Gaps 0;   |
| AC P21836   |  |    | Indels 0; Gaps 0;   |
| DT 01-MAY-1991 (Rel. 18, Created)   |  |    | Indels 0; Gaps 0;   |
| DT 01-MAY-1991 (Rel. 18, Last sequence update)  |  |    | Indels 0; Gaps 0;   |
| DN 15-FEB-2000 (Rel. 39, Last annotation update)  |  |    | Indels 0; Gaps 0;   |
| DE ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7).   |  |    | Indels 0; Gaps 0;   |
| GN ACHE.  |  |    | Indels 0; Gaps 0;   |
| OS Mus musculus (Mouse).  |  |    | Indels 0; Gaps 0;   |
| OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Sciuromorphata; Muridae; Murinae; Mus.   |  |    | Indels 0; Gaps 0;   |
| RN [1]  | SEQUENCE FROM N.A.   |    | Indels 0; Gaps 0;   |
| RX MEDLINE; 90380429.   |  |    | Indels 0; Gaps 0;   |
| RA Rachinsky T.L., Camp S., Li Y., Ekstroem T.J., Newton M., Taylor P.; "Molecular cloning of mouse acetylcholinesterase: tissue distribution of alternatively spliced mRNA species." ; |  |    | Indels 0; Gaps 0;   |
| RL Neuron 5:31-32 (1990).   |  |    | Indels 0; Gaps 0;   |
| RN [2]  | X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS) OF COMPLEX WITH FASCICULIN.        |    | Indels 0; Gaps 0;   |
| RX MEDLINE; 96067648.   |  |    | Indels 0; Gaps 0;   |
| Query   | Match Score 14; DB 1; Length 614;  |    | Indels 0; Gaps 0;   |
| Best Local Similarity 100.0%;   |  |    | Indels 0; Gaps 0;   |
| Matches 14; Conservative 0; Mismatches 0;   |  |    | Indels 0; Gaps 0;   |
| Db  | 586 AEPHRWSSYMWK 599   |    | Indels 0; Gaps 0;   |

|                                     |  |  |                            |                        |  |  |
|-------------------------------------|--|--|----------------------------|------------------------|--|--|
| RESULT                              | 5  |  |                            |                        |  |  |
| ACES_RAT                            |  | STANDARD;  | PRT;                       | 614 AA.                |  |  |
| ID                                  |  |  |                            |                        |  |  |
| AC                                  |  |  |                            |                        |  |  |
| P37136;                             |  |  |                            |                        |  |  |
| DT                                  | 01-OCT-1994  | (Rel. 30, Created)   |                            |                        |  |  |
| DT                                  | 01-OCT-1994  | (Rel. 30, Last sequence update)  |                            |                        |  |  |
| DT                                  | 15-FEB-2000  | (Rel. 39, Last annotation update)  |                            |                        |  |  |
| DE                                  |  | ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7.)   |                            |                        |  |  |
| GN                                  |  | ACHE.  |                            |                        |  |  |
| OS                                  | Rattus norvegicus (Rat).   |  |                            |                        |  |  |
| OC                                  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  |  |                            |                        |  |  |
| OC                                  | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus   |  |                            |                        |  |  |
| RN                                  | [1]  |  |                            |                        |  |  |
| RP                                  | SEQUENCE FROM N.A. (T FORM)  |  |                            |                        |  |  |
| RX                                  | MEDLINE: 93107932.   |  |                            |                        |  |  |
| RA                                  | Legry C., Bon S., Vernier P., Coussen F., Massoulie J.;  |  |                            |                        |  |  |
| RT                                  | "Cloning and expression of a rat acetylcholinesterase subunit:   |  |                            |                        |  |  |
| RT                                  | generation of multiple molecular forms and complementarity with a  |  |                            |                        |  |  |
| RT                                  | Torpedo collagenic subunit;  |  |                            |                        |  |  |
| RL                                  | J. Neurochem. 60:337-346(1993).  |  |                            |                        |  |  |
| RN                                  | [2]  |  |                            |                        |  |  |
| RP                                  | SEQUENCE FROM N.A. (H AND R FORMS).  |  |                            |                        |  |  |
| RX                                  | MEDLINE: 93114454.   |  |                            |                        |  |  |
| RA                                  | Legry C., Bon S., Massoulie J.;  |  |                            |                        |  |  |
| RT                                  | "Expression of a cDNA encoding the glycolipid-anchored form of rat   |  |                            |                        |  |  |
| RT                                  | acetylcholinesterase."   |  |                            |                        |  |  |
| RL                                  | FEBS Lett. 315:163-166(1993).  |  |                            |                        |  |  |
| CC                                  | -I - FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.   |  |                            |                        |  |  |
| CC                                  | -I - CATALYTIC ACTIVITY: ACETYLCHOLINE + H(2)O = CHOLINE + ACETATE.  |  |                            |                        |  |  |
| CC                                  | -I - SUBUNIT: OLIGOMER COMPOSED OF DISULFIDE-LINKED HOMODIMERS.  |  |                            |                        |  |  |
| CC                                  | CATALYTIC FORMS H (GPI-ANCHOR DIMER) AND T (ASYMMETRIC COLLAGEN-TAILED), WHICH DIFFER IN THEIR C-TERMINUS, ACCOUNT FOR ALL TYPES |  |                            |                        |  |  |
| CC                                  | OF KNOWN ACHE FORMS.   |  |                            |                        |  |  |
| CC                                  | -I - ALTERNATIVE PRODUCTS: THE DIFFERENT CATALYTIC SUBUNITS ARE ENCODED  |  |                            |                        |  |  |
| CC                                  | BY ALTERNATIVELY SPLICED MRNA'S THAT ARISE FROM A SINGLE GENE.   |  |                            |                        |  |  |
| CC                                  | IT IS NOT KNOWN WHETHER THE R FORM REPRESENTS A FUNCTIONAL   |  |                            |                        |  |  |
| CC                                  | SPECIES. THE T (ASYMMETRIC) FORM IS SHOWN HERE.  |  |                            |                        |  |  |
| CC                                  | -I - SIMILARITY: SPECIFICITY HAS BEEN FOUND IN CENTRAL NERVOUS SYSTEM AND  |  |                            |                        |  |  |
| CC                                  | MUSCLE. FOUND IN EMBRYONIC LIVER AND SPLEEN BUT NOT IN ADULT   |  |                            |                        |  |  |
| CC                                  | LIVER.   |  |                            |                        |  |  |
| CC                                  | -I - SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLIPASE FAMILY.   |  |                            |                        |  |  |
| CC                                  | -----  |  |                            |                        |  |  |
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| CC                                  | or send an email to license@isb-sib.ch).   |  |                            |                        |  |  |
| CC                                  | -----  |  |                            |                        |  |  |
| DR                                  | EMBL: S50879; AAB4586.1;   |  |                            |                        |  |  |
| DR                                  | EMBL: X77140; CAA9717.1;   |  |                            |                        |  |  |
| DR                                  | PIR: X70141; CAA9718.1;  |  |                            |                        |  |  |
| DR                                  | PIR: JH0811; JH0811.   |  |                            |                        |  |  |
| DR                                  | HSSP: P21836, 1MAH.  |  |                            |                        |  |  |
| PFAM: PF0135; Coesterase_1.         |  |  |                            |                        |  |  |
| PRINTS: PS00878; CHOLNESTERASE_B_1. |  |  |                            |                        |  |  |
| DR                                  | PROSITE: PS00122; CARBOXYLIPASE_B_2; 1.  |  |                            |                        |  |  |
| DR                                  | hydrolase; Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;  |  |                            |                        |  |  |
| KW                                  | Neurotransmitter degradation; Glycoprotein; Alternative splicing.  |  |                            |                        |  |  |
| FN                                  | SIGNAL_1   |  |                            |                        |  |  |
| CHAIN                               | 31   |  |                            |                        |  |  |
| FT                                  | ACT_31   |  |                            |                        |  |  |
| FT                                  | ACT_32   |  |                            |                        |  |  |
| FT                                  | ACT_33   |  |                            |                        |  |  |
| FT                                  | ACT_34   |  |                            |                        |  |  |
| FT                                  | ACT_35   |  |                            |                        |  |  |
| FT                                  | ACT_36   |  |                            |                        |  |  |
| FT                                  | ACT_37   |  |                            |                        |  |  |
| FT                                  | ACT_38   |  |                            |                        |  |  |
| FT                                  | ACT_39   |  |                            |                        |  |  |
| FT                                  | ACT_40   |  |                            |                        |  |  |
| FT                                  | ACT_41   |  |                            |                        |  |  |
| FT                                  | ACT_42   |  |                            |                        |  |  |
| FT                                  | ACT_43   |  |                            |                        |  |  |
| FT                                  | ACT_44   |  |                            |                        |  |  |
| FT                                  | ACT_45   |  |                            |                        |  |  |
| FT                                  | ACT_46   |  |                            |                        |  |  |
| FT                                  | ACT_47   |  |                            |                        |  |  |
| FT                                  | ACT_48   |  |                            |                        |  |  |
| FT                                  | DISULFID_100   |  |                            |                        |  |  |
| FT                                  | DISULFID_127   |  |                            |                        |  |  |
| FT                                  | DISULFID_288   |  |                            |                        |  |  |
| FT                                  | DISULFID_303   |  |                            |                        |  |  |
| FT                                  | DISULFID_440   |  |                            |                        |  |  |
| FT                                  | DISULFID_611   |  |                            |                        |  |  |
| FT                                  | CARBOHYD_296   |  |                            |                        |  |  |
| FT                                  | CARBONYL_381   |  |                            |                        |  |  |
| FT                                  | CARBONYL_381   |  |                            |                        |  |  |
| FT                                  | CARBONYL_495   |  |                            |                        |  |  |
| FT                                  | VARSPLIC   | 570  | 614                        |                        |  |  |
| FT                                  | VARSPLIC   | 570  | 614                        |                        |  |  |
| FT                                  | SEQUENCE   | 614 AA:  | 68196 MW:                  | 2EDAE/D4628E7/0 CRC64; |  |  |
| FT                                  | Query  | 1  | AEPHRWSSYMWHK              | 14                     |  |  |
| FT                                  | Db   | 586 AEFHRWSSYMWHK  | 599                        |                        |  |  |
| FT                                  | Query  | 1  | AEPHRWSSYMWHK              | 14                     |  |  |
| FT                                  | Db   | 586 AEFHRWSSYMWHK  | 599                        |                        |  |  |
| FT                                  | RESULT   | 6  |                            |                        |  |  |
| FT                                  | ACES_CHICK   |  |                            |                        |  |  |
| FT                                  | ID   |  |                            |                        |  |  |
| FT                                  | ACES   |  |                            |                        |  |  |
| FT                                  | CHICK  |  |                            |                        |  |  |
| FT                                  | STANDARD;  |  |                            |                        |  |  |
| FT                                  | PRT;   | 767 AA.  |                            |                        |  |  |
| FT                                  | AC   | P36196;  |                            |                        |  |  |
| FT                                  | DT   | 01-JUN-1994 (Rel. 29, Created)   |                            |                        |  |  |
| FT                                  | DT   | 01-JUN-1994 (Rel. 29, Last sequence update)  |                            |                        |  |  |
| FT                                  | DT   | 01-NOV-1995 (Rel. 32, Last annotation update)  |                            |                        |  |  |
| FT                                  | DE   | ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7.)   |                            |                        |  |  |
| FT                                  | GN   | Gallus gallus (Chicken).   |                            |                        |  |  |
| FT                                  | OS   | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  |                            |                        |  |  |
| FT                                  | OC   | Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  |                            |                        |  |  |
| FT                                  | OC   | Gallus.  |                            |                        |  |  |
| FT                                  | RN   | [1]  |                            |                        |  |  |
| FT                                  | RP   | SEQUENCE FROM N.A.   |                            |                        |  |  |
| FT                                  | RC   | TISSUE=MUSCLE;   |                            |                        |  |  |
| FT                                  | RA   | MEDLINE; 94325359.   |                            |                        |  |  |
| FT                                  | RA   | Randall W.R., Rimer M., Gough N.R.;  |                            |                        |  |  |
| FT                                  | RA   | "Cloning and analysis of chicken acetylcholinesterase transcripts  |                            |                        |  |  |
| FT                                  | RT   | from muscle and brain."  |                            |                        |  |  |
| FT                                  | RL   | Biochim. Biophys. Acta 1218:453-456(1994).   |                            |                        |  |  |
| FT                                  | CC   | -I - FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.   |                            |                        |  |  |
| FT                                  | CC   | -I - CATALYTIC ACTIVITY: ACETYLCHOLINE + H(2)O = CHOLINE + ACETATE.  |                            |                        |  |  |
| FT                                  | CC   | -I - SUBUNIT: OLIGOMER COMPOSED OF DISULFIDE-LINKED HOMODIMERS.  |                            |                        |  |  |
| FT                                  | CC   | -I - SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLIPASE/LIPASE FAMILY.  |                            |                        |  |  |
| FT                                  | CC   | -----  |                            |                        |  |  |
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| FT                                  | CC   | or send an email to license@isb-sib.ch).   |                            |                        |  |  |
| FT                                  | CC   | -----  |                            |                        |  |  |
| FT                                  | DR   | EMBL: U03472; AAA60456.1;  |                            |                        |  |  |
| FT                                  | DR   | HSSP: P21836; 1MAH.  |                            |                        |  |  |
| FT                                  | DR   | PF00135; Coesterase_2.   |                            |                        |  |  |
| FT                                  | DR   | PRINTS: PRO0878; CHOLNESTERASE.  |                            |                        |  |  |
| FT                                  | DR   | PROSITE: PS00941; CARBOXYLIPASE_B_2; 1.  |                            |                        |  |  |
| FT                                  | DR   | KW   |                            |                        |  |  |
| FT                                  | FT   | Neurtransmitter degradation; Glycoprotein.   |                            |                        |  |  |
| FT                                  | FT   | SIGNAL_1   | 19                         |                        |  |  |
| FT                                  | FT   | CHAIN  | 20                         |                        |  |  |
| FT                                  | FT   | ACT_SITE   | 227                        |                        |  |  |
| FT                                  | FT   | ACT_32   | 227                        |                        |  |  |
| FT                                  | FT   | ACT_33   | 520                        |                        |  |  |
| FT                                  | FT   | ACT_SITE   | 633                        |                        |  |  |
| FT                                  | FT   | ACT_34   | 633                        |                        |  |  |
| FT                                  | FT   | DISULFID_94  | 121                        |                        |  |  |
| FT                                  | FT   | DISULFID_281   | 292                        |                        |  |  |
| FT                                  | FT   | DISULFID_595   | 713                        |                        |  |  |
| FT                                  | FT   | DISULFID_764   | 764                        |                        |  |  |
| FT                                  | FT   | INTERCHAIN   | INTERCHAIN (BY SIMILARITY) |                        |  |  |
| FT                                  | FT   | CARBONYD_285   | 285                        |                        |  |  |
| FT                                  | FT   | CARBONYD_536   | 536                        |                        |  |  |
| FT                                  | FT   | CARBONYD_650   | 650                        |                        |  |  |
| FT                                  | FT   | CARBONYD_495   | 495                        |                        |  |  |

|    |   |           |      |         |
|----|---|-----------|------|---------|
| ID | HXD4-CHICK  | STANDARD; | PRT; | 235 AA. |
| AC | P12778;   |           |      |         |
| DT | 01-AUG-1990 (Rel. 15; Created)  |           |      |         |
| DT | 01-AUG-1990 (Rel. 15; Last sequence update)   |           |      |         |
| DT | 01-OCT-1996 (Rel. 34; Last annotation update)   |           |      |         |
| DE | HOMEBOX PROTEIN HOX-D4 (CHOX-A).  |           |      |         |
| GN | HOXD4 OR HOXD-4 OR CHOX-A.  |           |      |         |
| OS | Gallus gallus (Chicken).  |           |      |         |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Phasianidae; Galliformes; Galli; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.   |           |      |         |
| RN | [1]   |           |      |         |
| RP | SEQUENCE FROM N.A.  |           |      |         |
| RX | MEDLINE; 90245562.  |           |      |         |
| RA | Sasaki H., Tokuyama E., Kuroiwa A.;   |           |      |         |
| RT | "Specific DNA binding of the two chicken Deformed family homeodomain proteins, Chox-1.4 and Chox-a."  |           |      |         |
| RL | Nucleic Acids Res. 18:1739-1747(1990).  |           |      |         |
| CC | -!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.   |           |      |         |
| CC | -!- FUNCTION: BINDS TO SITES IN THE 5'-FLANKING SEQUENCE OF ITS CODING REGION WITH VARIOUS AFFINITIES. THE CONSENSUS SEQUENCES OF THE HIGH AND LOW AFFINITY BINDING SITES ARE TATGAC(C/G) AND CTAATT.   |           |      |         |
| CC | -!- SUBCELLULAR LOCATION: NUCLEAR.  |           |      |         |
| CC | -!- SIMILARITY: BELONGS TO THE ANTP FAMILY OF HOMEBOX PROTEINS. "DEFORMED" SUBFAMILY.   |           |      |         |
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| DR | EMBL; X52671; CAA36897.1; -.  |           |      |         |
| DR | EMBL; X52672; CAA36898.1; -.  |           |      |         |
| DR | PIR; S09256; S09256.  |           |      |         |
| DR | HSPP; P02833; ISAN.   |           |      |         |
| DR | TRANSFAC; T01753; -.  |           |      |         |
| DR | PF00046; homeobox; 1.   |           |      |         |
| DR | PRINTS; PR00024; HOMEBOX.   |           |      |         |
| DR | PRINTS; PR00025; ANTENNAPEDIA.  |           |      |         |
| DR | PROSITE; PS50027; HOMEBOX_2; 1.   |           |      |         |
| DR | PROSITE; PS50032; ANTENNAPEDIA_1.   |           |      |         |
| DR | Homeobox; DNA-binding; Developmental protein; Nuclear protein; Transcription regulation.  |           |      |         |
| KW | ANTP-TYPE HEXAPEPTIDE.  |           |      |         |
| FT | DOMAIN 123 128  |           |      |         |
| FT | DNA_BIND 144 203  |           |      |         |
| FT | DOMAIN 212 217  |           |      |         |
| SQ | SEQUENCE 235 AA; 266662 MW; B7115D434033E4B5 CRC64;   |           |      |         |
| DR | X82444; CAA57824.1; -.  |           |      |         |
| DR | REBASE; RB02888; M.SpoMI.   |           |      |         |
| DR | PFAM; PF00445; DNA_methylase_2.   |           |      |         |
| KW | Methyltransferase; Methylation.   |           |      |         |
| FT | ACT SITE 81 81 BY SIMILARITY  |           |      |         |
| SQ | SEQUENCE 330 AA; 37976 MW; 50A7121FA7CF58A1 CRC64;  |           |      |         |
| DR | X82444; CAA57824.1; -.  |           |      |         |
| DR | REBASE; RB02888; M.SpoMI.   |           |      |         |
| DR | PFAM; PF00445; DNA_methylase_2.   |           |      |         |
| KW | Methyltransferase; Methylation.   |           |      |         |
| FT | ACT SITE 81 81 BY SIMILARITY  |           |      |         |
| SQ | SEQUENCE 330 AA; 37976 MW; 50A7121FA7CF58A1 CRC64;  |           |      |         |
| DR | X82444; CAA57824.1; -.  |           |      |         |
| DR | REBASE; RB02888; M.SpoMI.   |           |      |         |
| DR | PFAM; PF00445; DNA_methylase_2.   |           |      |         |
| KW | Methyltransferase; Methylation.   |           |      |         |
| FT | ACT SITE 81 81 BY SIMILARITY  |           |      |         |
| SQ | SEQUENCE 330 AA; 37976 MW; 50A7121FA7CF58A1 CRC64;  |           |      |         |
| DR | X82444; CAA57824.1; -.  |           |      |         |
| DR | REBASE; RB02888; M.SpoMI.   |           |      |         |
| DR | PFAM; PF00445; DNA_methylase_2.   |           |      |         |
| KW | Methyltransferase; Methylation.   |           |      |         |
| FT | ACT SITE 81 81 BY SIMILARITY  |           |      |         |
| SQ | SEQUENCE 330 AA; 37976 MW; 50A7121FA7CF58A1 CRC64;  |           |      |         |
| DR | X82444; CAA57824.1; -.  |           |      |         |
| DR | REBASE; RB02888; M.SpoMI.   |           |      |         |
| DR | PFAM; PF00445; DNA_methylase_2.   |           |      |         |
| KW | Methyltransferase; Methylation.   |           |      |         |
| FT | ACT SITE 81 81 BY SIMILARITY  |           |      |         |
| SQ | SEQUENCE 330 AA; 37976 MW; 50A7121FA7CF58A1 CRC64;  |           |      |         |
| DR | X82444; CAA57824.1; -.  |           |      |         |
| DR | REBASE; RB02888; M.SpoMI.   |           |      |         |
| DR | PFAM; PF00445; DNA_methylase_2.   |           |      |         |
| KW | Methyltransferase; Methylation.   |           |      |         |
| FT | ACT SITE 81 81 BY SIMILARITY  |           |      |         |
| SQ | SEQUENCE 330 AA; 37976 MW; 50A7121FA7CF58A1 CRC64;  |           |      |         |
| DR | X82444; CAA57824.1; -.  |           |      |         |
| DR | REBASE; RB02888; M.SpoMI.   |           |      |         |
| DR | PFAM; PF00445; DNA_methylase_2.   |           |      |         |
| KW | Methyltransferase; Methylation.   |           |      |         |
| FT | ACT SITE 81 81 BY SIMILARITY  |           |      |         |
| SQ | SEQUENCE 330 AA; 37976 MW; 50A7121FA7CF58A1 CRC64;  |           |      |         |
| DR | X82444; CAA57824.1; -.  |           |      |         |
| DR | REBASE; RB02888; M.SpoMI.   |           |      |         |
| DR | PFAM; PF00445; DNA_methylase_2.   |           |      |         |
| KW | Methyltransferase; Methylation.   |           |      |         |
| FT | ACT SITE 81 81 BY SIMILARITY  |           |      |         |
| SQ | SEQUENCE 330 AA; 37976 MW; 50A7121FA7CF58A1 CRC64;  |           |      |         |
| DR | X82444; CAA57824.1; -.  |           |      |         |
| DR | REBASE; RB02888; M.SpoMI.   |           |      |         |
| DR | PFAM; PF00445; DNA_methylase_2.   |           |      |         |
| KW | Methyltransferase; Methylation.   |           |      |         |
| FT | ACT SITE 81 81 BY SIMILARITY  |           |      |         |
| SQ | SEQUENCE 330 AA; 37976 MW; 50A7121FA7CF58A1 CRC64;  |           |      |         |
| DR | X82444; CAA57824.1; -.  |           |      |         |
| DR | REBASE; RB02888; M.SpoMI.   |           |      |         |
| DR | PFAM; PF00445; DNA_methylase_2.   |           |      |         |
| KW | Methyltransferase; Methylation.   |           |      |         |
| FT | ACT SITE 81 81 BY SIMILARITY  |           |      |         |
| SQ | SEQUENCE 330 AA; 37976 MW; 50A7121FA7CF58A1 CRC64;  |           |      |         |
| DR | X82444; CAA57824.1; -.  |           |      |         |
| DR | REBASE; RB02888; M.SpoMI.   |           |      |         |
| DR | PFAM; PF00445; DNA_methylase_2.   |           |      |         |
| KW | Methyltransferase; Methylation.   |           |      |         |
| FT | ACT SITE 81 81 BY SIMILARITY  |           |      |         |
| SQ | SEQUENCE 330 AA; 37976 MW; 50A7121FA7CF58A1 CRC64;  |           |      |         |
| DR | X82444; CAA57824.1; -.  |           |      |         |
| DR | REBASE; RB02888; M.SpoMI.   |           |      |         |
| DR | PFAM; PF00445; DNA_methylase_2.   |           |      |         |
| KW | Methyltransferase; Methylation.   |           |      |         |
| FT | ACT SITE 81 81 BY SIMILARITY  |           |      |         |
| SQ | SEQUENCE 330 AA; 37976 MW; 50A7121FA7CF58A1 CRC64;  |           |      |         |
| DR | X82444; CAA57824.1; -.  |           |      |         |
| DR | REBASE; RB02888; M.SpoMI.   |           |      |         |
| DR | PFAM; PF00445; DNA_methylase_2.   |           |      |         |
| KW | Methyltransferase; Methylation.   |           |      |         |
| FT | ACT SITE 81 81 BY SIMILARITY  |           |      |         |
| SQ | SEQUENCE 330 AA; 37976 MW; 50A7121FA7CF58A1 CRC64;  |           |      |         |
| DR | X82444; CAA57824.1; -.  |           |      |         |
| DR | REBASE; RB02888; M.SpoMI.   |           |      |         |
| DR | PFAM; PF00445; DNA_methylase_2.   |           |      |         |
| KW | Methyltransferase; Methylation.   |           |      |         |
| FT | ACT SITE 81 81 BY SIMILARITY  |           |      |         |
| SQ | SEQUENCE 330 AA; 37976 MW; 50A7121FA7CF58A1 CRC64;  |           |      |         |
| DR | X82444; CAA57824.1; -.  |           |      |         |
| DR | REBASE; RB02888; M.SpoMI.   |           |      |         |
| DR | PFAM; PF00445; DNA_methylase_2.   |           |      |         |
| KW | Methyltransferase; Methylation.   |           |      |         |
| FT | ACT SITE 81 81 BY SIMILARITY  |           |      |         |
| SQ | SEQUENCE 330 AA; 37976 MW; 50A7121FA7CF58A1 CRC64;  |           |      |         |
| DR | X82444; CAA57824.1; -.  |           |      |         |
| DR | REBASE; RB02888; M.SpoMI.   |           |      |         |
| DR | PFAM; PF00445; DNA_methylase_2.   |           |      |         |
| KW | Methyltransferase; Methylation.   |           |      |         |
| FT | ACT SITE 81 81 BY SIMILARITY  |           |      |         |
| SQ | SEQUENCE 330 AA; 37976 MW; 50A7121FA7CF58A1 CRC64;  |           |      |         |
| DR | X82444; CAA57824.1; -.  |           |      |         |
| DR | REBASE; RB02888; M.SpoMI.   |           |      |         |
| DR | PFAM; PF00445; DNA_methylase_2.   |           |      |         |
| KW | Methyltransferase; Methylation.   |           |      |         |
| FT | ACT SITE 81 81 BY SIMILARITY  |           |      |         |
| SQ | SEQUENCE 330 AA; 37976 MW; 50A7121FA7CF58A1 CRC64;  |           |      |         |
| DR | X82444; CAA57824.1; -.  |           |      |         |
| DR | REBASE; RB02888; M.SpoMI.   |           |      |         |
| DR | PFAM; PF00445; DNA_methylase_2.   |           |      |         |
| KW | Methyltransferase; Methylation.   |           |      |         |
| FT | ACT SITE 81 81 BY SIMILARITY  |           |      |         |
| SQ | SEQUENCE 330 AA; 37976 MW; 50A7121FA7CF58A1 CRC64;  |           |      |         |
| DR | X82444; CAA57824.1; -.  |           |      |         |
| DR | REBASE; RB02888; M.SpoMI.   |           |      |         |
| DR | PFAM; PF00445; DNA_methylase_2.   |           |      |         |
| KW | Methyltransferase; Methylation.   |           |      |         |
| FT | ACT SITE 81 81 BY SIMILARITY  |           |      |         |
| SQ | SEQUENCE 330 AA; 37976 MW; 50A7121FA7CF58A1 CRC64;  |           |      |         |
| DR | X82444; CAA57824.1; -.  |           |      |         |
| DR | REBASE; RB02888; M.SpoMI.   |           |      |         |
| DR | PFAM; PF00445; DNA_methylase_2.   |           |      |         |
| KW | Methyltransferase; Methylation.   |           |      |         |
| FT | ACT SITE 81 81 BY SIMILARITY  |           |      |         |
| SQ | SEQUENCE 330 AA; 37976 MW; 50A7121FA7CF58A1 CRC64;  |           |      |         |
| DR | X82444; CAA57824.1; -.  |           |      |         |
| DR | REBASE; RB02888; M.SpoMI.   |           |      |         |
| DR | PFAM; PF00445; DNA_methylase_2.   |           |      |         |
| KW | Methyltransferase; Methylation.   |           |      |         |
| FT | ACT SITE 81 81 BY SIMILARITY  |           |      |         |
| SQ | SEQUENCE 330 AA; 37976 MW; 50A7121FA7CF58A1 CRC64;  |           |      |         |
| DR | X82444; CAA57824.1; -.  |           |      |         |
| DR | REBASE; RB02888; M.SpoMI.   |           |      |         |
| DR | PFAM; PF00445; DNA_methylase_2.   |           |      |         |
| KW | Methyltransferase; Methylation.   |           |      |         |
| FT | ACT SITE 81 81 BY SIMILARITY  |           |      |         |
| SQ | SEQUENCE 330 AA; 37976 MW; 50A7121FA7CF58A1 CRC64;  |           |      |         |
| DR | X82444; CAA57824.1; -.  |           |      |         |
| DR | REBASE; RB02888; M.SpoMI.   |           |      |         |
| DR | PFAM; PF00445; DNA_methylase_2.   |           |      |         |
| KW | Methyltransferase; Methylation.   |           |      |         |
| FT | ACT SITE 81 81 BY SIMILARITY  |           |      |         |
| SQ | SEQUENCE 330 AA; 37976 MW; 50A7121FA7CF58A1 CRC64;  |           |      |         |
| DR | X82444; CAA57824.1; -.  |           |      |         |
| DR | REBASE; RB02888; M.SpoMI.   |           |      |         |
| DR | PFAM; PF00445; DNA_methylase_2.   |           |      |         |
| KW | Methyltransferase; Methylation.   |           |      |         |
| FT | ACT SITE 81 81 BY SIMILARITY  |           |      |         |
| SQ | SEQUENCE 330 AA; 37976 MW; 50A7121FA7CF58A1 CRC64;  |           |      |         |
| DR | X82444; CAA57824.1; -.  |           |      |         |
| DR | REBASE; RB02888; M.SpoMI.   |           |      |         |
| DR | PFAM; PF00445; DNA_methylase_2.   |           |      |         |
| KW | Methyltransferase; Methylation.   |           |      |         |
| FT | ACT SITE 81 81 BY SIMILARITY  |           |      |         |
| SQ | SEQUENCE 330 AA; 37976 MW; 50A7121FA7CF58A1 CRC64;  |           |      |         |
| DR | X82444; CAA57824.1; -.  |           |      |         |
| DR | REBASE; RB02888; M.SpoMI.   |           |      |         |
| DR | PFAM; PF00445; DNA_methylase_2.   |           |      |         |
| KW | Methyltransferase; Methylation.   |           |      |         |
| FT | ACT SITE 81 81 BY SIMILARITY  |           |      |         |
| SQ | SEQUENCE 330 AA; 37976 MW; 50A7121FA7CF58A1 CRC64;  |           |      |         |
| DR | X82444; CAA57824.1; -.  |           |      |         |
| DR | REBASE; RB02888; M.SpoMI.   |           |      |         |
| DR | PFAM; PF00445; DNA_methylase_2.   |           |      |         |
| KW | Methyltransferase; Methylation.   |           |      |         |
| FT | ACT SITE 81 81 BY SIMILARITY  |           |      |         |
| SQ | SEQUENCE 330 AA; 37976 MW; 50A7121FA7CF58A1 CRC64;  |           |      |         |
| DR | X82444; CAA57824.1; -.  |           |      |         |
| DR | REBASE; RB02888; M.SpoMI.   |           |      |         |
| DR | PFAM; PF00445; DNA_methylase_2.   |           |      |         |
| KW | Methyltransferase; Methylation.   |           |      |         |
| FT | ACT SITE 81 81 BY SIMILARITY  |           |      |         |
| SQ | SEQUENCE 330 AA; 37976 MW; 50A7121FA7CF58A1 CRC64;  |           |      |         |
| DR | X82444; CAA57824.1; -.  |           |      |         |
| DR | REBASE; RB02888; M.SpoMI.   |           |      |         |
| DR | PFAM; PF00445; DNA_methylase_2.   |           |      |         |
| KW | Methyltransferase; Methylation.   |           |      |         |
| FT | ACT SITE 81 81 BY SIMILARITY  |           |      |         |
| SQ | SEQUENCE 330 AA; 37976 MW; 50A7121FA7CF58A1 CRC64;  |           |      |         |
| DR | X82444; CAA57824.1; -.  |           |      |         |
| DR | REBASE; RB02888; M.SpoMI.   |           |      |         |
| DR | PFAM; PF00445; DNA_methylase_2.   |           |      |         |
| KW | Methyltransferase; Methylation.   |           |      |         |
| FT | ACT SITE 81 81 BY SIMILARITY  |           |      |         |
| SQ | SEQUENCE 330 AA; 37976 MW; 50A7121FA7CF58A1 CRC64;  |           |      |         |
| DR | X82444; CAA57824.1; -.  |           |      |         |
| DR | REBASE; RB02888; M.SpoMI.   |           |      |         |
| DR | PFAM; PF00445; DNA_methylase_2.   |           |      |         |
| KW | Methyltransferase; Methylation.   |           |      |         |
| FT | ACT SITE 81 81 BY SIMILARITY  |           |      |         |
| SQ | SEQUENCE 330 AA; 37976 MW; 50A7121FA7CF58A1 CRC64;  |           |      |         |
| DR | X82444; CAA57824.1; -.  |           |      |         |
| DR | REBASE; RB02888; M.SpoMI.   |           |      |         |
| DR | PFAM; PF00445; DNA_methylase_2.   |           |      |         |
| KW | Methyltransferase; Methylation.   |           |      |         |
| FT | ACT SITE 81 81 BY SIMILARITY  |           |      |         |
| SQ | SEQUENCE 330 AA; 37976 MW; 50A7121FA7CF58A1 CRC64;  |           |      |         |
| DR | X82444; CAA57824.1; -.  |           |      |         |
| DR | REBASE; RB02888; M.SpoMI.   |           |      |         |
| DR | PFAM; PF00445; DNA_methylase_2.   |           |      |         |
| KW | Methyltransferase; Methylation.   |           |      |         |
| FT | ACT SITE 81 81 BY SIMILARITY  |           |      |         |
| SQ | SEQUENCE 330 AA; 37976 MW; 50A7121FA7CF58A1 CRC64;  |           |      |         |
| DR | X82444; CAA57824.1; -.  |           |      |         |
| DR | REBASE; RB02888; M.SpoMI.   |           |      |         |
| DR | PFAM; PF00445; DNA_methylase_2.   |           |      |         |
| KW | Methyltransferase; Methylation.   |           |      |         |
| FT | ACT SITE 81 81 BY SIMILARITY  |           |      |         |
| SQ | SEQUENCE 330 AA; 37976 MW; 50A7121FA7CF58A1 CRC64;  |           |      |         |
| DR | X82444; CAA57824.1; -.  |           |      |         |
| DR | REBASE; RB02888; M.SpoMI.   |           |      |         |
| DR | PFAM; PF00445; DNA_methylase_2.   |           |      |         |
| KW | Methyltransferase; Methylation.   |           |      |         |
| FT | ACT SITE 81 81 BY SIMILARITY  |           |      |         |
| SQ | SEQUENCE 330 AA; 37976 MW; 50A7121FA7CF58A1 CRC64;  |           |      |         |
| DR | X82444; CAA57824.1; -.  |           |      |         |
| DR | REBASE; RB02888; M.SpoMI.   |           |      |         |
| DR | PFAM; PF00445; DNA_methylase_2.   |           |      |         |
| KW | Methyltransferase; Methylation.   |           |      |         |
| FT | ACT SITE 81 81 BY SIMILARITY  |           |      |         |
| SQ | SEQUENCE 330 AA; 37976 MW; 50A7121FA7CF58A1 CRC64;  |           |      |         |
| DR | X82444; CAA57824.1; -.  |           |      |         |
| DR | REBASE; RB02888; M.SpoMI.   |           |      |         |
| DR | PFAM; PF00445; DNA_methylase_2.   |           |      |         |
| KW | Methyltransferase; Methylation.   |           |      |         |
| FT | ACT SITE 81 81 BY SIMILARITY  |           |      |         |
| SQ | SEQUENCE 330 AA; 37976 MW; 50A7121FA7CF58A1 CRC64;  |           |      |         |
| DR | X82444; CAA57824.1; -.  |           |      |         |
| DR | REBASE; RB02888; M.SpoMI.   |           |      |         |
| DR | PFAM; PF00445; DNA_methylase_2.   |           |      |         |
| KW | Methyltransferase; Methylation.   |           |      |         |
| FT | ACT SITE 81 81 BY SIMILARITY  |           |      |         |
| SQ | SEQUENCE 330 AA; 37976 MW; 50A7121FA7CF58A1 CRC64;  |           |      |         |
| DR | X82444; CAA57824.1; -.  |           |      |         |
| DR | REBASE; RB02888; M.SpoMI.   |           |      |         |
| DR | PFAM; PF00445; DNA_methylase_2.   |           |      |         |
| KW | Methyltransferase; Methylation.   |           |      |         |
| FT | ACT SITE 81 81 BY SIMILARITY  |           |      |         |
| SQ | SEQUENCE 330 AA; 37976 MW; 50A7121FA7CF58A1 CRC64;  |           |      |         |
| DR | X82444; CAA57824.1; -.  |           |      |         |
| DR | REBASE; RB02888; M.SpoMI.   |           |      |         |
| DR | PFAM; PF00445; DNA_methylase_2.   |           |      |         |
| KW | Methyltransferase; Methylation.   |           |      |         |
| FT |   |           |      |         |

OS Brachydanio rerio (zebrafish) (*zebra danio*).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostii; Euteleostei; Ostariophysi;  
 OC Cypriniformes; Cyprinoidea; Cyprinidae; Cyprinidae; Rasborinae; Danio.  
 [1]

RN "Zebrafish hox genes: genomic organization and modified colinear expression patterns in the trunk";  
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.

CC -!- SUBCELLULAR LOCATION: NUCLEAR.

CC -!- SIMILARITY: BELONGS TO THE ANTP FAMILY OF HOMEOBOX PROTEINS. "DEFORMED" SUBFAMILY.

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DR EMBL: Y4883; CAA4883\_1; ALT\_INIT.  
 DR EMBL: J03770; AAA20072\_1; ALT\_INIT.  
 DR EMBL: M87804; AAA37851\_1; -.  
 DR EMBL: U77364; AAB41222\_1; -.  
 DR PIR: A36170; A36170.  
 DR HSSP: P02833; 1SAN.  
 DR TRANSFAC: T01752; -.  
 DR MGII: 96200; HOXD4.  
 DR PFAM: PF00046; homeobox; 1.  
 DR PRINTS: PR00024; HOMEBOX.  
 DR PRINTS: PR00025; ANTENNAPEPIA.  
 DR PROSITE: PS00027; HOMEBOX\_1; 1.  
 DR PROSITE: PS00071; HOMEBOX\_2; 1.  
 DR PROSITE: PS00032; ANTENNAPEPIA; 1.  
 KW Homeobox; DNA binding; Developmental protein; Nuclear protein;  
 KW Transcription regulation.

FT DOMAIN 125 130 ANTP-TYPE HEXAPEPTIDE.

FT DNA\_BIND 146 205 HOMEBOX.

SEQUENCE 236 AA: 27132 MW: AAEBC8CF34F17B5E CRC64;

Query Match 35.7%; Score 5; DB 1; Length 236;  
 Best Local Similarity 100.0%; Pred. No. 20;  
 Matches 5; Conservative 0; Mismatches 0; Gaps 0;

QY 7 SSIMV 11  
 Db 4 SSIMV 8

RESULT 10  
 HXD4\_MOUSE STANDARD; PRT; 250 AA.  
 ID HXD4\_HUMAN STANDARD; PRT; 255 AA.  
 AC P010628; P97451; ID HXD4\_HUMAN  
 DT 01-JUL-1989 (Rel. 11, Created) AC P09056; ID HXD4\_HUMAN  
 DT 01-NOV-1995 (Rel. 32, Last sequence update) AC P09056; ID HXD4\_HUMAN  
 DT 15-DEC-1998 (Rel. 37, Last annotation update) AC P09056; ID HXD4\_HUMAN  
 DE HOMEOBOX PROTEIN HOX-D4 (HOX-4.2) (HOX-5.1).  
 GN HOXD4 OR HOXD-4 OR HOX-4.2.  
 OS Mus musculus (Mouse).  
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Mus.  
 [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 88263027.  
 RA Featherstone M.S., Baron A., Gaunt S.J., Mattei M.-G., Duboule D.;  
 RT "Hox-5.1 defines a homeobox-containing gene locus on mouse chromosome 2."  
 RT Proc. Natl. Acad. Sci. U.S.A. 85:4760-4764 (1988).  
 RN [2]  
 RP MEDLINE: 94173687.  
 RA Rambaldi I., Kovacs E.N., Featherstone M.S.;  
 RA "A Proline-rich transcriptional activation domain in murine HOXD-4 REVISIONS.  
 RP

RX MEDLINE; 90356367.  
 RA Cianetti L., di Cristofaro A., Zappavigna V., Bottero L.,  
 RA Boccoli G., Testa U., Russo G., Roncinelli E., Peschle C.;  
 RT "Molecular mechanisms underlying the expression of the human HOX-5.1  
 gene.";  
 RT Differential and stage-related expression in embryonic tissues of a  
 new human homeobox gene.";  
 RT Nature 324:664-668(1986).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 87090377.  
 RA Mavilio F., Simeone A., Giampaolo A., Paiella A., Zappavigna V.,  
 RA Acampora D., Poiana M., Russo G., Roncinelli E.;  
 RT "Differential and stage-related expression in embryonic tissues of a  
 new human homeobox gene.";  
 RT Nature 324:664-668(1986).  
 RN [3]  
 RP SEQUENCE OF 154-219 FROM N.A.  
 RX MEDLINE; 90215156.  
 RA Boncinelli E., Acampora D., Pannese M., D'Esposito M., Somma R.,  
 RA Gaudino G., Scornaiuolo A., Cafiero M., Paiella A., Simeone A.;  
 RT "Organization of human class I homeobox genes.";  
 RL Genome 31:745-756(1989).  
 CC -I- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF  
 CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH  
 CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.  
 CC -I- SUBCELLULAR LOCATION: NUCLEAR.  
 CC -I- SIMILARITY: BELONGS TO THE ANT DOMAIN OF HOMEBOX PROTEINS.  
 CC -I- "DEFORMED" SUBDOMAIN.  
 CC  
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 CC  
 DR EMBL; X17360; CAA3237.1; -.  
 DR PIR; X04706; CA28411.1; -.  
 DR PIR; S10985; WJH4B.  
 DR HSSP; P02833; 1SAN.  
 DR TRANSFAC; T00376; -.  
 DR MIM; 142981; -.  
 DR PFAM; PF00046; homeobox; 1.  
 DR PRINTS; PR00024; HOMEBOX.  
 DR PRINTS; PR00035; ANTENNAPEDIA.  
 DR PROSITE; PS00027; HOMEBOX\_1; 1.  
 DR PROSITE; PS00032; ANTENNAPEDIA\_1.  
 DR PROSITE; PS50071; HOMEBOX\_2; 1.  
 KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;  
 KW Transcription regulation.  
 FT DOMAIN 138 ANTP-TYPE HEXAPEPTIDE.  
 FT DOMAIN 213 HOMEobox.  
 FT DOMAIN 222 234 POLY-SER.  
 FT CONFLICT 123 123 P -> S (IN REF. 2).  
 FT CONFLICT 142 142 V -> A (IN REF. 2).  
 SQ SEQUENCE 255 AA; 27895 MW; 3920508CCCAF16FF CRC64;

DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 GN HYPOTHETICAL 31.5 KDA PROTEIN IN KATB 3' REGION.  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
 OC Bacillus/Staphylococcus group; Bacillus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-168 / BGSC1A;  
 RA Yoshida K.-I., Sano H., Seki S., Oda M., Fujimura M., Fujita Y.;  
 RL Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.  
 CC -I- SIMILARITY: TO E.COLI RNA AND M.GRISEORUBIDA MYRA.  
 CC  
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 CC  
 DR EMBL; DB8026; BAA11703.1; -.  
 DR EMBL; Z99123; CAB11927.1; -.  
 DR EMBL; Z99124; CAB15937.1; -.  
 DR SUBTLELIST; BG11151; YXJB.  
 KW Hypothetical protein.  
 SQ SEQUENCE 282 AA; 31473 MW; 35DE65D847D67E61 CRC64;

Query Match 35.7%; Score 5; DB 1; Length 282;  
 Best Local Similarity 100.0%; Pred. No. 21; Mismatches 0; Indels 0; Gaps 0;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHR 5  
 Db 172 AEFHR 176

RESULT 13  
 YFIN\_ECOLI STANDARD; PRT; 408 AA.  
 ID YFIN\_ECOLI STANDARD;  
 AC P46139; P76598;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE HYPOTHETICAL 46.0 KDA PROTEIN IN AROF-RPLS INTERGENIC REGION.  
 GN YFIN.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K12 / MG1655;  
 RX MEDLINE; 9742617.  
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Collado-Vides J., Glasner J.D., Goeddel D.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeddel M.A., Rose D.J.,  
 RA Mai B., Shao Y.;  
 RT "The complete genome sequence of Escherichia coli K-12.";  
 RL Science 277:153-1474 (1997).  
 RN [2]  
 RP SEQUENCE OF 330-408 FROM N.A.  
 RX MEDLINE; 8405772.  
 RA Bystroem A.S., Hjalmarsson K.J., Wikstrom P.M., Bjork G.R.;  
 RT "The nucleotide sequence of an Escherichia coli operon containing  
 RT genes for the tRNA<sup>Ala</sup>MIG methyltransferase, the ribosomal proteins S16  
 RT and L19 and a 21-K polypeptide.";  
 RL EMBO J. 2:899-905(1983).  
 RN [3]  
 RP IDENTIFICATION.  
 RX MEDLINE; 96032851.  
 RA Borodovsky M., McIninch J., Koontz E.V., Rudd K.E., Medigue C.,  
 RA Danchin A.;  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)

RESULT 12  
 YXJB\_BACSU STANDARD; PRT; 282 AA.  
 ID YXJB\_BACSU  
 AC P4213;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)

"Detection of new genes in a bacterial genome using Markov models for three gene classes"; Nucleic Acids Res. 23:3554-3562(1995).  
 -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  
 CC -!- SIMILARITY: BELONGS TO THE YALC / YFIN (E.COLI), YHCK (B.SUBTILLIS) FAMILY.  
 CC

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DR: AE000346; AAC75651.1; -;  
 DR: EMBL: X01818; -; NOT\_ANNOTATED\_CDS.  
 DR: ECOGENE: EG12880; YFIN.  
 DR: PFAM: PF00990; DUF9\_1.  
 KW: HYPOTHETICAL PROTEIN; Transmembrane.  
 FT: TRANSMEM 25 POTENTIAL.  
 FT: TRANSMEM 53 73 POTENTIAL.  
 FT: TRANSMEM 113 133 POTENTIAL.  
 FT: TRANSMEM 155 175 POTENTIAL.  
 SQ: SEQUENCE 408 AA; 45989 MW; 720B6539EF43DB16 CRC64;

Query Match 35.7%; Score 5; DB 1; Length 408;  
 Best Local Similarity 100.0%; Pred. No. 29;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHR 5  
 |||||  
 Db 215 AEFHR 219

SEQUENCE FROM N.A.

STRAIN=K12;

RA: Suzuki H., Kim E., Yamamoto N., Hashimoto W., Yamamoto K., Kumagai H.;  
 RT: "Mapping, cloning and DNA sequencing of pepB gene which encodes  
 peptidase B of Escherichia coli K-12.";  
 J. Ferment. Bioeng. 82:392-397(1996).  
 RN [2]

SEQUENCE FROM N.A.

STRAIN=K12;

RA: Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 Mau B., Shao Y.;  
 RT: "The complete genome sequence of Escherichia coli K-12.";  
 J. Bacteriol. 176:610-619 (1994).

SEQUENCE FROM N.A.

STRAIN=K12;

RA: Alba H., Baba T., Fujita K., Hayashi K., Honjoh A., Horiochi T.,  
 Ikeno K., Inada T., Isono K., Isono S., Itoh T., Kanai K.,  
 Kasai H., Kashimoto K., Kim S., Kimura S., Kitagawa M.,  
 Kitakawa M., Makino K., Masuda S., Mikl T., Mizobuchi K., Mori H.,  
 Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Oshima T.,

Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C.,  
 Yamanoto Y., Yano M.;  
 RA: Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
 RL: SEQUENCE OF 1-42 FROM N.A.  
 RN: RP  
 RX: RC  
 MEDLINE: 94131939.  
 RA: Kawula T.H., Lelivelt M.J.;  
 RT: "Mutations in a gene encoding a new Hsp70 suppress rapid DNA inversion and bg1 activation, but not proU derepression, in hns-1 mutant Escherichia coli".  
 J. Bacteriol. 176:610-619 (1994).  
 RL: -!  
 CC: -!- COFACTOR: ACTIVATED BY MANGANESE (BY SIMILARITY).  
 CC: -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M1; ALSO KNOWN AS THE CYTOSOL ANTIPEPTIDASE FAMILY.  
 CC: -!  
 CC: This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).  
 CC: -!  
 CC: EMBL: D84499; BAA12689.1;  
 DR: EMBL: AE000333; AAC75576.1; ALT\_INIT.  
 DR: EMBL: D90882; CAB2347.1;  
 DR: EMBL: D90883; CAB2357.1;  
 DR: EMBL: U01827; -; NOT\_ANNOTATED\_CDS.  
 DR: HSSP: P00727; LAP.  
 DR: ECOGENE: EG1210; PEPB.  
 DR: PFAM: PF00883; Peptidase\_M17\_1.  
 DR: PRINTS: PRO0481; LAMNOPTDASE.  
 DR: PROSITE: PS00031; CYTOSOL\_AP; 1.  
 DR: KW: Hydrolase; Manganese.  
 FT: METAL 195 195 MANGANESE (2) (BY SIMILARITY).  
 FT: METAL 200 200 MANGANESE (1 AND 2) (BY SIMILARITY).  
 FT: METAL 218 218 MANGANESE (2) (BY SIMILARITY).  
 FT: METAL 277 277 MANGANESE (1 AND 2) (BY SIMILARITY).  
 FT: METAL 279 279 MANGANESE (1 AND 2) (BY SIMILARITY).  
 FT: ACT\_SITE 207 207 POTENTIAL.  
 FT: ACT\_SITE 281 281 POTENTIAL.  
 FT: CONFLICT 155 155 Q->P (IN REF. 1).  
 FT: CONFLICT 375 426 STRAGFLSHFENYQQGWHLIDSATVKAPVQWSAGATG-LGVRTIANLT->TRRASCLTLTISKGCISARRL  
 FT: CONFLICT 41 41 TYERRNLGLRLDVC (IN REF. 1).  
 FT: CONFLICT 427 AA; 46180 MW; L->P (IN REF. 3).  
 SQ: SEQUENCE 427 AA; 46180 MW; 8299E7D440F5732E CRC64;

Query Match 35.7%; Score 5; DB 1; Length 427;  
 Best Local Similarity 100.0%; Pred. No. 30;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHR 5

Db 348 AEFHR 352

RESULT 15  
 ID NU4M.LOCM1 STANDARD; PRT; 444 AA.  
 ID NU4M.LOCM1 ID Q36424;  
 AC DT 01-NOV-1997 (Ref. 35, Created)  
 DT 01-NOV-1997 (Ref. 35, Last sequence update)  
 DT 01-NOV-1997 (Ref. 35, Last annotation update)  
 DE ND4.  
 SEQUENCE FROM N.A.

OS: Locusta migratoria (Migratory locust).  
 OG: Mitochondrion.  
 RA: Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC: Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;  
 OC: Acridoidea; Acridoidea; Acriidae; Oedipodinae; Locusta.

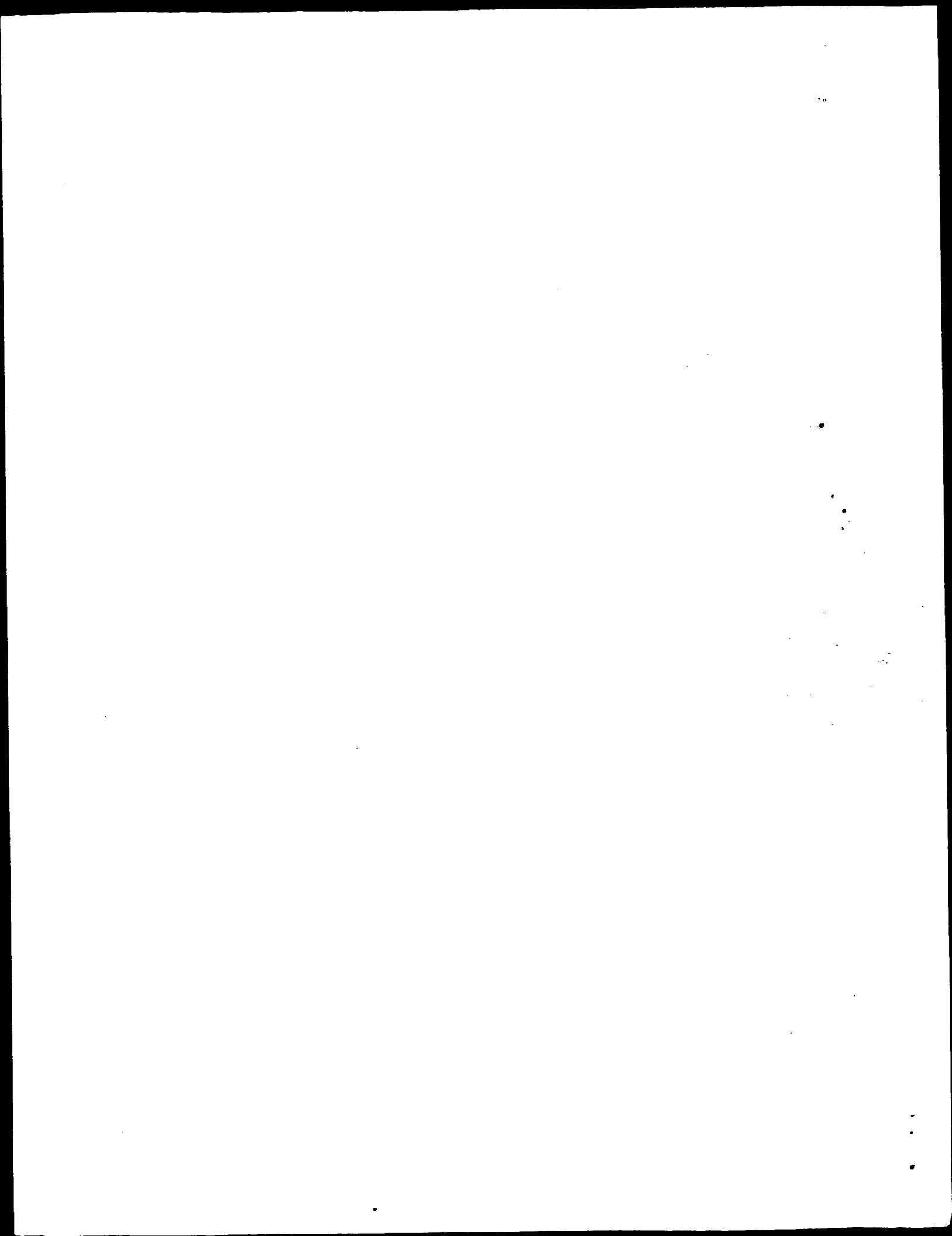
```

RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE: 96139026;
RA      Flock P.K., Rovelli C.H.F., Gelliissen G. ;
RT      "The sequence, organization, and evolution of the Locusta migratoria
RT      mitochondrial genome."
RL      J. Mol. Evol. 41:928-941(1995).
CC      -!- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: X80245; CAA56334.1; -
DR      PFAM: PF00361; Oxidored.q1; 1.
DR      PFAM: PF01059; Oxidored._S5_N; 1.
KW      Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SQ      SEQUENCE 444 AA; 51135 MW; B2D8DEC2584521BA CRC64;
```

```

Query Match      35.7%; Score 5; DB 1; Length 444;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      6 WSSYM 10
Db      376 WSSYM 380
```

Search completed: September 13, 2000, 02:27:53  
Job time: 170 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: September 13, 2000, 02:21:12 ; Search time 22.49 Seconds  
(without alignments)  
43.160 Million cell updates/sec

Title: US-09-155-076-1

Perfect score: 87 1 AEFFHRWSSTMVHVK 14

Sequence:

Scoring table: BLOSUM62

Gapop 10.0 Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 10%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL\_12:

- 1: sp\_archea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodont:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query | Match | Length | DB     | ID | Description        |
|------------|-------|-------|-------|--------|--------|----|--------------------|
| 1          | 87    | 100.0 | 611   | 6      | 062763 |    | 06763 felis silve  |
| 2          | 84    | 96.6  | 633   | 13     | 042275 |    | 042275 electrophor |
| 3          | 80    | 92.0  | 95    | 13     | Q9WY8  |    | QW6Y8 torpedo cal  |
| 4          | 76    | 80.5  | 95    | 13     | 073748 |    | 073748 bungarus fa |
| 5          | 56    | 64.4  | 602   | 6      | 062760 |    | 062760 felis silve |
| 6          | 56    | 64.4  | 602   | 6      | 062761 |    | 062761 panthera ti |
| 7          | 44    | 50.6  | 260   | 8      | 078338 |    | 078338 arabidopsis |
| 8          | 42    | 48.3  | 1788  | 4      | 060611 |    | 060611 homo sapien |
| 9          | 42    | 48.3  | 1788  | 4      | 060612 |    | 060612 homo sapien |
| 10         | 42    | 48.3  | 1792  | 6      | 046385 |    | 046385 bos taurus  |
| 11         | 42    | 48.3  | 2214  | 4      | 095425 |    | 09425 homo sapien  |
| 12         | 41    | 47.1  | 1323  | 11     | 062255 |    | 062255 mus musculu |
| 13         | 41    | 47.1  | 1687  | 10     | Q9KG9  |    | Q9XG9 oryza sativ  |
| 14         | 40.5  | 46.6  | 285   | 2      | 052970 |    | 052970 rhizobium m |
| 15         | 40.5  | 46.6  | 508   | 8      | 078332 |    | 078332 perugaria   |
| 16         | 40.5  | 46.6  | 508   | 8      | 078337 |    | 06177 pliocerpera  |
| 17         | 40.5  | 46.6  | 511   | 8      | 078334 |    | 078334 tylophora i |
| 18         | 40.5  | 46.6  | 511   | 8      | 078335 |    | 078335 vincetoxicu |
| 19         | 40    | 46.0  | 183   | 2      | Q57000 |    | 057000 zymomonas m |

RESULT 1  
062763 PRELIMINARY;  
ID 062763 PRT; 611 AA.  
AC 062763;  
DT 01-AUG-1998 (TREMBLrel. 07, Created)  
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)  
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
DE ACETYLCHOLINESTERASE COLLAGEN-TAILED OR GLOBULAR FORM PRECURSOR.  
DE ACHE.  
GN Felis silvestris catus (Cat).  
OS Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Felidae; Fissipedia; Felidae; Felis.  
RN [1].  
RP SEQUENCE FROM N.A.  
RA BATELLS C.F., XIE W.-H., MILLER-LINDOLM A.K., LOCRIDGE O.;  
RL Submitted (MR-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF053485; AAC089595.1; --.  
DR HSSP; P22303; 2CUL.  
DR PROSITE; PS00122; CARBOXYLESTERASE\_B-1; 1.  
DR PROSITE; PS00941; CARBOXYLESTERASE\_B-2; 1.  
DR PFAM; PF00155; Coesterase; 1.  
DR PRINTS; PRO0878; CHOLNESTRASE; 1.  
SQ SEQUENCE 611 AA; 67298 MW; 172DEB16 CRC32;

Query Match 100.0%; Score 87; DB 6; Length 611;  
Best Local Similarity 100.0%; Pred. No. 4.2-e-0;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
SEQUENCE 611 AA; 67298 MW; 172DEB16 CRC32;

QY 1 AEFHRWSSYYMVHK 14  
Db 583 AEFHRWSSYYMVHK 596

RESULT 2  
042275 PRELIMINARY;  
ID 042275 PRT; 633 AA.  
AC 042275;  
DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
DE ACETYLCHOLINESTERASE CATALYTIC SUBUNIT PRECURSOR (EC 3.1.1.7).

OS Electrophorus electricus (Electric eel). Vertebrata; Craniata; Vertebrata; Actinopterygii;  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;  
 OC Neopterygii; Teleostei; Buteleostii; Ostarlophysi; Gymnotiformes;  
 OC Gymnotoidei; Electrophoridae; Electrophorus.

[1]

RN

SEQUENCE FROM N.A.

RA

SIMON S., MASSOLIE J.

J. Biol. Chem. 0:0-0(1997);

DR EMBL; AF03422; AAB6605.1;

DR HSSP; P04058; IACL.

DR PROSITE; PS00122; CARBOXYLESTERASE\_B\_1;

DR PROSITE; PS00941; CARBOXYLESTERASE\_B\_2;

DR PFAM; PF00135; Coesterase\_2;

DR PRINTS; PR00878; CHOLNESTRASE.

KW SIGNAL; Hydrolase.

FT SIGNAL 1 23 POTENTIAL.

FT CHAIN 24 633 AA; 71814 MW; 6D50AB05 CRC32;

SQ

RESULT 3

Q9W6Y8

PRELIMINARY;

PRT; 95 AA.

AC Q9W6Y8;

DT 01-NOV-1999 (TREMBLrel. 12, Created)

DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)

Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFRHWSYYMHWK 14

Db 605 AEFRHWSYYMHWK 618

RESULT 4

O13748

PRELIMINARY;

PRT; 95 AA.

AC O13748;

DT 01-AUG-1998 (TREMBLrel. 07, Created)

DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)

Matches 12; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy 2 AEFRHWSYYMHWK 14

Db 68 EFHRWSSYYMHWK 80

RESULT 5

Q9W6Y8

PRELIMINARY;

PRT; 602 AA.

AC Q9W6Y8;

DT 01-AUG-1998 (TREMBLrel. 07, Created)

DT 01-NOV-1999 (TREMBLrel. 07, Last sequence update)

Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 EFHRWSSYYMHWK 14

Db 68 EFHRWSSYYMHWK 80

RESULT 6

Q9W6Y8

PRELIMINARY;

PRT; 602 AA.

AC Q9W6Y8;

DT 01-AUG-1998 (TREMBLrel. 07, Created)

DT 01-NOV-1999 (TREMBLrel. 07, Last sequence update)

Matches 8; Conservative 4; Mismatches 4; Indels 2; Gaps 0;

Qy 1 AEFRHWSYYMHWK 14

Db 573 AGFYRNNNNMDWK 586

RESULT 7

Q9W6Y8

PRELIMINARY;

PRT; 602 AA.

AC Q9W6Y8;

DT 01-AUG-1998 (TREMBLrel. 07, Created)

DT 01-NOV-1999 (TREMBLrel. 07, Last sequence update)

Matches 12; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy 1 AEFRHWSYYMHWK 14

Db 573 AGFYRNNNNMDWK 586

RESULT 8

Q9W6Y8

PRELIMINARY;

PRT; 602 AA.

AC Q9W6Y8;

DT 01-AUG-1998 (TREMBLrel. 07, Created)

DT 01-NOV-1999 (TREMBLrel. 07, Last sequence update)

Matches 12; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy 1 AEFRHWSYYMHWK 14

Db 573 AGFYRNNNNMDWK 586

RESULT 9

Q9W6Y8

PRELIMINARY;

PRT; 602 AA.

AC Q9W6Y8;

DT 01-AUG-1998 (TREMBLrel. 07, Created)

DT 01-NOV-1999 (TREMBLrel. 07, Last sequence update)

Matches 12; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy 1 AEFRHWSYYMHWK 14

Db 573 AGFYRNNNNMDWK 586

RESULT 10

Q9W6Y8

PRELIMINARY;

PRT; 602 AA.

AC Q9W6Y8;

DT 01-AUG-1998 (TREMBLrel. 07, Created)

DT 01-NOV-1999 (TREMBLrel. 07, Last sequence update)

Matches 12; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy 1 AEFRHWSYYMHWK 14

Db 573 AGFYRNNNNMDWK 586

RESULT 11

Q9W6Y8

PRELIMINARY;

PRT; 602 AA.

AC Q9W6Y8;

DT 01-AUG-1998 (TREMBLrel. 07, Created)

DT 01-NOV-1999 (TREMBLrel. 07, Last sequence update)

Matches 12; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy 1 AEFRHWSYYMHWK 14

Db 573 AGFYRNNNNMDWK 586

RESULT 12

Q9W6Y8

PRELIMINARY;

PRT; 602 AA.

AC Q9W6Y8;

DT 01-AUG-1998 (TREMBLrel. 07, Created)

DT 01-NOV-1999 (TREMBLrel. 07, Last sequence update)

Matches 12; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy 1 AEFRHWSYYMHWK 14

Db 573 AGFYRNNNNMDWK 586

RESULT 13

Q9W6Y8

PRELIMINARY;

PRT; 602 AA.

AC Q9W6Y8;

DT 01-AUG-1998 (TREMBLrel. 07, Created)

DT 01-NOV-1999 (TREMBLrel. 07, Last sequence update)

Matches 12; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy 1 AEFRHWSYYMHWK 14

Db 573 AGFYRNNNNMDWK 586

RESULT 14

Q9W6Y8

PRELIMINARY;

PRT; 602 AA.

AC Q9W6Y8;

DT 01-AUG-1998 (TREMBLrel. 07, Created)

DT 01-NOV-1999 (TREMBLrel. 07, Last sequence update)

Matches 12; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy 1 AEFRHWSYYMHWK 14

Db 573 AGFYRNNNNMDWK 586

RESULT 15

Q9W6Y8

PRELIMINARY;

PRT; 602 AA.

AC Q9W6Y8;

DT 01-AUG-1998 (TREMBLrel. 07, Created)

DT 01-NOV-1999 (TREMBLrel. 07, Last sequence update)

Matches 12; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy 1 AEFRHWSYYMHWK 14

Db 573 AGFYRNNNNMDWK 586

RESULT 16

Q9W6Y8

PRELIMINARY;

PRT; 602 AA.

AC Q9W6Y8;

DT 01-AUG-1998 (TREMBLrel. 07, Created)

DT 01-NOV-1999 (TREMBLrel. 07, Last sequence update)

Matches 12; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy 1 AEFRHWSYYMHWK 14

Db 573 AGFYRNNNNMDWK 586

RESULT 17

Q9W6Y8

PRELIMINARY;

PRT; 602 AA.

AC Q9W6Y8;

DT 01-AUG-1998 (TREMBLrel. 07, Created)

DT 01-NOV-1999 (TREMBLrel. 07, Last sequence update)

Matches 12; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy 1 AEFRHWSYYMHWK 14

Db 573 AGFYRNNNNMDWK 586

RESULT 18

Q9W6Y8

PRELIMINARY;

PRT; 602 AA.

AC Q9W6Y8;

DT 01-AUG-1998 (TREMBLrel. 07, Created)

DT 01-NOV-1999 (TREMBLrel. 07, Last sequence update)

Matches 12; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy 1 AEFRHWSYYMHWK 14

Db 573 AGFYRNNNNMDWK 586

RESULT 19

Q9W6Y8

PRELIMINARY;

PRT; 602 AA.

AC Q9W6Y8;

DT 01-AUG-1998 (TREMBLrel. 07, Created)

DT 01-NOV-1999 (TREMBLrel. 07, Last sequence update)

Matches 12; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy 1 AEFRHWSYYMHWK 14

Db 573 AGFYRNNNNMDWK 586

RESULT 20

Q9W6Y8

PRELIMINARY;

PRT; 602 AA.

AC Q9W6Y8;

DT 01-AUG-1998 (TREMBLrel. 07, Created)

DT 01-NOV-1999 (TREMBLrel. 07, Last sequence update)

Matches 12; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy 1 AEFRHWSYYMHWK 14

Db 573 AGFYRNNNNMDWK 586

RESULT 21

Q9W6Y8

PRELIMINARY;

PRT; 602 AA.

AC Q9W6Y8;

DT 01-AUG-1998 (TREMBLrel. 07, Created)

DT 01-NOV-1999 (TREMBLrel. 07, Last sequence update)

Matches 12; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy 1 AEFRHWSYYMHWK 14

Db 573 AGFYRNNNNMDWK 586

RESULT 22

Q9W6Y8

PRELIMINARY;

PRT; 602 AA.

AC Q9W6Y8;

DT 01-AUG-1998 (TREMBLrel. 07, Created)

DT 01-NOV-1999 (TREMBLrel. 07, Last sequence update)

Matches 12; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy 1 AEFRHWSYYMHWK 14

Db 573 AGFYRNNNNMDWK 586

RESULT 23

Q9W6Y8

PRELIMINARY;

PRT; 602 AA.

AC Q9W6Y8;

DT 01-AUG-1998 (TREMBLrel. 07, Created)

DT 01-NOV-1999 (TREMBLrel. 07, Last sequence update)

Matches 12; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy 1 AEFRHWSYYMHWK 14

Db 573 AGFYRNNNNMDWK 586

RESULT 24

Q9W6Y8

PRELIMINARY;

PRT; 602 AA.

AC Q9W6Y8;

DT 01-AUG-1998 (TREMBLrel. 07, Created)

DT 01-NOV-1999 (TREMBLrel. 07, Last sequence update)

Matches 12; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy 1 AEFRHWSYYMHWK 14

Db 573 AGFYRNNNNMDWK 586

RESULT 25

Q9W6Y8

PRELIMINARY;

PRT; 602 AA.

AC Q9W6Y8;

DT 01-AUG-1998 (TREMBLrel. 07, Created)

DT 01-NOV-1999 (TREMBLrel. 07, Last sequence update)

Matches 12; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy 1 AEFRHWSYYMHWK 14

Db 573 AGFYRNNNNMDWK 586

RESULT 26

Q9W6Y8

PRELIMINARY;

PRT; 602 AA.

AC Q9W6Y8;

DT 01-AUG-1998 (TREMBLrel. 07, Created)

DT 01-NOV-1999 (TREMBLrel. 07, Last sequence update)

Matches 12; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy 1 AEFRHWSYYMHWK 14

Db 573 AGFYRNNNNMDWK 586

RESULT 27

Q9W6Y8

PRELIMINARY;

PRT; 602 AA.

AC Q9W6Y8;

|                       |  |  |   |
|-----------------------|--|--|---|
| DR                    | EMBL; AF053484; AAC06262.1; -.   | RC   | TISSUE=CERVICAL CARCINOMA;  |
| DR                    | HSSP; P21836; 1MAH.  | RX   | MEDLINE: 98044228.  |
| DR                    | PROSITE; PS00122; CARBOXYESTERASE_B-1; 1.  | RA   | PESTONJAMASP K.N.; POPE R.K.; WULFKUHLE J.D.; LUNA E.J.;          |
| DR                    | PROSITE; PS00041; CARBOXYESTERASE_B-2; 1.  | RT   | "Supervillin (P205); A novel membrane-associated, F-actin-binding |
| DR                    | PRINTS; PF00135; Coesterase; 1.  | RT   | protein in the villin/gelsolin superfamily.";                     |
| DR                    | PRINTS; PRO0078; CHOLNESTERASE.  | RL   | J. Cell Biol. 139:1255-1269(1997).                                |
| KW                    | Signal 1.  | RN   | [2]   |
| FT                    | POTENTIAL.   | RP   | SEQUENCE FROM N.A.  |
| CHAIN                 | 1 28   | RC   | TISSUE=CERVICAL CARCINOMA;  |
| SEQNCE                | 29 602 AA; 68290 MW; B019C09B CRC32;   | RA   | POPE R.K.; SMITH K.P.; PESTONJAMASP K.N.; WULFKUHLE J.D.,         |
| SQ                    |  | LAURENCE J.B.; LUNA E.J.;                        |   |
| Query Match           | 64.4%; Score 56; DB 6; Length 602;   | RL   | Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.           |
| Best Local Similarity | 57.1%; Pred. No. 0.29;   | DR   | EMBL; AF051850; AAC64695.1; -.                                    |
| Matches               | 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;                                     | DR   | HSSP; P02640; 1VII.   |
| Qy                    | 1 AEPHRWSSYMHWK 14   | DR   | PFAM; PF000626; Gelsolin; 1.                                      |
| Db                    | 573 AGFYRWNYYMMDWK 586   | SQ   | SEQUENCE 1788 AA; 200792 MW; 25862FCB CRC32;                      |
| RESULT                | 7  | Query Match                                      | 48.3%; Score 42; DB 4; Length 1788;                               |
| ID                    | 078318 PRELIMINARY; PRT; 260 AA.   | Best Local Similarity                            | 46.2%; Pred. No. 1.4e+02;   |
| AC                    | 078318; 01-NOV-1998 (TREMBLrel. 08, Created)   | Matches  | 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;                |
| DT                    | 01-NOV-1998 (TREMBLrel. 12, Last annotation update)                                    | Qy   | 2 EFHRWSSYMHWK 14   |
| DE                    | NADH DEHYDROGENASE SUBUNIT F (FRAGMENT).   | Db   | 1348 QFHEDGDAYVVKWK 1360  |
| GN                    | Arabidopsis thaliana (Mouse-ear cress).  | RESULT   | 9   |
| OS                    | Chloroplast.   | ID   | 060612 PRELIMINARY; PRT; 1788 AA.                                 |
| OC                    | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;                     | AC   | 060612; 1998 (TREMBLrel. 07, Created)                             |
| OC                    | euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;                          | DT   | 01-AUG-1998 (TREMBLrel. 07, Last sequence update)                 |
| OC                    | core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;                        | DE   | SUPERVILLIN.  |
| OC                    | Arabidopsis.   | OS   | Homo sapiens (Human).   |
| RN                    | [1]  | OC   | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;     |
| RP                    | SEQUENCE FROM N.A.   | Eutheria; Primates; Catarrhini; Hominidae; Homo. |   |
| RA                    | GALLOWAY G.L., MALMBERG R.L., PRICE R.A.;  | RN   | [1]   |
| RT                    | "Phylogenetic utility of the nuclear gene arginine decarboxylase within Brassicaceae". | RP   | SEQUENCE FROM N.A.  |
| RL                    | Mol. Biol. Evol. 0:0-(1998).   | RC   | TISSUE-KIDNEY;  |
| RL                    | ENBM: AF064554; AAC68593.1; -.   | RX   | MEDLINE; 98044228.  |
| DR                    | MENDEL; 30386; Arath; ndhf30386.   | RA   | PESTONJAMASP K.N.; POPE R.K.; WULFKUHLE J.D.; LUNA E.J.;          |
| DR                    | PFAM; PF01010; oxidored_q1_C; 1.   | RT   | "Supervillin (P205); A novel membrane-associated, F-actin-binding |
| KW                    | Chloroplast.   | RT   | protein in the villin/gelsolin superfamily.";                     |
| ET                    | NON_TER 1 1  | RL   | J. Cell Biol. 139:1255-1269(1997).                                |
| ET                    | NON_TER 260 260  | RN   | [2]   |
| SEQUENCE              | 260 AA; 30565 MW; 916B2FFC CRC32;  | RP   | SEQUENCE FROM N.A.  |
| Qy                    | 3 PHRWSSYMHWK 14   | RC   | TISSUE-KIDNEY;  |
| Db                    | 192 FQKWNKRRIHVE 203   | RA   | POPE R.K.; SMITH K.P.; PESTONJAMASP K.N.; WULFKUHLE J.D.,         |
| RESULT                | 8  | RA   | LAWRENCE J.B.; LUNA E.J.;   |
| 060611                | ID 060611 PRELIMINARY; PRT; 1788 AA.   | RL   | Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.           |
| ID                    | 060611; 01-AUG-1998 (TREMBLrel. 07, Created)   | DR   | EMBL; AF051851; AAC64696.1; -.                                    |
| AC                    | 060611; 01-AUG-1998 (TREMBLrel. 07, Last sequence update)                              | DR   | HSSP; P02640; 1VII.   |
| DT                    | 01-NOV-1999 (TREMBLrel. 12, Last annotation update)                                    | DR   | PFAM; PF00626; Gelsolin; 1.                                       |
| DE                    | SUPERVILLIN.   | SQ   | SEQUENCE 1788 AA; 200820 MW; DEBAE76B CRC32;                      |
| OS                    | Homo sapiens (Human).  | RESULT   | 10  |
| OC                    | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;                          | ID   | 046385 PRELIMINARY; PRT; 1792 AA.                                 |
| OC                    | Eutheria; Primates; Catarrhini; Hominidae; Homo.                                       | AC   | 046385;   |
| RN                    | [1]  | DT   | 01-JUN-1998 (TREMBLrel. 06, Created)                              |
| RP                    | SEQUENCE FROM N.A.   | DT   | 01-JUN-1998 (TREMBLrel. 06, Last sequence update)                 |

DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
DE SUPERVILLIN.  
OS Bos taurus (Bovine).  
OC Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovinae; Bos.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 98044228.  
RA PESTONJAMASP K.N., POPE R.K., WULFKUHLE J.D., LUNA E.J.;  
RT "Supervillin (P205): A novel membrane associated, F-actin-binding  
protein in the villin/gelsolin superfamily.";  
RL J. Cell. Biol. 139:1255-1269(1997).  
DR EMBL: AF025996; AAC48783.1; -.  
DR HSSP: P02640; IIVI.  
DR PFAM: PF00626; Gelsolin; 1.  
SQ SEQUENCE 1792 AA; 200625 MW; 29AEEB3CE CRC32;

Query Match 48 3%; Score 42; DB 6; Length 1792;  
Best Local Similarity 46.2%; Pred. No. 1.4e+02; Indels 0; Gaps 0;  
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 EFHRWSSYAVHWK 14  
Db 1352 QFHEGDAYVVKW 1364

RESULT 11  
ID 095425 PRELIMINARY; PRT; 2214 AA.  
AC 095425; PRELIMINARY;  
DT 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
DB ARCHYLLIN.  
GN SVIL.  
OS Homo sapiens (Human).  
OC Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Primates; Catarrhini; Homindae; Homo.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 99058997.  
RA POPE R.K., PESTONJAMASP K.N., SMITH K.P., WULFKUHLE J.D.,  
RA STRASSEL C.P., LAWRENCE J.B., LUNA E.J.,  
RT "Cloning, characterization, and chromosomal localization of human  
superillin (SVIL)".  
RL Genomics 52:342-351(1998).  
DR EMBL: AF109135; ADI4682.1; -.  
DR HSSP: P02640; IIVI.  
SQ SEQUENCE 2214 AA; 247704 MW; 0204DCB9 CRC32;

Query Match 48 3%; Score 42; DB 4; Length 2214;  
Best Local Similarity 46.2%; Pred. No. 1.7e+02; Indels 0; Gaps 0;  
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 EFHRWSSYAVHWK 14  
Db 1774 QFHEGDAYVVKW 1786

RESULT 12  
ID Q62255 PRELIMINARY; PRT; 1323 AA.  
AC Q62255; PRELIMINARY;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-NOV-1998 (TREMBLrel. 12, Last annotation update)  
DE SPALT HOMOLOGUE (SPALT PROTEIN) (FRAGMENT).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Mus musculus. SPALT OR MSAL.

OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 96391179.  
RA OTT T., KAESNER K.H., MONAGHAN A.P., SCHUTZ G.;  
RT "The mouse homolog of the region specific homeotic gene spalt of  
Drosophila is expressed in the developing nervous system and in  
mesoderm-derived structures.";  
RT Mech. Dev. 56:117-128(1996).  
RL EMBL; X97581; CAA66196.1; -.  
DR HSSP; P07248; IARE.  
MGI; MGI-109295; Spalt.  
DR PROSITE; PS00028; ZINC\_FINGER\_C2H2; 9.  
PFAM; PF00096; zf-C2H2; 10.  
KW Zinc finger; Metal-binding; DNA-binding.  
FT NON-TER 1 Zinc finger; Metal-binding; DNA-binding.  
SQ SEQUENCE 1323 AA; 139070 MW; DAD82AAD CRC32;

Query Match 47.1%; Score 41; DB 11; Length 1323;  
Best Local Similarity 42.9%; Pred. No. 1.4e+02; Indels 0; Gaps 0;

Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AEFFRKWSSYAVHWK 14  
Db 29 AEFFRKWADFLQHKK 42

RESULT 13  
ID Q9XGN9 PRELIMINARY; PRT; 1687 AA.  
AC Q9XGN9; PRELIMINARY;  
DT 01-NOV-1999 (TREMBLrel. 12, Created)  
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
DE SIMILAR TO SEC7 PROTEIN.  
OS Oryza sativa (Rice).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;  
OC Poaceae; Oryza.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAN=CV\_NIPPONBARE;  
RA SASAKI T., MATSUMOTO T., YAMAMOTO K.;  
RT "Oryza sativa Nipponbare (GA3) genomic DNA, chromosome 2, PAC  
clone P0431H03 (contig b)";  
RT clone P0431H03 (contig b);  
RT Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AP000367; BAA82387.1; -.  
SQ SEQUENCE 1687 AA; 18179 MW; 6E0EDFF9 CRC32;

Query Match 47.1%; Score 41; DB 10; Length 1687;  
Best Local Similarity 63.6%; Pred. No. 1.8e+02; Indels 0; Gaps 0;

Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 EFHRWSSYAVHW 12  
Db 1492 ETHRNSFYAER 1502

RESULT 14  
ID Q52970 PRELIMINARY; PRT; 285 AA.  
AC Q52970; PRELIMINARY;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
DE NODULATION GENES NODA, NODB AND NOC.  
OS Rhizobium meliloti.  
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
OC Rhizobiaceae; Sinorhizobium.  
RN [1]  
RP SEQUENCE FROM N.A.

RX MEDLINE; 85087953.  
 RA TOEROEK I., KONDOROSI E., STEPCKOWSKI T., POSPAI J., KONDOROSI A.;  
 RT "Nucleotide sequence of Rhizobium meliloti nodule genes.",  
 RL Nucleic Acids Res. 12:9509-9524 (1984).  
 EMBL X01649; CAAJ5807.1;  
 DR SEQUENCE 285 AA; 32342 MW; 157B9F20 CRC32;

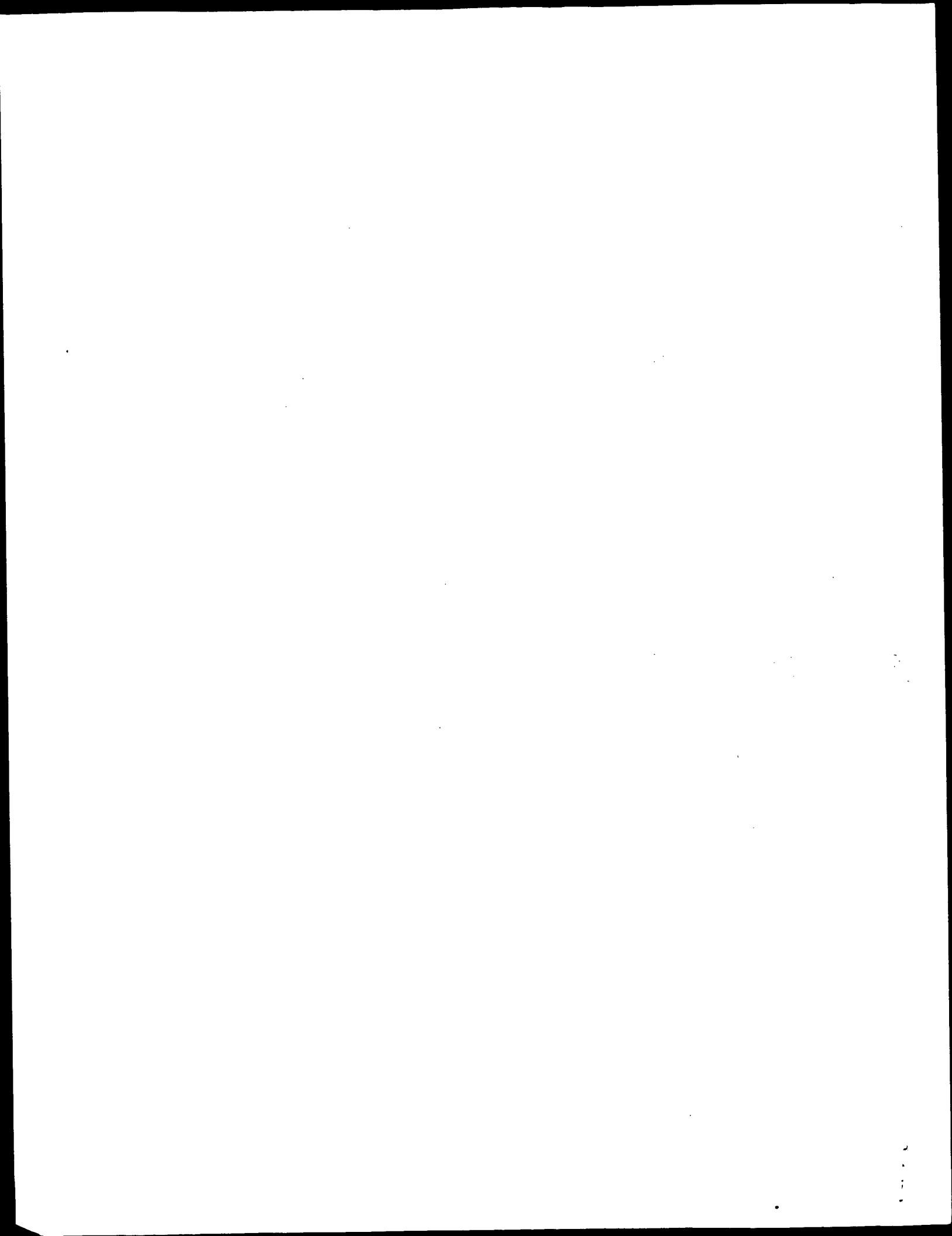
Query Match 46.6%; Score 40.5; DB 2; Length 285;  
 Best Local Similarity 56.2%; Pred. No. 36;  
 Matches 9; Conservative 0; Mismatches 4; Indels 3; Gaps 1;  
 QY 2 EPHRWSYM--VHVK 14  
 Db 82 ETHWSSYMSLVKWK 97

RESULT 15  
 078332 PRELIMINARY; PRT; 508 AA.  
 ID 078332  
 AC 078332;  
 DT 01-NOV-1998 (TRIMBLRE1. 08. Created)  
 DT 01-MAY-1999 (TRIMBLRE1. 10. Last sequence update)  
 DT 01-NOV-1999 (TRIMBLRE1. 12. Last annotation update)  
 DE MURASE (FRAGMENT).  
 GN YCF14 OR MATK.  
 OS Perigularia daemita.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 eukaryophytes; Spermatophyta; Magnoliophyta; eudicotyledons;  
 core eudicots; Asteridae; euasterids I; Gentianales; Asclepiadaceae;  
 OC Perigularia.  
 RN [1]

SEQUENCE FROM N. A.

RX MEDLINE; 98334575.  
 RA CIVEYREL L., LE THOMAS A., FERGUSON K., CHASE M.W.;  
 RT "Critical reexamination of palynological characters used to delimit  
 Asclepiadaceae in comparison to the molecular phylogeny obtained from  
 plastid matK sequences.",  
 RL Phylogenet. Evol. 9:517-527 (1998).  
 DR EMBL Z98191; CAB10879.2;  
 MENDEL 30397; Perdys; ycf14; 30397.  
 DR PFAM; PF01348; Intron\_maturas2; 1.  
 KW Chloroplast.  
 FT NON-TER 1  
 SQ SEQUENCE 508 AA; 60145 MW; EC02C198 CRC32;

Query Match 46.6%; Score 40.5; DB 8; Length 508;  
 Best Local Similarity 50.0%; Pred. No. 65;  
 Matches 6; Conservative 4; Mismatches 1; Indels 1; Gaps 1;  
 QY 4 HRWSSYMHVK 14  
 Db 299 NKWKSYLVHEWQ 310



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OM of: US-09-155-076-1 to: EST:*    out_format : pfs
Date: Sep 13, 2000 2:42 AM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Inc.

Command line parameters:
-MODEL:frame=p2n,model -DEV=x1P
-0=cgn2_1/USPTO_spool/US091155076/runat_29082000_092504_15735/app_qr
-DB=EST -QFMT=fastpack -SUFFIX=rst -GAPEXT=4.000
-MINMAX=0.100 -LOOP0=0.000 -LOOP1=0.000 -LOOP2=0.000 -GAPPOP=4.500
-QGAPEXT=0.050 -YGAPOP=10.000 -XGAPEXT=0.500 -PGAPOP=6.000
-QGAPEXT=7.000 -YGAPEXT=10.000 -YGAPEXT=0.500 -DELOR=6.000
-DELEXIT=7.000 -START=1 -MATRIXBLOCK=662 -TRANS=human40 cdi
-LIST=45 -DOCALIGN=200 -THER SCORE=pot -THER MAX=100 -THR MIN=0
-ALIGN15 -MODE=LOCAL -OUTFILE=pfs -NORMext -MINLEN=0
-MA maxlen=1000000 -USER=US091155076 -CCNN1.1-1327 -ICPU=6 -ICPU=3

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Align seg 1/1 to: N90761 from: 1 to: 248

1 AlaGluPheHisArgGTPSerSerTyrMetValIstrPlys 14  
1 ||||| ||||| ||||| ||||| ||||| |||||  
11 GCGAGTTCCACGGCTTACAGTGCACTGAG 52

seq\_name: gb\_est52:T28280

seq\_documentation\_block:  
 LOCUS T28280 254 bp mRNA 06-SEP-1995  
 DEFINITION ESTN35080 Human Embryo Homo sapiens cDNA 5' end similar to acetylcholinesterase (HT:518), mRNA sequence.

VERSION T28280.1 GI:610378

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE Adams, M.D., Kerlavage, A.R., Fleischman, R.D., Fulder, R.A., Bult, C.J., Lee, N., Kirchner, F.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chin, M.-W., Clayton, R.A., Cline, R.T., Cotton, M.D., Earle, J., Fritchman, J.L., Geoghegan, N.S.M., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkley Jr., P.S., Kelley, J.M., Klimek, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palancas, R.F., McDonald, L.A., Nguyen, D.T., Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.-J., Dimle, D., Feng, P., Ferrie, A., Fischer, J., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M., Gruber, J., Hudson, P., Kim, A., Korak, D.L., Kunsch, C., Ji, J.H., Li, H., Meissner, P. S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C., Yu, G.-L., Ruben, S.M., Dillon, P.J., Pannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.  
 TITLE Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 83 Million Basepairs of cDNA Sequence Nature 377, 3-174 (1995)  
 JOURNAL MEDLINE On May 10, 1995 this sequence version replaced gi:805490.  
 COMMENT Other ESTs: THC20766 Contact: Venter, JC  
 The Institute for Genomic Research  
 932 Clapper Rd, Gaithersburg, MD 20878  
 Tel: 301859056  
 Fax: 3018599423  
 Email: tdbinfo@tigr.org

Information related to this EST, please contact the TIGR Database (tdbinfo@tigr.org) Insert Length: 1145 Std Error: 0.00 Seq Primer: M13 Reverse High quality sequence stop: 187.

FEATURES source

Organism: "Homo sapiens"  
 /db\_xref="AFC (Inhost):101797  
 /db\_xref="Saxon:9606"  
 /clone\_id="Human Embryo"

/tissue\_type="embryo".

BASE COUNT 45 a 89 c 78 g 41 t 1 others

ORIGIN

alignment\_scores: Quality: 87.00 Length: 14  
 Ratio: 6.214 Gaps: 0 Percent Identity: 100.000  
 Percent Similarity: 100.000 alignment\_block: US-09-155-076-1 x T28280 ..

Align seg 1/1 to: T28280 from: 1 to: 254

1 AlaGluPheHisArgGTPSerSerTyrMetValIstrPlys 14  
1 ||||| ||||| ||||| ||||| ||||| |||||  
138 GCCGAGTTCCACGGCTTACAGTGCACTGAG 179

seq\_name: gb\_est25:MI764103

seq\_documentation\_block:  
 LOCUS AR64103 362 bp mRNA 25-JUN-1999  
 DEFINITION UI-R-YO-acy-h-04-0-UI-S1 UI-R-YO Rattus norvegicus CDNA clone  
 ACCESSION AI64103  
 VERSION AI64103  
 KEYWORDS EST.  
 SOURCE Norway rat.

ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Murinae;

Rattus (bases 1 to 362)

REFERENCE 1 (bases 1 to 362)  
 AUTHORS Bonaldo, M.F., Lennon, G., and Soares, M.B.  
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery  
 JOURNAL Genom. Res. 6 (9), 791-806 (1996)

COMMENT MEDLINE  
 Contact: Soares, MB  
 Program for Rat Gene Discovery and Mapping  
 University of Iowa  
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA  
 Tel: 319 335 9550  
 Fax: 319 335 9565

Email: msoares@blue.weeg.uiowa.edu  
 The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bona fide poly A tail. The sequence tag present in the cDNA between the Not I site and the oligo-dT track served to verify it as a clone from the normalized Eye library cDNA Library Preparation. M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com). The following repetitive elements were found in this cDNA sequence: 1-30, >Poly\_A#Simple\_repeat Seq primer: M13 Forward POLYA:Yes.

FEATURES source

Organism: "Rattus norvegicus"  
 /strain="Sprague-Dawley"  
 /db\_xref="Taxon:10116"  
 /clone="UI-R-YO-acy-h-04-0-UI"  
 /clone.lib="UI-R-YO"  
 /dev\_stage="adult"  
 /lab\_host="DH10B (Life Technologies)"  
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; site\_1: Not I; site\_2: Eco RI; The UI-R-YO library is a subtracted library derived from an individually-tagged normalized whole-eye (minus the lens) library. The driver for the subtraction consisted of a pool of all previous libraries (UI-R-AL, UI-R-EL, UI-R-E0, UI-R-EL1, UI-R-C0, and UI-R-CL). The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-YO) was constructed as follows: PCR amplified cDNA inserts from previous library clones from which 3' EMS had been derived were used as a driver in a hybridization with the normalized whole-eye library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography converted to double-stranded circles and incorporated into DH10B bacteria (Life Technologies) to generate the UI-R-YO

library. This procedure has been previously described (Bonaldi, Lennon and Soares, Genome Research 6: 791-806 1996; TAG\_LIBUI-R-Y0; TAG\_TISSUE=Eye; TAG\_SEQ=CATG" 71 a 87 c 116 g 88 t

**BASE COUNT**

**ORIGIN**

**alignment\_scores:**

|                     |         |                   |         |
|---------------------|---------|-------------------|---------|
| Quality:            | 87.00   | Length:           | 14      |
| Ratio:              | 6.214   | Gaps:             | 0       |
| Percent Similarity: | 100.000 | Percent Identity: | 100.000 |

**alignment\_block:**  
US-09 155-076-1 x AI764103/rev ..

**Align seg 1/1 to reverse of: AI764103 from: 1 to: 362**

1 AlaGlutheHisArgTrpSerTyrMetValHistDlys 14  
 ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 340 GCGGAGTTCACCGCTGAGCTTACATGGTCACTGGAG 299

**seq\_name: qb\_est48:f27586**

**seq\_documentation\_block:**

|                     |   |        |              |                                   |
|---------------------|---|--------|--------------|-----------------------------------|
| LOCUS               | F27586  | 378 bp | mRNA         | EST                               |
| DEFINITION          | HSPD15598   | HM3    | Homo sapiens | clone s4000002G06, mRNA sequence. |
| ACCESION            | F27586  |        |              |                                   |
| VERSION             | F27586.1  |        |              |                                   |
| KEYWORDS            | EST.  |        |              |                                   |
| SOURCE              | human.  |        |              |                                   |
| ORGANISM            | Homo sapiens  |        |              |                                   |
| REFERENCE           | Eukaryota; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.   |        |              |                                   |
| AUTHORS             | 1 (bases 1 to 378)  |        |              |                                   |
| TITLE               | Lanfranchi,G., Muraro,T., Caldara,F., Pacchioni,B., Pallavicini,A., Pandolfi,D., Toppo,S., Trevisan,S., Scarso,S. and Valle,G.  |        |              |                                   |
| JOURNAL             | Identification of 4370 expressed sequence tags from a 3'-end-specific cDNA library of human skeletal muscle by DNA sequencing and filter hybridization  |        |              |                                   |
| MEDLINE             | 96276048  |        |              |                                   |
| COMMENT             | On Jul 7, 1999 this sequence version replaced gi:5410190.   |        |              |                                   |
| LOCATION/QUALIFIERS | Contact: Valle G.   |        |              |                                   |
| FEATURES            | Source  |        |              |                                   |
| Source              | /organism="Homo sapiens"<br>/note="vector: PCDNAII (Invitrogen; Site_1: BstXI;<br>Site_2: NotI; The library was constructed by G.<br>Lanfranchi. This library is not subtracted nor normalized.<br>The first strand cDNA was primed with a biotinylated<br>oligo-dT-NotI primer<br>(5'-biotin AACCAGGCCTGAGGGCCGCTTTTTTTTTTTTTT-3'). The<br>ds cDNA was sonicated and size-selected in the range<br>350-550 bp. The 3' specific fragments were selected by<br>streptavidin coated magnetic beads, ligated to non-palindromic BstXI adaptors, NotI digested and<br>directionally cloned into BstXI-NotI cut PCDNAII vector." 65 a 147 c 102 g 64 t |        |              |                                   |
| BASE COUNT          |   |        |              |                                   |
| ORIGIN              |   |        |              |                                   |

```

Align seg 1/1 to: AA933814 from: 1 to: 380
  1 AlaGluPheHisArgTrpSerSerTyrMetValHistDlys 14
    ||||| | | | | | | | | | | | | | | | | | | | |
    115 GCGGAGTTCCACCGCTTCACTGGACTCATCTGGACTGGAG 156

seq_name: gb-sest44 AW612795
seq_documentation.block:
LOCUS      AW612795      384 bp      mRNA      EST      23-MAR-2000
DEFINITION hni3a07_x1 NCI_CGAP_LU24 Homo sapiens CDNA clone IMAGE:2956884 3'
SIMILARITY similar to contains PTRS.t3 PTRS5 repetitive element ; mRNA
sequence.
ACCESSION AW612795
VERSION    AW612795.1
KEYWORDS   EST
SOURCE     Homo sapiens
ORGANISM  Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 384)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert.Strausberg, Ph.D.
          Tel: (301) 496-1550
          Email: Robert.Strausberg@nih.gov
          Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
          Emmert-Buck, M.D., Ph.D.
          cDNA Library Preparation: M. Bento Soares, Ph.D.
          cDNA Library Arrayed by: Greg Lennon, Ph.D.
          DNA Sequencing by: Washington University Genome Sequencing Center
          Clone distribution: NCI-CGAP Clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          image.llnl.gov/image/html/resources.shtml

Possible reversed clone: polyT not found
Seq primer: -40UP from Gibco.
  1. .384
  Location/Qualifiers
    1. .384
      source
        /organism="Homo sapiens"
        /db_xref="Taxon:9606"
        /clone="IMAGE:2956884"
        /clone.lib="NCI CGAP Lu24"
        /tissue.type="carcinoïd"
        /lab.host="DH10B"
        /note="Organ: lung; Vector: pTTT3D-Pac (Pharmacia) with a
modified polylinker; Plasmid DNA from the normalized
library NCI_CGAP_Lu5 was prepared, and ss circles were
made in vitro. Following HAP purification, this DNA was
used as tracer in a subtractive hybridization reaction.
The driver was PCR-amplified cDNAs from a pool of 5,000
clones made from the same library (clones IDs
1414920-1417991 and 1520904-1522439). Subtraction by Bento
Soares and M. Fatima Bonaldo."
  BASE COUNT   66 a 154 c 96 g 68 t
  ORIGIN

alignment_scores:
  Quality: 87.00
  Ratio: 6.214
  Percent Similarity: 100.0000
  alignment_block:
    US-09-155-076-1 x AW612795 ..
  Align seg 1/1 to: AW612795 from: 1 to: 384
  1 AlaGluPheHisArgTrpSerSerTyrMetValHistDlys 14

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ORIGIN

alignment\_scores:

|                             |                           |
|-----------------------------|---------------------------|
| Quality: 87.00              | Length: 14                |
| Ratio: 6.214                | Gaps: 0                   |
| Percent Similarity: 100.000 | Percent Identity: 100.000 |

alignment\_block:  
US-09-155-076-1 x AA998511/rev ..

Align seg 1/1 to reverse of: AA998511 from: 1 to: 395

1 AlagliupheHisArgTrpSerSerTyrMetValHistPlys 14  
 ||||||| ||||| ||||| ||||| ||||| ||||| |||||  
 327 GCCGAGTTACCCGCTGGACTCCTACATGGCACTGGAG 286

seq\_name: qb\_est25:AI766812

seq\_documentation\_block:  
LOCUS AI84791 395 bp mRNA EST 15-JUL-1999  
 DEFINITION UI-M-AKI-aev-f-02-0-UI s1 NIH\_BMAP\_MHY\_N Mus musculus cDNA clone  
 ACCESSION AI84791  
 VERSION AI84791.1 GI:5491697

seq\_name: qb\_est26:AI847791

seq\_documentation\_block:  
LOCUS AI84791 395 bp mRNA EST 15-JUL-1999  
 DEFINITION UI-M-AKI-aev-f-02-0-UI s1 NIH\_BMAP\_MHY\_N Mus musculus cDNA clone  
 ACCESSION AI84791  
 VERSION AI84791.1 GI:5491697

ORGANISM Mus musculus

KEYWORDS house mouse.

REFERENCE 1 (bases 1 to 395)  
 AUTHORS Bonaldo, M. F., Lennon, G. and Soares, M. B.  
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 9704477

COMMENT On Apr 7, 1998 this sequence version replaced gi:3035605.

Contact: Chin, H  
 National Institute of Mental Health  
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD  
 Tel: 301 443 1706  
 Fax: 301 443 9890

Email: mEST@mail.nih.gov

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bona fide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the normalized hypothalamus library cDNA Library Preparation: M.B. Soares Lab Clone distribution: NIH\_BMAP cDNA Clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined.

Seq primer: M13 Forward

POLY-A-Yes

FEATURES

source 1. .395 Location/Qualifiers

1. .395 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2400478"  
 /clone\_id="NCI\_CGAP\_Kid12"  
 /tissue\_type="2 Pooled tumors (clear cell type)"  
 /lab\_host="DH10B"  
 /note="Organ: kidney; Vector: PT7T3D-Pac (Pharmacia) with a modified Polylinker; Site\_1: Not I; Site\_2: Eco RI;  
 Plasmid DNA from the normalized library NCI\_CGAP\_Kid5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clone IDs 1323912-125831, 141368-147903 and 1492104-1493255). Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 64 a 155 c 107 g 69 t

ORIGIN

align\_scores:

alignment\_scores: Quality: 87.00 Length: 14  
Percent Similarity: 100.000 Gaps: 0  
Alignment\_block: US-09-155-076-1 x AI847791/rev  
Align seg 1/1 to reverse of: AI847791 from: 1 to: 395  
seq\_name: gb\_est19\_AI360141

seq\_documentation\_block:  
LOCUS AI360141 410 bp mRNA EST  
DEFINITION similaar to gb:M55040 ACETYLCHOLINESTERASE PRECURSOR  
(HUMAN); contains PTR5..b2 TARI repetitive element ; mRNA sequence.  
ACCESSION AI360141  
VERSION 1  
KEYWORDS EST.  
ORGANISM Homo sapiens  
SOURCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Etheria; Primates; Catarrhini; Homidae; Homo.  
Human.

JOURNAL Unpublished (1998)  
COMMENT On Jun 22, 1998 this sequence replaced gi:3247207.  
Contact: Robert Straussberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Straussberg@nih.gov  
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,  
National Cancer Institute / National Institute of Neurological  
Disorders and Stroke, Brain Tumor Genome Anatomy Project  
(CGAP/BTGP), Tumor Gene Index  
Unpublished (1998)  
On Jun 22, 1998 this sequence replaced gi:3247207.  
Contact: Robert Straussberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Straussberg@nih.gov  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LINL at:  
[www-bio.llnl.gov/bbrp/](http://www-bio.llnl.gov/bbrp/)  
Insert Length: 440 Std Error: 0.00  
Seq Primer: -40UP from Gibco.  
Location/Qualifiers 1..410

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/db\_xref="taxon:9606"  
/clone IMAGE:2018611"  
/clone\_lib="NCI-CGAP\_Brn25"  
/tissue\_type="anaplastic oligodendroglioma"  
/lab\_host="DH10B"  
/note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a  
modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dt) primer [5'  
TGTTTACCAATCTGAATGGAGGCCATAGTTTTTTTTTTTTTTT  
T 3']; double-stranded cDNA was ligated to Eco RI  
adaptors (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of the modified pT73 vector.  
Library is normalized, and was constructed by Bento  
Soares and M. Fatima Bonaldo."  
BASE COUNT 66 a 163 c 113 g 69 t 1 others

alignment\_scores: Quality: 87.00 Length: 14  
Percent Similarity: 100.000 Gaps: 0  
Alignment\_block: US-09-155-076-1 x AI360141 ..  
Align seg 1/1 to: AI360141 from: 1 to: 410  
seq\_name: gb\_est24\_AI690171

seq\_documentation\_block:  
LOCUS AI690171 411 bp mRNA EST  
DEFINITION similar to gb:M55040 ACETYLCHOLINESTERASE PRECURSOR  
(HUMAN); contains PTR5..b2 TARI repetitive element ; mRNA sequence.  
ACCESSION AI690171.1  
VERSION 1  
KEYWORDS EST.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Etheria; Primates; Catarrhini; Homidae; Homo.  
Human.

JOURNAL Unpublished (1998)  
COMMENT On Jan 19, 1998 this sequence version replaced gi:2286587.  
Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert\_Strausberg@nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LINL at:  
[www-bio.llnl.gov/bbrp/](http://www-bio.llnl.gov/bbrp/)  
Insert Length: 458 Std Error: 0.00  
Seq Primer: -40UP from Gibco.  
Location/Qualifiers 1..411

FEATURES Source  
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/db\_xref="taxon:9606"  
/clone IMAGE:2271338"  
/clone\_lib="NCI-CGAP\_Lu24"  
/tissue\_type="carcinoïd"  
/lab\_host="DH10B"  
/note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a  
modified polylinker; Plasmid DNA from the normalized  
library NCI-CGAP Lu5 was prepared, and ss circles were  
made in vitro. Following HAP purification, this DNA was  
used as tracer in a subtractive hybridization reaction.  
The driver was PCR-amplified cDNAs from a pool of 5,000  
clones made from the same library (cloneIDs  
141920-141799 and 152090-1522439). Subtraction by Bento  
Soares and M. Fatima Bonaldo."  
BASE COUNT 66 a 162 c 113 g 70 t  
ORIGIN alignment\_scores:  
" Quality: 87.00 Length: 14  
Ratio: 6.214 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000  
alignment\_block:

US-09-155-076-1 x A1690171 ..

1 Align GlnGluPheHisArgTrpSerSerTyrMetValHistDPLys 14  
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 119 GCGGACTTCACCGCTTACATGGACTGTGAAAG 160

seq\_name: qb\_est7:AA401251

seq\_documentation\_block:

LOCUS Aw653940 496 bp mRNA taurinus CDNA 5', mRNA sequence.

DEFINITION Aw653940

ACCESSION Aw653940

VERSION Aw653940.1 GI:7419766

SOURCE EST.

ORGANISM Bos taurus

KEYWORDS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Catarrhini; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

REFERENCE Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A. and Keele, J.W.

TITLE Design and use of four pooled tissue normalized cDNA libraries for EST discovery in cattle

JOURNAL Unpublished (2000)

COMMENT Contact: Smith, T.P.L.  
 USDA, ARS, US Meat Animal Research Center  
 PO Box 166, Clay Center, NE 68933-0166, USA  
 Tel.: 402 762 4366  
 Fax: 402 762 4390  
 Email: smitht@mail.marc.usda.gov

SINGLE PASS SEQUENCING BASES CALLED AND ALT\_TRIMMED WITH PHRED v0.880904.e. VECTOR IDENTIFIED BY CROSS\_MATCH WITH THE -MINSCORE 18

PCR PRIMERS FORWARD: AGGAACAGCTTGTGACCAT  
 BACKWARD: GTTTCCAGTCAGCAGC

Plate: 112 row: B column: 5

/clone\_lib="MARC\_BOV"  
 /clone\_type="pooled"  
 /lab\_host=DH10B

Seq primer: ATTAGGTGACACTTGTAG.

FEATURES source

1..496  
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 /db\_xref="taxon:9113"  
 /clone.lib="MARC\_BOV"  
 /clone.type="pooled"  
 /lab.host=DH10B

/note="vector: PCMV\_SPORT6; Site 1: xbaI; Site 2: XbaI;  
 Library made from pooled tissue from lymph node, ovary,  
 fat, hypothalamus, and pituitary."

BASE COUNT 91 a 177 c 137 g 91 t

ORIGIN

alignment\_scores:

Quality: 87.00 Length: 14  
 Ratio: 6.214 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-155-076-1 x AW653940 ..

Align seg 1/1 to: AW653940 from: 1 to: 496

1 AlaGluPheHisArgTrpSerSerTyrMetValHistDPLys 14  
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 186 GCCGACTTCATCGCTGGACTCTACATGGCACTGGAAAG 227

seq\_name: qb\_est1:AR030863

seq\_documentation\_block:

LOCUS AA30863 501 bp mRNA

DEFINITION m145c07 r1 Soares mouse embryo NbME13.5 14.5 Mus musculus CDNA

PRCURSOR (HUMAN); SP: X56518 Mouse mRNA for acetylcholinesterase (MOUSE); mRNA sequence.

alignment\_scores:

Quality: 87.00 Length: 14  
 Ratio: 6.214 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-155-076-1 x AA401251 ..

Align seg 1/1 to: AA401251 from: 1 to: 413

1 AlaGluPheHisArgTrpSerSerTyrMetValHistDPLys 14



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 13, 2000, 02:25:26 ; Search time 14:59 Seconds  
(without alignments)  
16.811 Million cell updates/sec

Title: US-09-155-076-2  
Perfect score: 16  
Sequence: 1 DAEFRHDSGYEVHHQK 16

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 152396 seqs, 15329161 residues

Word size : 0

Total number of hits satisfying chosen parameters: 152396

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Listing first 45 summaries

Database : Issued\_Patents\_AA:  
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 2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:  
 3: /cgn2\_6/ptodata/2/iaa/6\_COMB.pep:  
 4: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:  
 5: /cgn2\_6/ptodata/2/iaa/backfile1.pep:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query | Match | Length | DB ID             | Description       |
|------------|-------|-------|-------|--------|-------------------|-------------------|
| 1          | 16    | 100.0 | 16    | 1      | US-08-322-808-10  | Sequence 10, Appl |
| 2          | 16    | 100.0 | 16    | 2      | US-08-966-948-10  | Sequence 10, Appl |
| 3          | 16    | 100.0 | 21    | 2      | US-08-659-984A-18 | Sequence 18, Appl |
| 4          | 16    | 100.0 | 21    | 1      | US-08-141-324-11  | Sequence 11, Appl |
| 5          | 16    | 100.0 | 27    | 1      | US-08-141-324-12  | Sequence 12, Appl |
| 6          | 16    | 100.0 | 27    | 1      | US-08-541-902-11  | Sequence 11, Appl |
| 7          | 16    | 100.0 | 27    | 1      | US-08-541-904-12  | Sequence 12, Appl |
| 8          | 16    | 100.0 | 28    | 1      | US-08-346-849-4   | Sequence 4, Appl  |
| 9          | 16    | 100.0 | 28    | 1      | US-08-320-888-7   | Sequence 7, Appl  |
| 10         | 16    | 100.0 | 28    | 2      | US-08-659-050-2   | Sequence 2, Appl  |
| 11         | 16    | 100.0 | 28    | 2      | US-08-986-948-7   | Sequence 7, Appl  |
| 12         | 16    | 100.0 | 28    | 2      | US-08-293-284A-4  | Sequence 4, Appl  |
| 13         | 16    | 100.0 | 28    | 2      | US-08-161-216-2   | Sequence 2, Appl  |
| 14         | 16    | 100.0 | 30    | 2      | US-08-059-050-3   | Sequence 3, Appl  |
| 15         | 16    | 100.0 | 33    | 2      | US-08-609-080-4   | Sequence 4, Appl  |
| 16         | 16    | 100.0 | 33    | 2      | US-08-559-944A-16 | Sequence 16, Appl |
| 17         | 16    | 100.0 | 35    | 1      | US-08-304-585-6   | Sequence 6, Appl  |
| 18         | 16    | 100.0 | 35    | 2      | US-08-612-585B-15 | Sequence 15, Appl |
| 19         | 16    | 100.0 | 35    | 2      | US-08-612-785B-38 | Sequence 38, Appl |
| 20         | 16    | 100.0 | 36    | 2      | US-08-059-050-6   | Sequence 6, Appl  |
| 21         | 16    | 100.0 | 38    | 1      | US-08-302-808-1   | Sequence 1, Appl  |
| 22         | 16    | 100.0 | 38    | 2      | US-07-371-371E-68 | Sequence 68, Appl |
| 23         | 16    | 100.0 | 38    | 2      | US-08-386-948-1   | Sequence 1, Appl  |
| 24         | 16    | 100.0 | 39    | 1      | US-08-302-808-2   | Sequence 2, Appl  |
| 25         | 16    | 100.0 | 39    | 2      | US-08-059-050-7   | Sequence 7, Appl  |
| 26         | 16    | 100.0 | 39    | 2      | US-08-682-245A-1  | Sequence 1, Appl  |
| 27         | 16    | 100.0 | 39    | 2      | US-08-986-248-2   | Sequence 2, Appl  |
| 28         | 16    | 100.0 | 40    | 1      | US-07-744-767A-2  | Sequence 1, Appl  |

## ALIGNMENTS

RESULT 1  
US-08-302-808-10  
; Sequence 10, Application US/08302808  
; Patent No. 5750349  
; GENERAL INFORMATION:  
; APPLICANT: SUZUKI, No. 5750349hiro  
; APPLICANT: ODAKA, Asano  
; APPLICANT: KITADA, Chieko  
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR DERIVATIVES AND USE THEREOF  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
; STREET: 130 WATER STREET  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02119  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/302,808  
; FILING DATE: 15-SEP-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/JP94/00089  
; FILING DATE: 24-JAN-1994  
; APPLICATION NUMBER: 01032/1993  
; FILING DATE: 25-JAN-1993  
; APPLICATION NUMBER: 019035/1993  
; FILING DATE: 05-FEB-1993  
; APPLICATION NUMBER: 286385/1993  
; FILING DATE: 16-NOV-1993  
; APPLICATION NUMBER: 334773/1993  
; FILING DATE: 28-DEC-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DAVID, RESNICK, S  
; REGISTRATION NUMBER: 34,235  
; REFERENCE/DOCKET NUMBER: 44631  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-523-3400  
; TELEFAX: 617-523-3440  
; TELEX: 200291 STRE  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQ ID CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single

TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: N-terminal  
 ORIGINAL SOURCE:  
 US-08-302-808-10

Query Match 100.0%; Score 16; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 6.8e-12;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHK 16  
 Db 1 DAEFRHDSGYEVHK 16  
 1 DAEFRHDSGYEVHK 16  
 1 DAEFRHDSGYEVHK 16

RESULT 2  
 US-08-986-948-10  
 Sequence 10, Application US/08986948  
 Patent No. 5955317  
 GENERAL INFORMATION:  
 APPLICANT: SUZURI, No. 5955317uhiro  
 APPLICANT: ODAKA, Asano  
 APPLICANT: KITARA, Chieko  
 TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR DERIVATIVES AND USE THEREOF  
 NUMBER OF SEQUENCES: 14  
 ADDRESSEE: DIRE, BRONSTEIN, ROBERTS & CUSHMAN  
 STREET: 130 WATER STREET  
 CITY: BOSTON  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02119  
 COMPUTER READABLE FORM:  
 COMPUTER TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASSEQ Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/986,948  
 FILING DATE:  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/485,152  
 FILING DATE: 07-JUN-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Heslin, James M.  
 REGISTRATION NUMBER: 29,541  
 REFERENCE/DOCKET NUMBER: 15270-0022810US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-326-2400  
 TELEFAX: 415-326-2422  
 INFORMATION FOR SEQ ID NO: 18:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 21 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-659-984A-18

RESULT 3  
 US-08-659-984A-18  
 Sequence 18, Application US/08659984A  
 GENERAL INFORMATION:  
 APPLICANT: Anderson, John P.  
 PATENT NO. 594400  
 APPLICANT: Siniha, Sukanto  
 APPLICANT: Jacobson-Croak, Kirsten L.  
 TITLE OF INVENTION: Assays for Detecting Beta-Secretase  
 NUMBER OF SEQUENCES: 21  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend and Crew LLP  
 STREET: Two Embarcadero Ctr., 8th Floor  
 CITY: San Francisco  
 STATE: California  
 COUNTY: USA  
 ZIP: 94111-3834  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/659,984A  
 FILING DATE: 07-JUN-1996  
 CLASSIFICATION: 436  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/485,152  
 FILING DATE: 07-JUN-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Heslin, James M.  
 REGISTRATION NUMBER: 29,541  
 REFERENCE/DOCKET NUMBER: 15270-0022810US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-326-2400  
 TELEFAX: 415-326-2422  
 INFORMATION FOR SEQ ID NO: 18:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 21 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-659-984A-18

RESULT 4  
 Query Match 100.0%; Score 16; DB 2; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 8.5e-12;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 DAEFRHDSGYEVHK 16  
 1 DAEFRHDSGYEVHK 16  
 6 DAEFRHDSGYEVHK 21

US-08-141-324-11  
; Sequence 11, Application US/08141324  
; Patent No. 5475097

GENERAL INFORMATION:  
; APPLICANT: Travis, James  
; APPLICANT: Potempa, Jan S.  
; APPLICANT: Barr, Philip J.  
; APPLICANT: Pavloff, Nadine  
; APPLICANT: Pike, Robert N.

TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Greenlee and Winner, P.C.  
; STREET: 5370 Manhattan Circle, Suite 201  
CITY: Boulder  
STATE: CO  
COUNTRY: US  
ZIP: 80303

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/141-324  
FILING DATE: 21-OCT-1993  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Feber, Donna M.  
REGISTRATION NUMBER: 33,878  
REFERENCE DOCKET NUMBER: 44-93  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 303-499-8080  
TELEFAX: 303-499-8080  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-141-324-12

Query Match 100.0%; Score 16; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 1.1e-11;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6  
US-08-541-902-11  
Sequence 11, Application US/08541902  
Patent No. 5107620

GENERAL INFORMATION:  
APPLICANT: Travis, James  
APPLICANT: Potempa, Jan S.  
APPLICANT: Barr, Philip J.  
APPLICANT: Pavloff, Nadine  
APPLICANT: Pike, Robert N.  
TITLE OF INVENTION: Protease  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Greenlee and Winner, P.C.  
; STREET: 5370 Manhattan Circle, Suite 201  
CITY: Boulder  
STATE: CO  
COUNTRY: US  
ZIP: 80303

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/541,902  
FILING DATE: 21-OCT-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/141-324  
FILING DATE: 21-OCT-1993  
ATTORNEY/AGENT INFORMATION:

NAME: Ferber, Donna M.  
 REGISTRATION NUMBER: 33,878  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 303-499-8080  
 TELEX/FAX: 303-499-8089  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 27 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 US-08-541-902-11

Query Match Score 16; DB 1; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-11;  
 Matches 16; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHK 16  
 Db 9 DAEFRHDSGYEVHK 24

RESULT 8  
 US-08-346-849-4  
 Sequence 4, Application US/08346849  
 Patent No. 5670483

GENERAL INFORMATION:  
 APPLICANT: Zhang, Shuguang  
 APPLICANT: Lockshin, Curtis  
 APPLICANT: Rich, Alexander  
 APPLICANT: Holmes, Todd  
 TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES THEREFOR

NUMBER OF SEQUENCES: 64

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
 STREET: Two Militia Drive  
 CITY: Lexington  
 STATE: Massachusetts  
 COUNTRY: U.S.A.  
 ZIP: 02173-4799

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/346,849  
 FILING DATE: 28 DECEMBER 1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/973,326  
 FILING DATE: 28 DECEMBER 1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Brook, David E.  
 REGISTRATION NUMBER: 22,592

REFERENCE/DOCKET NUMBER: MIT-6008  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 861-6240  
 TELEFAX: (617) 861-5540  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 28 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide

US-08-346-849-4

Query Match Score 16; DB 1; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-11;  
 Matches 16; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHK 16  
 Db 1 DAEFRHDSGYEVHK 16

RESULT 9  
 US-08-302-808-7

; Sequence 7, Application US/08302808  
; Patient No. 5750349  
; GENERAL INFORMATION:  
; APPLICANT: SUZUKI, No. 5750349uhirō  
; COMPUTER: ODAKA, Asano  
; APPLICANT: KITADA, Chieko  
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR  
; TITLE OF INVENTION: DERIVATIVES AND USE THEREOF  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; STREET: 130 WATER STREET  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02019  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/302,808  
; FILING DATE: 15-SEP-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/JP94/00089  
; FILING DATE: 24-JAN-1994  
; APPLICATION NUMBER: 010132/1993  
; FILING DATE: 25-JAN-1993  
; APPLICATION NUMBER: 019035/1993  
; FILING DATE: 05-FEB-1993  
; APPLICATION NUMBER: 286985/1993  
; FILING DATE: 16-NOV-1993  
; APPLICATION NUMBER: 334173/1993  
; FILING DATE: 28-DEC-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DAVID, RESNICK S  
; REGISTRATION NUMBER: 34,235  
; REFERENCE/DOCKET NUMBER: 44631  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-523-3400  
; TELEFAX: 617-523-6440  
; TELEX: 200291 STRE  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 28 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:  
; US-08-302-808-7

Query Match Score 16; DB 1; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.1e-11;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHK 16  
Db 1 DAEFRHDSGYEVHK 16

RESULT 10  
US-08-609-090-2  
; Sequence 2, Application US/08609090  
; Patent No. 5840838  
; GENERAL INFORMATION:  
; APPLICANT: HENSLEY, Kenneth

; APPLICANT: BUTTERFIELD, D. A.  
; APPLICANT: CARNEY, John M.  
; APPLICANT: ARSENOV, Michael  
; TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF  
; TITLE OF INVENTION: AN OLIGOPEPTIDE OR POLYPEPTIDES  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LOWE PRICE LEBLANC & BECKER  
; STREET: 99 Canal Center Plaza, Suite 300  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/609-090  
; FILING DATE: 29-FEB-1996  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kraus, Eric J.  
; REGISTRATION NUMBER: 36,190  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-684-1111  
; TELEFAX: 703-684-1124  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 28 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-609-090-2

Query Match Score 16; DB 2; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.1e-11;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHK 16  
Db 1 DAEFRHDSGYEVHK 16

RESULT 11  
US-08-986-948-7  
; Sequence 7, Application US/08986948  
; Patent No. 5955317  
; GENERAL INFORMATION:  
; APPLICANT: SUZUKI, No. 5955317uhiro  
; APPLICANT: ODAKA, Asano  
; APPLICANT: KITADA, Chieko  
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
; STREET: 130 WATER STREET  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02119  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/986,948

PATENT APPLICATION FORM  
FILING DATE: US/08/293,284A  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/302,808  
FILING DATE: 15-SEP-1994  
APPLICATION NUMBER: PCT/JP94/00089  
FILING DATE: 24-JAN-1994  
APPLICATION NUMBER: 010132/1993  
FILING DATE: 25-JAN-1993  
APPLICATION NUMBER: 010135/1993  
FILING DATE: 05-FEB-1993  
APPLICATION NUMBER: 286985/1993  
FILING DATE: 16-NOV-1993  
APPLICATION NUMBER: 334713/1993  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
TELEX: 200291 STRE  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
US-08-986-948-7

Query Match 100.0%; Score 16; DB 2; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.1e-11; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 0;

QY 1 DAEFRHDSSGYEVHQK 16  
Db 1 DAEFRHDSSGYEVHQK 16

RESULT 13  
US-08-461-216-2  
Sequence 2, Application US/08461216  
Patent No. 5958833

TITLE OF INVENTION: ANIMAL MODELS OF HUMAN AMYLOIDOSSES  
NUMBER OF SEQUENCES: 8  
GENERAL INFORMATION:  
APPLICANT: Show, A.D.  
TITLE OF INVENTION: ANIMAL MODELS OF HUMAN AMYLOIDOSSES  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADRESSEE: Christensen, O'Connor, Johnson and Kindness  
STREET: 1420 Fifth Avenue, Suite 2800  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98101-2347

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage  
COMPUTER: IBM PC/386 Compatible  
OPERATING SYSTEM: MS-DOS 4.01  
SOFTWARE: Word for Windows-t  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461-216  
FILING DATE:  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/969,734  
FILING DATE: October 23, 1992  
APPLICATION NUMBER: 07/950,417  
FILING DATE: September 23, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Broderick, Thomas F.  
REGISTRATION NUMBER: 31,332  
REFERENCE/DOCKET NUMBER: DOFW-1-6707  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 1-206-682-8100; 1-206-224-0709 (direct)  
TELEFAX: 1-206-224-0779  
TELEX: 493802  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28 amino acids  
TYPE: amino acid  
STRANDEDNESS: single

RESULT 12  
US-08-293-284A-4  
Sequence 4, Application US/08293284A  
GENERAL INFORMATION:  
APPLICANT: Holmes, Todd  
APPLICANT: Zhang, Shuguang  
APPLICANT: Rich, Alexander  
APPLICANT: DiPersio, C. Michael  
APPLICANT: Lockshin, Curtis  
TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY  
TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02173-4799  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent-In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

TOPOLGY: linear  
 MOLECULE TYPE: peptide  
 DESCRIPTION: (SYMBOL 98 \f "Symbol")/A4(1-28);  
 ;  
 ; DESCRIPTION: page 83, line 31  
 US-08-461-216-2

|                          | Query Match     | Score 16;          | DB 2;     | Length 28; |
|--------------------------|-----------------|--------------------|-----------|------------|
| Best Local Similarity    | 100.0%          | Pred. No. 1.1e-11; | Indels 0; | Gaps 0;    |
| Matches 16;              | Conservative 0; | Mismatches 0;      | Indels 0; | Gaps 0;    |
| Qy 1 DAEFRHDSGYEVHHQK 16 |                 |                    |           |            |
| Db 1 DAEFRHDSGYEVHHQK 16 |                 |                    |           |            |

RESULT 14  
 US-08-609-090-3  
 Sequence 3, Application US/08609090  
 ; Patent No. 5840838

; GENERAL INFORMATION:  
 ; APPLICANT: HENSLEY, Kenneth  
 ; COMPUTER: BUTTERFIELD, D. A.  
 ; APPLICANT: CARNEY, John M.  
 ; COMPUTER: IBM PC compatible  
 ; APPLICANT: AKSENOV, Michael  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF  
 ; NUMBER OF SEQUENCES: 11  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: LOWE PRICE LEBLANC & BECKER  
 ; STREET: 99 Canal Center Plaza, Suite 300  
 ; CITY: Alexandria  
 ; STATE: Virginia  
 ; COUNTRY: USA  
 ; ZIP: 22314  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/609,090  
 ; FILING DATE: 29-FEB-1996  
 ; CLASSIFICATION: 530  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Kraus, Eric J.  
 ; REGISTRATION NUMBER: 36,190  
 ; REFERENCE/DOCKET NUMBER: 434-059  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 703-684-1111  
 ; TELEFAX: 703-684-1124  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 33 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: Peptide  
 ; US-08-609-090-4

Query Match 100.0%; Score 16; DB 2; Length 33;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-11; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 1 DAEFRHDSGYEVHHQK 16  
 DB 1 DAEFRHDSGYEVHHQK 16

Search completed: September 13, 2000, 02:25:26  
 Job time: 169 sec

RESULT 15  
 US-08-609-090-4  
 ; Sequence 4, Application US/08609090



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Date: Sep 13, 2000 3:47 AM

About: Results were produced by the Gencore software, version 4.5,
Copyright (C) 1993-2000 Compugen Ltd.

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-Q=/cgn2_1/ruspio_spool/US0915576/runat_29082000_092538_16909/app_query
-DB=GenEmbl -QFNT=fastap -SUFIX=rge -GPOP=4.500 -GAPEXT=0.050
-MINMATCH=0.100 -LOORCL=0.000 -LOORPEXT=0.000 -QGAPOP=4.500
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Search information block:

TITLE gene-targeted mice with humanized A<sub>beta</sub>. sequence and Swedish FAD mutation  
 JOURNAL Patent: US 5777194-A 15 07-JUL-1998;  
 FEATURES Location/Qualifiers  
 SOURCE 1...58  
 BASE COUNT /organism="unknown"  
 ORIGIN 23 a 11 C 11 g 13 t

**WARN:** **XGAPEXT** and **IGAPEXT** must be equal. Assuming **XGAPEXT**=**60.000**

Singer 115

seq\_name : gb\_pat:A49528  
seg\_documentation\_block:  
LOCUS A49528 85 bp DNA  
DEFINITION Sequence 10 from Patient W09608561.  
ACCESSION A49528  
VERSION A49528.1 GI:2302985  
KEYWORDS

|            |   |                 |                           |
|------------|---|-----------------|---------------------------|
| ORGANISM   | unclassified                              |                 |                           |
| REFERENCE  | 1 (bases 1 to 85)                         |                 |                           |
| AUTHORS    | Chaudhuri, B. and Stephan, C.             |                 |                           |
| TITLE      | METHOD FOR DETECTION OF MALFOLDED PROTEIN |                 |                           |
| JOURNAL    | PATENT: WO 960561-A                       | 10 21 MAR 1996; |                           |
| COMMENT    | CIBA GEIGY AG (CH)                        |                 |                           |
| FEATURES   | Other publication                         | AU 3521595      | 960329.                   |
| source     | Location/Qualifiers                       | 1.              |                           |
|            |   | 85              |                           |
|            |   |                 | "organism"="unidentified" |
|            |   |                 | /db_xref="taxon:32644"    |
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|            |   | 18              | 21                        |
|            |   |                 | t                         |

alignment\_scores      Quality: 16.00      Length: 16  
                        Ratio: 1.000      Gaps: 0



**ORIGIN**

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 Quality: 16.00 Length: 16  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

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 18 GACGCCGAGTTCCGACATGACTCAGGATACGAGTCATCATAGAAA 65

**seq\_name:** gb\_om:CFAPPMR

**seq\_documentation\_block:**

LOCUS CRAPPMR mRNA 176 bp NAM 14-JUL-1992  
 DEFINITION Oryctolagus sp. mRNA for amyloid precursor protein (APP) (partial).  
 VERSION X56129  
 KEYWORDS amyloid polypeptide.  
 SOURCE Oryctolagus cuniculus.  
 ORGANISM Oryctolagus cuniculus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
 Lagomorpha; Leporidae; Oryctolagus.  
 1 (bases 1 to 176)  
 Johnstone, E.M.

REFERENCE 1  
 AUTHORS Johnstone, E.M.  
 TITLE Direct Submission  
 JOURNAL Submitted (24-SEP-1990) E.M. Johnstone, ELI LILLY AND COMPANY,  
 LILY CORPORATE CENTER 0424, INDIANAPOLIS IN 46285, USA

REFERENCE 2  
 (bases 1 to 176)  
 AUTHORS Johnstone, E.M., Chaney, M.O., Norris, F.H., Pascual, R. and  
 Little, S.P.

TITLE Conservation of the sequence of the Alzheimer's disease amyloid  
 peptide in dog, polar bear and five other mammals by cross-species  
 polymerase chain reaction analysis  
 Brain Res. Mol. Brain Res. 10 (4), 299-305 (1991)

JOURNAL  
 MEDLINE  
 FEATURES 92017079 Location/Qualifiers

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 /tissue\_type="brain"  
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 ORIGIN

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 Quality: 16.00 Length: 16  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
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**seq\_documentation\_block:**

LOCUS CSAPPMR mRNA 176 bp ROD 14-JUL-1992  
 DEFINITION Cavia sp. mRNA for amyloid precursor protein (APP) (partial).  
 VERSION X56126  
 KEYWORDS amyloid polypeptide.  
 SOURCE Cavia sp.  
 Cavia sp.  
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Cavia;  
 Rodentia; Hystricognathi; Caviidae; Cavia.  
 1 (bases 1 to 176)  
 Johnstone, E.M.

REFERENCE 1  
 AUTHORS Johnstone, E.M.  
 TITLE Direct Submission  
 JOURNAL Submitted (24-SEP-1990) E.M. Johnstone, ELI LILLY AND COMPANY,  
 LILY CORPORATE CENTER 0424, INDIANAPOLIS IN 46285, USA

alignment\_scores:  
 Quality: 16.00 Length: 16  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
 US-09-155-076-2 x CFAPPMR ..

Align seg 1/1 to: CFAPPMR from: 1 to: 176

1 ASPAlaGluPheArgHisAspSerGlyTyGluValHisGlnLys 16  
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 19 GATGGGAGTCGACATGACTCAGGATATGAAGTCAATCAAAA 66

REFERENCE 2 (bases 1 to 176)  
 AUTHORS Johnstone, E.M., Chaney, M.O., Norris, F.H., Pascual, R. and Little, S.P.  
 TITLE Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis  
 JOURNAL Brain Res. Mol. Brain Res. 10 (4), 299-305 (1991)  
 MEDLINE 92017079  
 FEATURES source  
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 /db\_xref="taxon:10143"  
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 BASE COUNT 52 a 30 c 46 g 48 t  
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 seq\_name: gb\_om:CSAPPMR  
 seq\_documentation\_block:  
 LOCUS CSAPPMR 178 bp mRNA MAM  
 DEFINITION Ovis sp. mRNA for amyloid precursor protein (APP) (partial).  
 ACCESSION X56130  
 VERSION X56130.1 GI:1829  
 KEYWORDS amyloid polypeptide.  
 SOURCE Ovis sp.  
 ORGANISM Ovis sp.  
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
 Artiodactyla; Ruminantia; Pecora; Bovidae; Caprinae;  
 Ovis.  
 1 (bases 1 to 178)  
 REFERENCE 1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisHisGlnLys 16  
 AUTHORS Johnstone, E.M., Chaney, M.O., Norris, F.H., Pascual, R. and Little, S.P.  
 TITLE Direct Submission  
 JOURNAL Submitted (24-SEP-1990) E.M. Johnstone, ELI LILLY AND COMPANY,  
 LILLY CORPORATE CENTER 0424, INDIANAPOLIS IN 46285, USA  
 2 (bases 1 to 178)  
 REFERENCE 1 (bases 1 to 177)  
 AUTHORS Johnstone, E.M., Chaney, M.O., Norris, F.H., Pascual, R. and Little, S.P.  
 TITLE Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis  
 JOURNAL Brain Res. Mol. Brain Res. 10 (4), 299-305 (1991)  
 MEDLINE 92017079  
 FEATURES source  
 LOCUS BTAPPMR 177 bp mRNA MAM  
 DEFINITION B.taurus mRNA for amyloid precursor protein (APP) (partial).  
 ACCESSION X56124  
 VERSION X56124.1 GI:82  
 KEYWORDS amyloid polypeptide.  
 SOURCE Bos taurus.  
 ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
 Artiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
 REFERENCE 1 (bases 1 to 177)  
 AUTHORS Johnstone, E.M., Chaney, M.O., Norris, F.H., Pascual, R. and Little, S.P.  
 TITLE Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis  
 JOURNAL Brain Res. Mol. Brain Res. 10 (4), 299-305 (1991)  
 MEDLINE 92017079  
 FEATURES source  
 JOURNAL Direct Submission  
 (24-SEP-1990) E.M. Johnstone, ELI LILLY AND COMPANY,  
 LILLY CORPORATE CENTER 0424, INDIANAPOLIS IN 46285, USA  
 REFERENCE 1 (bases 1 to 177)  
 AUTHORS Johnstone, E.M.  
 TITLE Direct Submission  
 Submitted (24-SEP-1990) E.M. Johnstone, ELI LILLY AND COMPANY,  
 LILLY CORPORATE CENTER 0424, INDIANAPOLIS IN 46285, USA  
 alignment\_scores:  
 Quality: 16.00 Length: 16  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000  
 alignment\_block:  
 US-09-155-076-2 x OVAPPMR ..  
 Align seg 1/1 to: OVAPPMR from: 1 to: 178  
 /db\_xref="SEVKMDAERFRHDSGYEVHHQKLVFFAEVDGSNKGAIIGLMYGG  
 /translation="ISEVKMDAERFRHDSGYEVHHQKLVFFAEVDGSNKGAIIGLMYGG  
 /db\_xref="taxon:9013"  
 /tissue\_type="brain"  
 <1..>177  
 /codon\_start=1  
 /product="amyloid precursor protein"  
 /protein\_id="CAA39589.1"  
 /db\_xref="GI:83"

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisHisGlnLys 16  
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 18 GATGCGAAATTCCGACATGATTGGATATGAAGTCATCATCAAAA 65

**seq\_name:** gb\_pr1:HUMAPP4A1

**seq\_documentation\_block:**  
**LOCUS** HUMAPP4A1 189 bp DNA PRI 31-OCT-1994  
**DEFINITION** Human amyloid protein, exon X.  
**ACCESSION** M29269  
**VERSION** M29269\_1 GI:178862  
**KEYWORDS** SEGMENT 1 of 2  
**SOURCE** Human DNA (library of T. Maniatis), Clone lambda-41.  
**ORGANISM** Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Hominidae; Homo.  
**REFERENCE** Johnstone, E.M., Chaney, M.O., Moore, R.E., Ward, K.E., Norris, F.H. and Little, S.P.  
**AUTHORS**  
**TITLE** Alzheimer's disease amyloid peptide is encoded by two exons and shows similarity to soybean trypsin inhibitor  
**JOURNAL** Biochem. Biophys. Res. Commun. 163 (3), 1248-1255 (1989)  
**MEDLINE** 89392030  
**FEATURES**  
**source** 1..189  
 /organism="Homo sapiens"  
 /db\_xref="9606"  
 /map="21q21.2"  
**introns**  
 <1..42  
 /gene="APP"  
 /note="intron X-1; G00-119-692"  
 43..143  
 /gene="APP"  
 /note="exon X; G00-119-692"  
**BASE COUNT** 59 a 32 c 38 g 60 t  
**ORIGIN** 73 bp upstream of BglII site; chromosome 21q21.2.

**alignment\_scores:**  
**aligner** US-09-155-076-2 x HUMAPP4A1  
**target** Align seg 1/1 to: HUMAMYBBL1 from: 1 to: 242  
**score** 1 ASPAlaGluPheArgHisAspSerGlyTyrGluValHisHisGlnLys 16  
 ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 154 GATGCGAAATTCCGACATGGACTCAGGATATGAAGTCATCATCAAAA 201

**seq\_name:** gb\_pr2:560721

**seq\_documentation\_block:**  
**LOCUS** S60721 246 bp mRNA PRI 23-JUL-1993  
**DEFINITION** beta-amyloid peptide precursor [clone 1] [human, mRNA Partial Mutant, 246 nt].  
**ACCESSION** S60721  
**VERSION** S60721\_1 GI:299644  
**KEYWORDS**  
**SOURCE** human  
**ORGANISM** Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Hominidae; Homo.

**REFERENCE** 1 (bases 1 to 246)  
**AUTHORS** Denman, R.B., Rosenzwaig, R., and Miller, D.L.  
**TITLE** A system for studying the effect(s) of familial Alzheimer disease mutations on the processing of the beta amyloid peptide precursor  
**JOURNAL** JOURNAL Biochem. Biophys. Res. Commun. 192 (1), 96-103 (1993)  
**MEDLINE** 93236601  
**REMARK** GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 129915] from the original journal article.  
 This sequence comes from Fig. 1.  
**Map** Map location: 21.

**FEATURES**  
**source** 1..246  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"

**gene** 1..246  
 /partial  
 /gene="beta-amyloid peptide precursor, beta APP"  
**CDS** 1..246  
 /partial  
 /gene="beta-amyloid peptide precursor, beta APP"  
**REMARK** 1 (bases 1 to 242)  
**AUTHORS** Levy, E., Carman, M.D., Fernandez-Madrid, I.J., Power, M.D., Lieberburg, I., van Duinen, S.G., Bots, G.T., Luyendijk, W., and Frangione, B.  
**TITLE** Mutation of the Alzheimer's disease amyloid gene in hereditary

/protein\_id="AAB26263\_1"  
 /db\_xref="Gv:299645"  
 /translation="GSLLNIKTEESEVRMDAEPFRPHDSGYEVHQKLVFFAEVDVSK  
 KGAIIGLMVGGVVIATVIFTIVMLRKWNTSIHGGVE"

BASE COUNT 72 a 40 c 69 g 65 t ORIGIN

alignment\_scores:  
 Quality: 16.00 Length: 16  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
 US-09-155-076-2 x S60721 ..

Align seg 1/1 to: S60721 from: 1 to: 246

seq\_name: gb\_pr2:S61383

seq\_documentation\_block:  
 LOCUS S61383 246 bp mRNA  
 DEFINITION beta-amyloid peptide precursor [clone 3] [human, mRNA Partial  
 Mutant, 246 nt].

ACCESSION S61383  
 VERSION S61383\_1 GI:299648

KEYWORDS human.

ORGANISM Homo sapiens  
 Eukaryota; Primates; Catarrhini; Hominidae; Homo.  
 Butheria; Primates; Catarrhini; Hominidae.

REFERENCE 1 (bases 1 to 246)  
 AUTHORS Deman, R.B., Rosenzwaig, R. and Miller, D.L.  
 TITLE A system for studying the effect(s) of familial Alzheimer disease mutations on the processing of the beta-amyloid peptide precursor

JOURNAL Biochem. Biophys. Res. Commun. 192 (1), 96-103 (1993)

MEDLINE 93236601  
 REMARK Genbank staff at the National Library of Medicine created this entry [NCBI gibbsq 132966] from the original journal article.  
 This sequence comes from Fig. 1.  
 Map location: 21.

FEATURES Location/Qualifiers

source 1. .246  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"

gene 1. .246  
 /partial  
 /gene="beta-amyloid peptide precursor, beta APP"  
 CDS 1. .246  
 /partial  
 /gene="beta-amyloid peptide precursor, beta APP"  
 /note="This sequence comes from Fig. 1; Protein sequence is in conflict with the conceptual translation; mismatches(698[K->N],727[W->Y],730[I->N]); beta APP mismatched(698[K->N],727[W->Y],730[I->N]); beta APP"

JOURNAL Biochem. Biophys. Res. Commun. 192 (1), 96-103 (1993)

MEDLINE 93236601  
 REMARK Genbank staff at the National Library of Medicine created this entry [NCBI gibbsq 132963] from the original journal article.  
 This sequence comes from Fig. 1.  
 Map location: 21.

FEATURES Location/Qualifiers

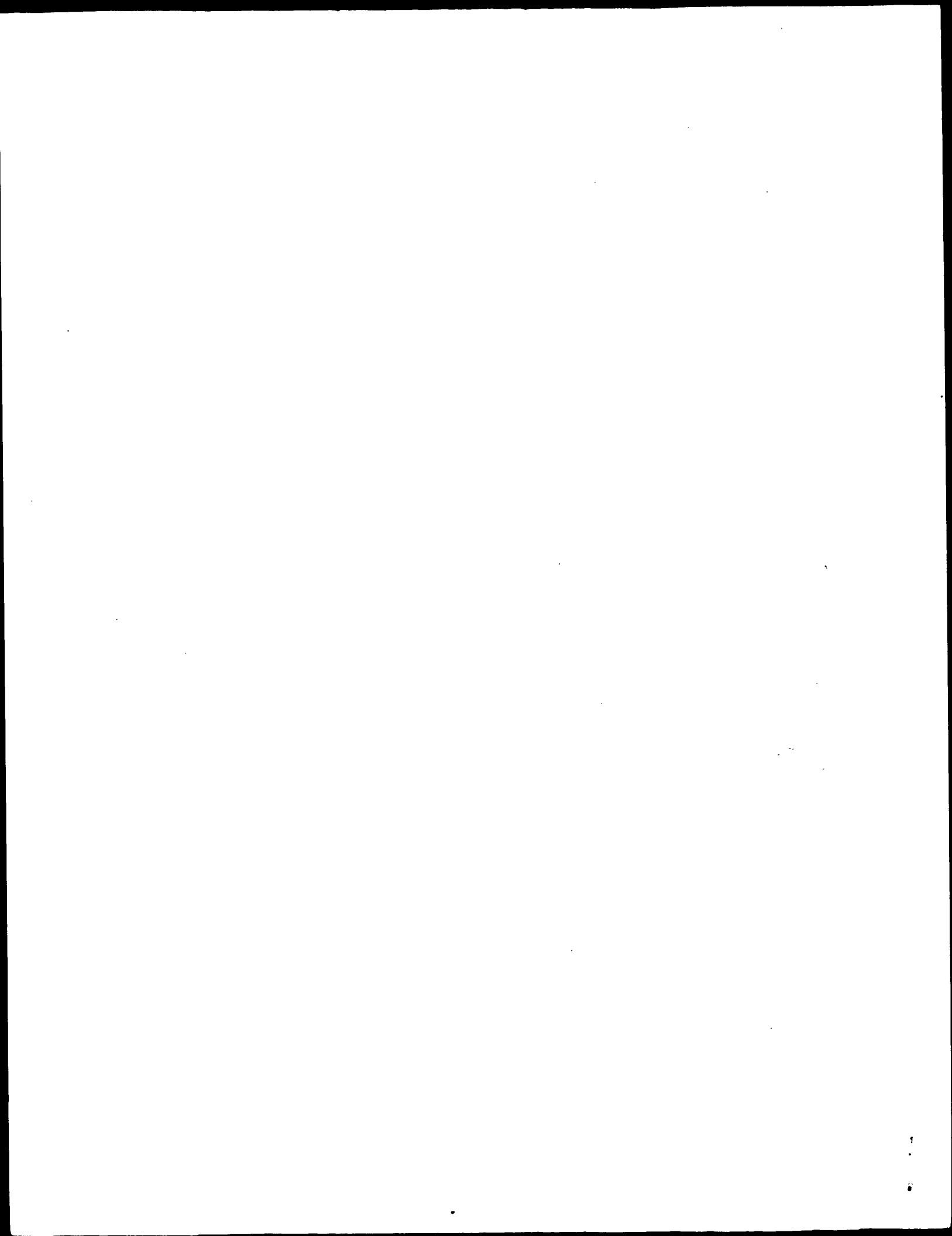
source 1. .246  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"

gene 1. .246  
 /partial  
 /gene="beta-amyloid peptide precursor, beta APP"  
 CDS 1. .246  
 /partial  
 /gene="beta-amyloid peptide precursor, beta APP"  
 /note="This sequence comes from Fig. 1; Protein sequence is in conflict with the conceptual translation; mismatches(44[K->N],743[W->Y],76[I->N]); beta APP"  
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 /protein\_id="AAB26264\_1"  
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 /translation="GSGLNIKTEESEVRMDAEPFRPHDSGYEVHQKLVFFAEVDVSK  
 KGAIIGLMVGGVVIATVIFTIVMLRKWNTSIHGGVE"

BASE COUNT 73 a 40 c 69 g 64 t ORIGIN

alignment\_scores:  
 Quality: 16.00 Length: 16  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000









1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisHisGlnLys 16  
 58 GATGCCAGATTCCGACGACGACTGGATATGAGTCATCATCAAAA 105

seq\_name: N\_Geneseq\_36:v23754

seq\_documentation\_block:

ID V23754 standard; DNA; 262 BP.

AC V23754;

DT 18-AUG-1998 (first entry)

DE Alzasi coding sequence.

KW Dsas; DSAsp; Alzasi's syndrome; diagnosis; therapy; human; Alzheimer's disease; ss.

KW Homo sapiens.

OS Homo sapiens.

FT 50..205 /tag= a /product= "ALZASp1"

FT /note= "specifically claimed fragment"

PN W09807850-A2.

PD 26-FEB-1998.

PF 22-AUG-1997; E04599.

PR 22-AUG-1998; CA 183901.

PA (BERG) BERGMANN J E.

PA (PREDDIE) PREDDIE E R.

PI Bergmann JE, Preddie ER;

WPI: 98-169155/15.

DR P-PSDB; W53984.

PT Nucleic acid molecules dsas, and alzas - used for detecting and treating Down's syndrome and Alzheimer's disease

PS Claim 13; Fig 11; 90pp; English.

CC This sequence represents the human alzas1 nucleic acid. The dsas and alzas DNA sequences are the nucleic acids of the invention. Reagents specifically for DSAsP can be used for the diagnosis of Down's syndrome in humans and especially in pregnant women. Molecules that inhibit the activity of the Promoters (PDS1, PDS2, PDS3, and PDS4) for dsas can be used for treating Down's syndrome. The reagent capable of detecting alzas can be used for detecting Alzheimer's disease, especially in the pre-symptomatic stage. Substances that inhibit the promoters for alzas can be used in treating Alzheimer's disease.

CC Sequence 262 BP; 96 A; 43 C; 52 G; 71 T;

alignment\_scores:

Quality: 16.00 Length: 16 Gaps: 0 Percent Identity: 100.000

aligner\_block:

US-09-155-076-2 x V23754 ..

Align seg 1/1 to: V23754 From: 1 to: 262

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisHisGlnLys 16  
 53 GATGCCAGATTCCGACGACGACTGGATATGAGTCATCATCAAAA 100

seq\_name: N\_Geneseq\_36:Q88696

seq\_documentation\_block:

ID Q88696 standard; cDNA to mRNA; 297 BP.

AC Q88696;

DT 11-Nov-1995 (first entry)

DE Beta-amyloid precursor protein C-terminal peptide gene.

RW Human; beta-amyloid precursor protein C-terminal peptide; transgenic animal; Alzheimer disease model;

KW gene transfer; transgenic animal; Alzheimer disease model;

OS Homo sapiens.

PN EP-653154-A.

PD 17-MAY-1995.

PF 07-NOV-1994; 117512.

PR 12-NOV-1995; JP-306026.

PA (FARH ) HOECHST JAPAN LTD.

PA (FARH ) HOECHST JAPAN KK.

PI Kawarabayashi T, Kobayashi T, Sato M, Shoji M, Tada N;

DR WPI: 95-180492/24.

DR P-PSDB; R74695.

PT Transgenic animal model for Alzheimer's disease - contains DNA encoding part of beta-amyloid precursor protein in a gene construct designed for over-expression in various cell types

Claim 2; Page 11; 32pp; English.

PA (FARH ) HOECHST JAPAN LTD.

PA (FARH ) HOECHST JAPAN KK.

CC The sequence encodes a human brain beta-amyloid precursor protein (APP) mutant C-terminal peptide, and differs from Q88696 by a Glu to Gln conversion at codon-22. The DNA may be transferred along with an APP signal peptide gene (e.g. Q88695) into somatic and germ cells of a non-human mammal, and the resulting transgenic animal may be used as a model for Alzheimer disease (AD). The animal model exhibits symptoms similar to AD, producing large quantities of APP C-terminal peptide, death of neuron cells in pyramidal cells at cerebral amyloid regions, increases in glial cells and deposition of abnormally phosphorylated tau protein. The animal model may be used to develop new therapies for AD, including gene therapy strategies.

Sequence 297 BP; 86 A; 65 C; 77 G; 69 T;



PI Cordell B, Ponte PA;  
WP; 93-205383/25.  
DR P-PSDB: R37866  
PT DNA sequence useful for detection of Alzheimer's disease - for encoding beta amyloid core protein  
Disclosure: Fig 5; 40pp; English  
CC A clone was obtained from the genomic library described in Lawn et al.,  
CC encodes amino acids 1-18 of the beta-amyloid protein, immediately  
preceded by a Methionine. A HindIII/Asai fragment derived from the  
genomic clone and containing the 57bp segment was used to isolate cDNA  
fragments from a library prepared from temporal and parietal cortical  
tissue from a normal human brain. Lambda clone SMW3 (Q42664) contains  
a 5' region segment which has a 6bp overlap with the 3' end of clone  
SNW4 (Q42653). The full-length beta-amyloid protein coding sequence  
(Q42655), including an initiator Met residue which is probably  
processed in vivo, was obtained by combining the sequences of the  
two overlapping clones.  
Sequence 300 BP; 87 A; 65 C; 78 G; 70 T;

alignment\_scores:  
Quality: 16.00 Length: 16  
Ratio: 1.000 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
US-09-155-076-2 x Q42665 ..

Align seg 1/1 to: Q42665 from: 1 to: 300

1 AsPAlaGluPheArgHisAspSerGlytyrGluValHisHisGlnLys 16  
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
4 GATGCCGAATTGGACATGACTCAGGATGAACTCATCACAAAA 51

seq\_name: N\_Geneseq\_36:Q88699

seq\_documentation\_block:  
ID Q88699 standard; cDNA to mRNA; 309 BP.  
AC 088699..  
DT 11-NOV-1995 (first entry)  
DE Beta-amyloid precursor protein C-terminal peptide gene.  
KW Human; beta-amyloid precursor protein; C-terminal peptide;  
KW gene transfer; transgenic animal; Alzheimer disease model;  
KW gene therapy; ss.  
OS Homo sapiens.  
PN EP-65154-A.  
PD 17-MAY-1995.  
PR 12-NOV-1993; JP-306026.  
(FARH ) HOECHST JAPAN LTD.  
PA Kawarabayashi T, Kobayashi T, Sato M, Shoji M, Tada N;  
WPI: 95-180492/24.  
DR P-PSDB; R74697.

Transgenic animal model for Alzheimer's disease - contains DNA encoding part of beta=amyloid precursor protein in a gene construct designed for over-expression in various cell types  
Claim 2; Page 15; 32pp; English.  
The sequence encodes a human brain beta-amyloid precursor protein (APP) mutant C-terminal peptide, and differs from Q88699 by conversion of Lys to Asn at codon-3 and Met to Leu at codon-4. The DNA may be transferred along with an APP signal peptide gene (e.g. Q88695) into somatic and germ cells of a non-human mammal, and the resulting transgenic animal may be used as a model for Alzheimer disease (AD). The animal model exhibits symptoms similar to AD, producing large quantities of APP C-terminal peptide, death of neuron cells in pyramidal cells at cerebral amyloid regions, increases in glial cells and deposition of abnormally phosphorylated tau protein. The animal model may be used to develop new therapies for AD, including gene therapy strategies.  
Sequence 309 BP; 90 A; 65 C; 82 G; 72 T;

alignment\_scores:  
Quality: 16.00 Length: 16  
Ratio: 1.000 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
US-09-155-076-2 x Q88699 ..

Align seg 1/1 to: Q88699 from: 1 to: 309

1 AsPAlaGluPheArgHisAspSerGlytyrGluValHisHisGlnLys 16  
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
13 GATGCCGAATTGGACATGACTCAGGATGAACTCATCACAAAA 60

seq\_name: N\_Geneseq\_36:Q88700

seq\_documentation\_block:  
ID T18082 standard; DNA; 336 BP.  
AC T18082;  
DT 10-OCT-1996 (first entry)

DE Familial Alzheimer's disease APP isoform 751 gene fragment.  
 APP; amyloid precursor protein; isoform 751; inherent; familial;  
 KW Alzheimer's disease; mutation; diagnosis; transgenic model; study;  
 KW cognitive; beta A4 domain; exon 17; sensitivity; ss.  
 OS Homo sapiens. Location/Qualifiers  
 FH Key  
 FT 1..336  
 FT /\*tag= a  
 FT /number= 17  
 FT /transl\_except= pos: 175-177, aa: Ile  
 FT /note= "encodes amino acids 640-751 of full APP  
 isofrom 751, the translation exception at posn. 175-177 is the site of a Val to Ile mutation in isoform 751, bases 175-177 probably should be ATC and not TTC."  
 FT misc\_feature 43..168  
 FT /\*tag= b  
 FT /note= "encodes the beta -A4 domain"  
 PN W09606927-A1.  
 PD 07-MAR-1996.  
 PR 28-AUG-1995; U10920.  
 PR 01-SEP-1994; US-29872.  
 PA (MERCK & CO INC.  
 Chen HY, Heavens RP, Singh G, Srinathsinghji DJS;  
 Smith DW, Trumboer ME, Van Der Ploeg LHT, Vongs A;  
 PI Zheng H;  
 DR WPI; 96-160358/16.  
 DR P-PSDB; R93356.  
 PT transgenic animal expressing familial form of human amyloid precursor protein - used to evaluate compounds affecting Alzheimer's disease and other cognitive disorders  
 PT precursor protein - used to evaluate compounds affecting Alzheimer's disease and other cognitive disorders  
 Example 1: Fig 7; 32pp; English.  
 CC T10802 represents exon 17 of the amyloid precursor protein (APP) isofrom 751 gene from a patient diagnosed with familial Alzheimer's disease (FAD). The sequence given corresponds to the coding sequence for amino acids 640-751 of FAD APP 751. A feature of FAD is a Val to Ile substitution at posn. 698 of the full APP (encoded by bases 175 to 177 of this sequence). DNA encoding this sequence was used to construct expression vectors for the production of transgenic animals (esp. mice) carrying the FAD APP 751 mutation. The transgenic animals are useful for the evaluation of test cpd's, affecting Alzheimer's disease and other cognitive disorders and for identification of new targets in Alzheimer's disease since the progression of the disease can be followed gradually.  
 CC N.B. the V-I mutation encoded at base 175-177 is given in the specification as a TTC codon (most probably this should be ATC).  
 CC Sequence 336 BP; 102 A; 69 C; 88 G; 77 T;  
 SQ 16..16  
 alignment\_scores:  
 Quality: 16.00 Length: 16  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000  
 alignment\_block:  
 US-09-155-076-2 x T18082 ..  
 Align seg 1/1 to: T18082 from: 1 to: 336

seq\_name: N\_Geneseq\_36\_V20380

seq\_documentation\_block:  
 ID V20380 standard; DNA: 354 BP.  
 AC V20380;  
 DT 26-JUN-1998 (first entry)  
 DE DNA for APP C-terminal fragment mutant SPA4CT Thr43Ala/Val46Phe.  
 KW Human; amyloid precursor protein; App; carboxy-terminal fragment; A4CT; mutant SPA4CT Thr43Ala/Val46Phe; disease model; treatment; Alzheimer's disease; ss.  
 OS Homo sapiens.  
 PH Synthetic.

Location/Qualifiers  
 FH Key  
 FT 1..354  
 FT /\*tag= a  
 FT /note= "stop codon not given"

seq\_name: N\_Geneseq\_36\_V20380

seq\_documentation\_block:  
 ID V20380 standard; DNA: 354 BP.  
 AC V20380;  
 DT 26-JUN-1998 (first entry)  
 DE DNA for APP C-terminal fragment mutant SPA4CT Thr43Ala/Val46Phe.  
 KW Human; amyloid precursor protein; App; carboxy-terminal fragment; A4CT; mutant SPA4CT Thr43Ser; disease model; treatment; Alzheimer's disease; ss.

seq\_name: N\_Geneseq\_36\_V20380

seq\_documentation\_block:  
 ID V20380 standard; DNA: 354 BP.  
 AC V20380;  
 DT 26-JUN-1998 (first entry)  
 DE DNA for APP C-terminal fragment mutant SPA4CT Thr43Ser.  
 KW Human; amyloid precursor protein; App; carboxy-terminal fragment; A4CT; mutant SPA4CT Thr43Ser; disease model; treatment; Alzheimer's disease; ss.

seq\_name: N\_Geneseq\_36\_V20380

seq\_documentation\_block:  
 ID V20380 standard; DNA: 354 BP.  
 AC V20380;  
 DT 26-JUN-1998 (first entry)  
 DE DNA for APP C-terminal fragment mutant SPA4CT Thr43Ala/Val46Phe.  
 KW Human; amyloid precursor protein; App; carboxy-terminal fragment; A4CT; mutant SPA4CT Thr43Ala/Val46Phe; disease model; treatment; Alzheimer's disease; ss.

seq\_name: N\_Geneseq\_36\_V20380

seq\_documentation\_block:  
 ID V20380 standard; DNA: 354 BP.  
 AC V20380;  
 DT 26-JUN-1998 (first entry)  
 DE DNA for APP C-terminal fragment mutant SPA4CT Thr43Ala/Val46Phe.  
 KW Human; amyloid precursor protein; App; carboxy-terminal fragment; A4CT; mutant SPA4CT Thr43Ser; disease model; treatment; Alzheimer's disease; ss.

PT or transformed cells, used for identifying potential drugs for  
PT Alzheimer's disease  
PS Claim 10; Page 11; 15pp; English.  
CC The present sequence encodes the human amyloid precursor protein  
CC (APP) C-terminal fragment (A4CT) mutant SPA4CT Thr13Ala/Val146Phe.  
CC The mutation results in a higher ratio of beta A4 1-42 to beta A4  
CC 1-40, useful in disease models to identify potential drugs for the  
SQ treatment of Alzheimer's disease.  
Sequence 354 BP; 91 A: 82 C: 98 G: 83 T:

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alignment_scores:
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  Percent: 100.00
  Identif.: 100.00
  Gaps: 0
  Length: 16
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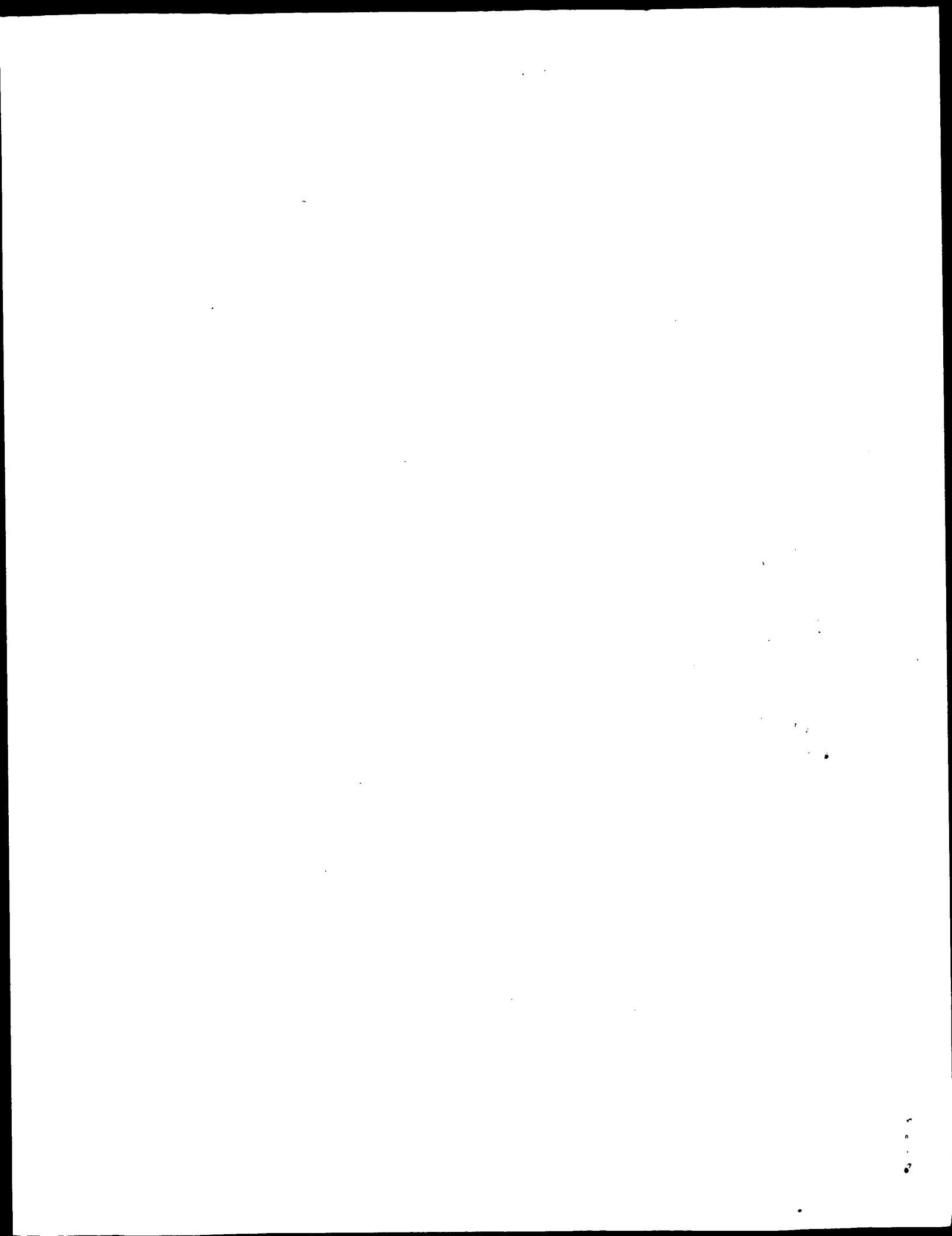
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alignment_block:
US-09-155-076-2 x V20380   ..

Align seg 1/1  to: V20380  from: 1  to: 354

 1 ASP ALA Glu Pro Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys 16
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 58 GAT GCG AAATT CGC GAC ATG GACT CAG AAT TGA GAA CTC TCA TCA CTC 105

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 Date: Sep 13, 2000 3:48 AM  
 About: Results were produced by the GenCore software, version 4.5,  
 Copyright (c) 1993-2000 Compugen Ltd.

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 Database: Issued\_Patents\_NA: \*  
 Database sequences: 243080  
 Database length: 68777915  
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WARNING: XGAPOP and YGAPOP must be equal. Assuming YGAPEXT=XGAPEXT=60.000  
 WARNING: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=60.000

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| Sequence                             | Strd              | Orig | ZScore | EScore | Len     | Documentn | Length: | Alignment_scores:   |
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| /cgn2_6/ptodata/2/ina/backfiles1.seq | 518153-3          | +    | 16.00  | 325.83 | 1.2e-10 | 485       | 16      | seq_documentation_block:  |
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| /cgn2_6/ptodata/2/ina/5C_COMB.seq    | US-08-104-165-7   | +    | 16.00  | 312.94 | 6.1e-10 | 3353      | 16      | seq_documentation_block:  |
| /cgn2_6/ptodata/2/ina/backfiles1.seq | 5218100-1         | +    | 16.00  | 312.94 | 6.1e-10 | 3353      | 16      | seq_documentation_block:  |
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 ; Sequence 15, Application US/08636876  
 ; Patient No. 5777194  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Scott, Richard W.  
 ; APPLICANT: Beaume, Andrew G.  
 ; APPLICANT: Trusko, Stephen P.  
 ; TITLE OF INVENTION: GENE-TARGETED NON-HUMAN MAMMAL WITH HUMANIZED AB SEQUENCE AND SWEDISH FAD MUTATIONS  
 ; NUMBER OF SEQUENCES: 16  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Fish & Richardson P.C.  
 ; STREET: 225 Franklin Street Suite 3100  
 ; CITY: Boston  
 ; STATE: MA  
 ; COUNTRY: USA  
 ; ZIP: 02110-2804  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/636876  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Clark, Paul T.  
 ; REGISTRATION NUMBER: 30,162  
 ; REFERENCE/DOCKET NUMBER: 02655/055001  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (617) 542-5070  
 ; TELEFAX: (617) 542-8906  
 ; TELEX: 2010154  
 ; INFORMATION FOR SEQ ID NO: 15:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 58 base pairs  
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 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; US-08-636-876-15

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 ; alignment\_block:  
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 ; seq\_documentation\_block:  
 ; Sequence 8, Application PC/TUS9404026  
 ; GENERAL INFORMATION:  
 ; APPLICANT:

TITLE OF INVENTION: Transgenic Animal Models for Alzheimer's Disease  
 NUMBER OF SEQUENCES: 12  
 CORRESPONDENCE ADDRESS: ADDRESSEE: Marchall, O'Toole, Gerstein, Murray & Borun  
 STREET: 6300 Sears Tower - 233 South Wacker Drive  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60606-6402

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT-US94/04026  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Clough, Ph.D., David W.  
 REGISTRATION NUMBER: 36,107  
 REFERENCE/DOCKET NUMBER: 31188  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312/474-6300  
 TELEFAX: 312/474-0448  
 INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 189 base pairs  
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 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 ORIGINAL SOURCE:  
 ORGANISM: Human  
 PCT-US94-04026-8

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 Sequence 3, Application US/08339708A

GENERAL INFORMATION:

APPLICANT: Sato, Masahiro  
 APPLICANT: Takashi, Kobayashi  
 APPLICANT: Tada, No. 6037521hiro

APPLICANT: Shoji, Mikio

APPLICANT: Kavarabayashi, Takeshi

TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR ALZHEIMER'S

TITLE OF INVENTION: DISEASE  
 NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner  
 STREET: 3000 K Street, N.W., Suite 500  
 CITY: Washington  
 STATE: D.C.

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
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 APPLICATION NUMBER: US/08-339-708A  
 FILING DATE: 14-NOV-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 306026/93  
 FILING DATE: 12-NOV-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: SANDERCOCK, COLIN G.  
 REGISTRATION NUMBER: 31,298  
 REFERENCE/DOCKET NUMBER: 026083/0159  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202)672-5300  
 TELEX: (202)672-5399  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 297 base Pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA to mRNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: homo sapiens  
 STRAIN: human brain  
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 NAME/KEY: CDS  
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 ; OTHER INFORMATION: precursor; 2. C-terminal peptide"  
 US-08-339-708A-3

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 Sequence 5, Application US/08339708A  
 GENERAL INFORMATION:  
 APPLICANT: Sato, Masahiro  
 APPLICANT: Takashi, Kobayashi  
 APPLICANT: Tada, No. 6037521hiro  
 APPLICANT: Shoji, Mikio  
 APPLICANT: Kavarabayashi, Takeshi  
 TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR ALZHEIMER'S  
 TITLE OF INVENTION: DISEASE  
 NUMBER OF SEQUENCES: 23  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Foley & Lardner  
 STREET: 3000 K Street, N.W., Suite 500  
 CITY: Washington  
 STATE: D.C.  
 ZIP: 20007-5109  
 COUNTRY: USA  
 COMPUTER READABLE FORM:

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; COMPUTER READABLE FORM:
; COMPUTER TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,708A
; FILING DATE: 14-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 306026/93
; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SANDERCOCK, COLIN G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 026083/0159
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 297 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: homo sapiense
; STRAIN: human brain
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..297
; OTHER INFORMATION: /note= "1. human beta-amyloid
; OTHER INFORMATION: precursor; 2. C-terminal peptide"
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; OTHER INFORMATION: precursor; 2. C-terminal peptide"
US-08-339-708A-5

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; Sequence 7, Application US/08339708A
; GENERAL INFORMATION:
; APPLICANT: Sato, Masahiro
; APPLICANT: Takashi, Kobayashi
; APPLICANT: Tada, No. 6037521hiro
; APPLICANT: Shoji, Mikio
; APPLICANT: Kawarabayashi, Takeshi
; TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR ALZHEIMER'S
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339-708A
; FILING DATE: 14-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 306026/93
; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SANDERCOCK, COLIN G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 026083/0159
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 297 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: homo sapiense
; STRAIN: human brain
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..297
; OTHER INFORMATION: /note= "1. human beta-amyloid
; OTHER INFORMATION: precursor; 2. C-terminal peptide"
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; OTHER INFORMATION: precursor; 2. C-terminal peptide"
US-08-339-708A-7

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; Patent No. 5220013
; APPLICANT: PONTE, PHYLIS A.; CORDELL, BARBARA
; TITLE OF INVENTION: DNA SEQUENCE USEFUL FOR THE DETECTION
; OF ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/444,118
; FILING DATE: 30-NOV-1989
; PRO/OP APPLICATION DATA:
; APPLICATION NUMBER: 87,002
; FILING DATE: 18-AUG-1987
; APPLICATION NUMBER: 87,810
; FILING DATE: 30-JAN-1987
; APPLICATION NUMBER: 948,376
; FILING DATE: 31-DEC-1986
; APPLICATION NUMBER: 932,193

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TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR ALZHEIMER'S DISEASE  
 TITLE OF INVENTION: DISEASE  
 NUMBER OF SEQUENCES: 23  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Foley & Lardner  
 STREET: 3000 K Street, N.W., Suite 500  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20007-5109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08-339,708A  
 FILING DATE: 14-NOV-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 306026/93  
 FILING DATE: 12-NOV-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: SANDERCOCK, COLIN G.  
 REGISTRATION NUMBER: 31,298  
 REFERENCE/DOCKET NUMBER: 026083/0159  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 672-5300  
 TELEFAX: (202) 672-5399  
 TELEX: 904136  
 INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 309 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA to mRNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: homo sapiense  
 STRAIN: human brain  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1..309  
 OTHER INFORMATION: /note= "1. human beta-amyloid  
 precursor; 2. C-terminal peptide"  
 US-08-339-708A-9  
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 Sequence 9, Application US/08339708A  
 GENERAL INFORMATION:  
 Patent No. 6037521  
 Sequence 11, Application US/08339708A  
 GENERAL INFORMATION:  
 Patent No. 6037521  
 GENERAL INFORMATION:  
 Sato, Masahiro  
 APPLICANT: Takashi, Kobayashi  
 APPLICANT: Tada, No. 6037521hiro  
 APPLICANT: Shoji, Mikio  
 APPLICANT: Kawarabayashi, Takeshi  
 APPLICANT: Shoji, Mikio  
 APPLICANT: Tada, No. 6037521hiro  
 APPLICANT: Sato, Masahiro  
 APPLICANT: Takashi, Kobayashi  
 APPLICANT: Tada, No. 6037521hiro  
 APPLICANT: Shoji, Mikio

APPLICANT: Kawarabayashi, Takeshi  
 TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR ALZHEIMER'S  
 NUMBER OF SEQUENCES: 23  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Foley & Lardner  
 STREET: 3000 K Street, N.W., Suite 500  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20007-5109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/339,708A  
 FILING DATE: 14-NOV-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 306026/93  
 FILING DATE: 12-NOV-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: SANDERCOCK, COLIN G.  
 REGISTRATION NUMBER: 31,298  
 REFERENCE/DOCKET NUMBER: 026083/0159  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 672-5300  
 TELEFAX: (202) 672-5599  
 TELEX: 901136  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 309 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA to mRNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: homo sapiense  
 STRAIN: human brain  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1..309  
 OTHER INFORMATION: /note= "1. human beta-amyloid  
 2. C-terminal peptide"  
 US-08-339-708A-11

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alignment\_scores:  
 Quality: 16.00 Length: 16  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
 US-09-155-076-2 x US-08-339-708A-11

Align seq 1/1 to: US-08-339-708A-11 from: 1 to: 309

1 AsparagluphearghisAspserGlytyrgluvalIshishGlnlys 16  
 13 GATGCAGAATTCGGACATGACTCAGGATATGAAGTCATCAAAA 60

seq\_name: /cgn2\_6/ptodata/2/ina/backfiles1.seq:5187153-3

seq\_documentation\_block:

; Patent No. 5187153

; APPLICANT: CORDELL, BARBARA; SCHILLING, JAMES W.; KATUNUMA, NOBUHIKO

; TITLE OF INVENTION: METHODS OF TREATMENT USING ALZHEIMER'S

; AMYLOID POLYPEPTIDE DERIVATIVES

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/502,273

; FILING DATE: 29-MAR-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 361,912

; FILING DATE: 06-JUN-1989

; APPLICATION NUMBER: 359,911

; FILING DATE: 12-MAY-1989

; APPLICATION NUMBER: 87,002

TITLE OF INVENTION: EXPRESSING FLAG-APP-C100 FUSION PROTEIN  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fish & Richardson P.C.  
 STREET: 225 Franklin Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: US  
 ZIP: 02110-2804  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEQ Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/729,345  
 FILING DATE: 16-OCT-1996  
 CLASSIFICATION: 800  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Clark, Paul T.  
 REGISTRATION NUMBER: 30,162  
 REFERENCE/DOCKET NUMBER: 04843/027001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-542-5070  
 TELEFAX: 617-542-8906  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 354 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: Linear  
 FEATURE:  
 NAME/KEY: Coding Sequence  
 LOCATION: 1..351  
 OTHER INFORMATION:  
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 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000  
 alignment\_block:  
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 Align seq 1/1 to: US-08-729-345-2 from: 1 to: 354  
 1 AsparagluphearghisAspserGlytyrgluvalIshishGlnlys 16  
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 seq\_name: /cgn2\_6/ptodata/2/ina/backfiles1.seq:5187153-3

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; FILING DATE: 18-AUG-1987
; APPLICATION NUMBER: 8,810
; FILING DATE: 30-JAN-1987
; APPLICATION NUMBER: 948,376
; FILING DATE: 31-DEC-1986
; APPLICATION NUMBER: 932,193
; FILING DATE: 17-NOV-1986
; SEQ ID NO:3;
; LENGTH: 485
; 5187153-3

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Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Identity: 100.000

alignment_block:
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seq_name: /cgn2_6/ptodata/2/ina/backfiles1.seq:5220013-3

seq_documentation_block:
; Patent No. 5220013
; APPLICANT: PONTE, PHYLLIS A.; CORDELL, BARBARA
; TITLE OF INVENTION: DNA SEQUENCE USEFUL FOR THE DETECTION
; OF ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 30
; CURRENT APPLICATION DATA:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US-07/444,118
; FILING DATE: 30-NOV-1989
; FILING DATE: 18-AUG-1987
; APPLICATION NUMBER: 8,810
; FILING DATE: 30-JAN-1987
; APPLICATION NUMBER: 948,376
; FILING DATE: 31-DEC-1986
; APPLICATION NUMBER: 932,193
; FILING DATE: 17-NOV-1986
; SEQ ID NO:3;
; LENGTH: 486
; 5220013-3

alignment_scores:
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Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Identity: 100.000

alignment_block:
US-09-155-076-2 x 5220013-3 .

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seq_documentation_block:
; Sequence 9, Application US/08268348A
; Patent No. 5750374
; GENERAL INFORMATION:
; APPLICANT: Dobeli, Heinz
; APPLICANT: Draeger, Nicholas
; APPLICANT: Trottman, Gerd H
; APPLICANT: Jakob, Peter
; APPLICANT: Stuber, Dietrich
; TITLE OF INVENTION: Process for Producing Hydrophobic
; Polypeptides and Proteins, and Fusion Proteins for Use in
; Title of Invention: Producing Same
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US-08/268,348A
; FILING DATE: 29-JUN-1994
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: EP 93110755.1
; FILING DATE: 06-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Parisi, John P.
; REGISTRATION NUMBER: 34,403
; REFERENCE/DOCKET NUMBER: 4105/157
; TELECOMMUNICATION INFORMATION:
;
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;TELEPHONE: (201) 235-6326
;TELEFAX: (201) 235-3500
;INFORMATION FOR SEQ ID NO: 9:
;SEQUENCE CHARACTERISTICS:
; LENGTH: 520 base Pairs
; TYPE: Ducleic acid
; STRANDEDNESS: single
; TOPOLOGY: Linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE: LOCATION: 115-516
; OTHER INFORMATION: /product= "Amyloid Protein AA"
; US-08-268-348A-9

alignment_scores:
Quality: 16.00 Length: 16
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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1 ASPAlaGluPheArgHisAspSerGlyTyrGluValHisHisGlnLys 16
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1222 GATGAGAATTCCGACATGACTCAGGATATGAAGTTCATCATCAAAA 1269

alignment_scores:
Quality: 16.00 Length: 16
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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Align seg 1/1 to: US-08-268-348A-9 from: 1 to: 520
1 ASPAlaGluPheArgHisAspSerGlyTyrGluValHisHisGlnLys 16
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388 GATGGGGAGTCCTCGTCATGATTCAGCTATGAAGTCCACATCAAAA 435

seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq;US-08-480-498-3

seq_documentation_block:
Sequence 3 Application US/08480498
; Patent No. 5744346
; GENERAL INFORMATION:
; APPLICANT: Chrysler, Susanna M.S.
; APPLICANT: Sinha, Subranto
; APPLICANT: Keim, Pamela S.
; APPLICANT: Anderson, John P.
; TITLE OF INVENTION: Beta-Secretase
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Stewart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Parentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,498
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Reslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 015570-002200
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2422
; TELEFAX: 415-326-2400
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1521 base Pairs
; TYPE: Ducleic acid
; STRANDEDNESS: single
; TOPOLOGY: Linear
; MOLECULE TYPE: DNA (genomic)
; US-08-480-498-3

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GenCore version 4.5  
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## OM protein - protein search, using sw model

Run on: September 13, 2000, 02:25:55 ; Search time 17:58 Seconds  
(without alignments)  
56.323 Million cell updates/sec

Title: US-09-155-076-2  
Perfect score: 16  
Sequence: 1 DAEFRHDSGYEVHKQ 16

Scoring table: OLIGO  
Gappp 60.0 , Gapext 60.0

Searched: 178050 seqs, 61884766 residues

Word size : 0

Total number of hits satisfying chosen parameters: 178050

Minimum DB seq length: 0  
Maximum DB seq length: 1000000

## Post-processing: Listing first 45 summaries

Database : PIR64:  
1: pirl:  
2: PIR2:  
3: PIR3:  
4: PIR4:  
A:Residues: 1-42 <SH1>  
C:Superfamily: Alzheimer's disease amyloid beta protein; amyloid

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID    | Description          |
|------------|-------|-------------|--------|----------|----------------------|
| 1          | 16    | 100.0       | 42     | 2 PN0512 | beta-amyloid prote   |
| 2          | 16    | 100.0       | 57     | 2 E60045 | Alzheimer's disease  |
| 3          | 16    | 100.0       | 57     | 2 F60045 | Alzheimer's disease  |
| 4          | 16    | 100.0       | 57     | 2 G60045 | Alzheimer's disease  |
| 5          | 16    | 100.0       | 57     | 2 D60045 | Alzheimer's disease  |
| 6          | 16    | 100.0       | 57     | 2 A60045 | Alzheimer's disease  |
| 7          | 16    | 100.0       | 57     | 2 B60045 | Alzheimer's disease  |
| 8          | 16    | 100.0       | 82     | 2 PQ0438 | Alzheimer's disease  |
| 9          | 16    | 100.0       | 695    | 1 A49795 | Alzheimer's disease  |
| 10         | 16    | 100.0       | 770    | 1 QRHUA4 | Alzheimer's disease  |
| 11         | 7     | 43.8        | 747    | 2 JH0773 | Alzheimer's disease  |
| 12         | 6     | 37.5        | 122    | 2 S54715 | probable aspartate   |
| 13         | 6     | 37.5        | 284    | 2 S04723 | genome polypeptide   |
| 14         | 6     | 37.5        | 313    | 2 JT0960 | polypeptide - polype |
| 15         | 6     | 37.5        | 327    | 2 S11435 | genome polypeptide   |
| 16         | 6     | 37.5        | 330    | 2 A26205 | coot protein precu   |
| 17         | 6     | 37.5        | 379    | 2 S13556 | genome polypeptide   |
| 18         | 6     | 37.5        | 380    | 2 G69277 | branched-chain ami   |
| 19         | 6     | 37.5        | 397    | 2 T11786 | aspartate transam    |
| 20         | 6     | 37.5        | 427    | 2 JA0073 | genome polypeptide   |
| 21         | 6     | 37.5        | 453    | 2 C69543 | hypothetical prote   |
| 22         | 6     | 37.5        | 519    | 2 PC1012 | nuclear inclusion    |
| 23         | 6     | 37.5        | 761    | 2 T15776 | hypothetical prote   |
| 24         | 6     | 37.5        | 846    | 2 A60678 | genome polypeptide   |
| 25         | 6     | 37.5        | 1555   | 2 JT0959 | polypeptide - polyp  |
| 26         | 6     | 37.5        | 3063   | 1 JN0545 | genome polypeptide   |
| 27         | 6     | 37.5        | 3063   | 2 JS0166 | genome polypeptide   |
| 28         | 5     | 31.2        | 58     | 2 D69449 | hypothetical prote   |
| 29         | 5     | 31.2        | 203    | 1 BYECRV | periplasmic divale   |

## ALIGNMENTS

| RESULT  | Match  | Score  | Length | DB  | Score  | Length | DB  | Score  | Length | DB  | Score  | Length | DB  | Score  | Length | DB  | Score  | Length | DB  |
|---|--|--------|--------|---|--|--------|---|--|--------|---|--|--------|---|--|--------|---|--|--------|---|
| PN0512  | beta-amyloid protein - guinea pig (fragment) | 100.0% | 42     | PN0512  | beta-amyloid protein - guinea pig (fragment) | 100.0% | PN0512  | beta-amyloid protein - guinea pig (fragment) | 100.0% | PN0512  | beta-amyloid protein - guinea pig (fragment) | 100.0% | PN0512  | beta-amyloid protein - guinea pig (fragment) | 100.0% | PN0512  | beta-amyloid protein - guinea pig (fragment) | 100.0% | PN0512  |
| C:Species: Cavia Porcellus (guinea pig)   |  |        |        | C:Species: Cavia Porcellus (guinea pig)   |  |        | C:Species: Cavia Porcellus (guinea pig)   |  |        | C:Species: Cavia Porcellus (guinea pig)   |  |        | C:Species: Cavia Porcellus (guinea pig)   |  |        | C:Species: Cavia Porcellus (guinea pig)   |  |        | C:Species: Cavia Porcellus (guinea pig)   |
| C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999           |  |        |        | C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999           |  |        | C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999           |  |        | C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999           |  |        | C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999           |  |        | C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999           |  |        |   |
| C:Accession: PN0512   |  |        |        | C:Accession: PN0512   |  |        | C:Accession: PN0512   |  |        | C:Accession: PN0512   |  |        | C:Accession: PN0512   |  |        | C:Accession: PN0512   |  |        | C:Accession: PN0512   |
| R;Shimohigashi, Y.; Matsunoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno |  |        |        | R;Shimohigashi, Y.; Matsunoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno |  |        | R;Shimohigashi, Y.; Matsunoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno |  |        | R;Shimohigashi, Y.; Matsunoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno |  |        | R;Shimohigashi, Y.; Matsunoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno |  |        | R;Shimohigashi, Y.; Matsunoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno |  |        |   |
| A:Title: Receptor-mediated specific biological activity of a beta-amyloid protein fra |  |        |        | A:Title: Receptor-mediated specific biological activity of a beta-amyloid protein fra |  |        | A:Title: Receptor-mediated specific biological activity of a beta-amyloid protein fra |  |        | A:Title: Receptor-mediated specific biological activity of a beta-amyloid protein fra |  |        | A:Title: Receptor-mediated specific biological activity of a beta-amyloid protein fra |  |        | A:Title: Receptor-mediated specific biological activity of a beta-amyloid protein fra |  |        | A:Title: Receptor-mediated specific biological activity of a beta-amyloid protein fra |
| A:Reference number: PN0512; MUID:93290653   |  |        |        | A:Reference number: PN0512; MUID:93290653   |  |        | A:Reference number: PN0512; MUID:93290653   |  |        | A:Reference number: PN0512; MUID:93290653   |  |        | A:Reference number: PN0512; MUID:93290653   |  |        | A:Reference number: PN0512; MUID:93290653   |  |        | A:Reference number: PN0512; MUID:93290653   |
| A:Molecule type: Protein  |  |        |        | A:Molecule type: Protein  |  |        | A:Molecule type: Protein  |  |        | A:Molecule type: Protein  |  |        | A:Molecule type: Protein  |  |        | A:Molecule type: Protein  |  |        | A:Molecule type: Protein  |
| C:Keywords: alternative splicing; amyloid   |  |        |        | C:Keywords: alternative splicing; amyloid   |  |        | C:Keywords: alternative splicing; amyloid   |  |        | C:Keywords: alternative splicing; amyloid   |  |        | C:Keywords: alternative splicing; amyloid   |  |        | C:Keywords: alternative splicing; amyloid   |  |        | C:Keywords: alternative splicing; amyloid   |

Query Match Score 16; Length 42;  
Best Local Similarity 100.0%; Pred. No. 4.2e-12; Mismatches 0; Indels 0; Gaps 0;

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Best Local Similarity 100.0%; Pred. No. 4.2e-12; Mismatches 0; Indels 0; Gaps 0;

Query Match Score 16; Length 57;  
Best Local Similarity 100.0%; Pred. No. 5.5e-12; Mismatches 0; Indels 0; Gaps 0;

Query Match Score 16; Length 57;  
Best Local Similarity 100.0%; Pred. No. 5.5e-12; Mismatches 0; Indels 0; Gaps 0;

Query Match Score 16; Length 57;  
Best Local Similarity 100.0%; Pred. No. 5.5e-12; Mismatches 0; Indels 0; Gaps 0;

Query Match Score 16; Length 57;  
Best Local Similarity 100.0%; Pred. No. 5.5e-12; Mismatches 0; Indels 0; Gaps 0;

| RESULT   | 3  | Query Match<br>Best Local Similarity<br>Matches | 100.0%;<br>16; Conservat | Score 16;<br>DB 2; Length 57; |  |
|--|--|---|--------------------------|-------------------------------|--|
| F60045   | A: Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)        |   |                          |                               |  |
| C;Species: Sus scrofa domestica (domestic pig)   |  |   |                          |                               |  |
| C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999              |  |   |                          |                               |  |
| R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.                 |  |   |                          |                               |  |
| A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, |  |   |                          |                               |  |
| A;Reference number: A60045; MUID:92017079  |  |   |                          |                               |  |
| A;Molecule type: mRNA  |  |   |                          |                               |  |
| A;Residues: 1-57 <JOH>   |  |   |                          |                               |  |
| A;Cross-references: EMBL:X56127; NIDB:gi1895; PIDN:AA30592_1; PID:gi1896                 |  |   |                          |                               |  |
| C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1 |  |   |                          |                               |  |
| C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain                    |  |   |                          |                               |  |
| Query Match<br>Best Local Similarity<br>Matches  | 100.0%;<br>16; Conservat   | Score 16;<br>Pred. No. 5.5e-12;                 | DB 2; Length 57;         |                               |  |
| Qy 1 DAEFRHDSGYEVHK 16   |  |   |                          |                               |  |
| Db 6 DAEFRHDSGYEVHK 21   |  |   |                          |                               |  |
| RESULT   | 4  | Query Match<br>Best Local Similarity<br>Matches | 100.0%;<br>16; Conservat | Score 16;<br>DB 2; Length 57; |  |
| G60045   | A: Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment) |   |                          |                               |  |
| C;Species: Cavia porcellus (guinea pig)  |  |   |                          |                               |  |
| C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995              |  |   |                          |                               |  |
| R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.                 |  |   |                          |                               |  |
| A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, |  |   |                          |                               |  |
| A;Reference number: A60045; MUID:92017079  |  |   |                          |                               |  |
| A;Molecule type: mRNA  |  |   |                          |                               |  |
| A;Residues: 1-57 <JOH>   |  |   |                          |                               |  |
| A;Cross-references: EMBL:X56126  |  |   |                          |                               |  |
| C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1 |  |   |                          |                               |  |
| C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain                    |  |   |                          |                               |  |
| Query Match<br>Best Local Similarity<br>Matches  | 100.0%;<br>16; Conservat   | Score 16;<br>Pred. No. 5.5e-12;                 | DB 2; Length 57;         |                               |  |
| Qy 1 DAEFRHDSGYEVHK 16   |  |   |                          |                               |  |
| Db 6 DAEFRHDSGYEVHK 21   |  |   |                          |                               |  |
| RESULT   | 5  | Query Match<br>Best Local Similarity<br>Matches | 100.0%;<br>16; Conservat | Score 16;<br>DB 2; Length 57; |  |
| D60045   | A: Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)     |   |                          |                               |  |
| C;Species: Bos primigenius taurus (cattle)   |  |   |                          |                               |  |
| C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995              |  |   |                          |                               |  |
| R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.                 |  |   |                          |                               |  |
| A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, |  |   |                          |                               |  |
| A;Reference number: A60045; MUID:92017079  |  |   |                          |                               |  |
| A;Molecule type: mRNA  |  |   |                          |                               |  |
| A;Residues: 1-57 <JOH>   |  |   |                          |                               |  |
| A;Cross-references: EMBL:X56124  |  |   |                          |                               |  |
| C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1 |  |   |                          |                               |  |
| C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain                    |  |   |                          |                               |  |
| Query Match<br>Best Local Similarity<br>Matches  | 100.0%;<br>16; Conservat   | Score 16;<br>Pred. No. 5.5e-12;                 | DB 2; Length 57;         |                               |  |
| Qy 1 DAEFRHDSGYEVHK 16   |  |   |                          |                               |  |
| Db 6 DAEFRHDSGYEVHK 21   |  |   |                          |                               |  |
| RESULT   | 8  | Query Match<br>Best Local Similarity<br>Matches | 100.0%;<br>16; Conservat | Score 16;<br>DB 2; Length 57; |  |
| PQ0438   | A: Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)          |   |                          |                               |  |
| C;Species: Oryctolagus cuniculus (domestic rabbit)                                       |  |   |                          |                               |  |
| C;Date: 30-Sep-1993 #sequence_revision 19-Oct-1995                                       |  |   |                          |                               |  |
| R;Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.                             |  |   |                          |                               |  |
| Biochem. Biophys. Res. Commun. 188, 905-911, 1992  |  |   |                          |                               |  |
| A;Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precurs    |  |   |                          |                               |  |
| A;Reference number: PQ0438; MUID:93075180  |  |   |                          |                               |  |

A; Accession: P00438  
 A; Molecule type: DNA  
 A; Residues: 1-82 <D&gt;  
 A; Cross-references: GB:M83558; GB:M83657  
 Brain Res., E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
 Brain Res. Mol. Brain Res. 10, 289-305, 1991  
 A; Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
 A; Reference number: A60045; MUID:92017079  
 A; Accession: C60045  
 A; Molecule type: mRNA  
 A; Residues: 12-68 <JOF>  
 A; Cross-references: EMBL:X56129  
 C; Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1  
 C; Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 100.0%; Score 16; DB 2; Length 82;  
 Best Local Similarity 100.0%; Pred. No. 7.6e-12;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHK 16  
 Db 17 DAEFRHDSGYEVHK 32

RESULT 9

A49795 Alzheimer's disease amyloid beta protein precursor - crab-eating macaque  
 C; Species: Macaca fascicularis (crab-eating macaque)  
 C; Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 R; Podlisny, M.B.; Tolan, D.R.; Selkoe, D.J.  
 Am J Pathol. 138, 1423-1435, 1991  
 A; Title: Homology of the amyloid beta protein precursor in monkey and human supports a P  
 A; Reference number: A49795; MUID:91273117  
 A; Accession: A49795  
 A; Status: preliminary  
 A; Molecule type: mRNA  
 A; Residues: 1-695 <P0D>  
 A; Cross-references: GB:M58727; NID:9142062; PIDN:AAA36839; PID:9342063  
 C; Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1  
 C; Keywords: alternative splicing

Query Match 100.0%; Score 16; DB 1; Length 95;  
 Best Local Similarity 100.0%; Pred. No. 5e-11;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHK 16  
 Db 597 DAEFRHDSGYEVHK 612

RESULT 10

Q9HQA4 Alzheimer's disease amyloid beta protein precursor - human  
 N; Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor XIa inhibitor  
 N; Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular  
 protein precursor splice form APP(770)

C; Species: Homo sapiens (man)  
 C; Date: 30-Jun-1987 #sequence\_revision 28-Jul-1995 #text\_change 24-Nov-1999  
 C; Accession: S02260; S05194; A32277; A31260; A35466; I39451; I39453; I59562; A444668; A28581; A23302; A6005; JU0038; SO6121; A60355; A59011; A38384; S29076; S38222; S38224  
 R; Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayne, R.M.; Unterbeck, A.; Bey  
 Nucleic Acids Res. 17, 517-522, 1989  
 A; Title: The ProA4 (695) precursor protein of Alzheimer's disease A4 amyloid is encoded by  
 A; Reference number: S02260; MUID:89128427  
 A; Accession: S02260  
 A; Molecule type: DNA  
 A; Residues: 1-288, 'V', 365-770 <LEM1>  
 A; Cross-references: EMBL:X13466  
 A; Note: alternative splice form APP(695)  
 R; Lemaire, H.G.

Alzheimer's disease amyloid beta protein precursor - human  
 N; Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular  
 protein precursor splice form APP(770)

C; Date: 30-Jun-1987 #sequence\_revision 28-Jul-1995 #text\_change 24-Nov-1999  
 C; Accession: S02260; S05194; A32277; A31260; A35466; I39451; I39453; I59562; A444668; A28581; A23302; A6005; JU0038; SO6121; A60355; A59011; A38384; S29076; S38222; S38224  
 R; Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayne, R.M.; Unterbeck, A.; Bey  
 Nucleic Acids Res. 17, 517-522, 1989  
 A; Title: The ProA4 (695) precursor protein of Alzheimer's disease A4 amyloid is encoded by  
 A; Reference number: S02260; MUID:89128427  
 A; Molecule type: DNA  
 A; Residues: 1-288, 'V', 365-770 <LEM1>  
 A; Cross-references: EMBL:X13466  
 A; Note: alternative splice form APP(695)  
 R; Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayne, R.M.; Unterbeck, A.; Bey  
 Nucleic Acids Res. 17, 517-522, 1989  
 A; Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for t

Submitted to the EMBL Data Library, November 1998  
 A; Reference number: S05194  
 A; Accession: S05194  
 A; Molecule type: DNA  
 A; Residues: 1-14, 'W', 17-288, 'V', 365-770 <LEM2>  
 A; Cross-references: EMBL:X13166; NID:935598; PIDN:CAA31830.1; PID:9171360  
 A; Note: alternative splice form APP(695)  
 R; La Fauci, G.; Lahiru, D.K.; Salton, S.R.J.; Robakis, N.K.  
 Biochem. Biophys. Res. Commun. 159, 297-304, 1989  
 A; Title: Characterization of the 5'-end region and the first two exons of the beta-pr  
 A; Reference number: A32277  
 A; Accession: A32277  
 A; Molecule type: DNA  
 A; Residues: 1-75 <AF>  
 A; Cross-references: GB:M24546; GB:M24547; NID:9341202; PIDN:AA1364.1; PID:9151604  
 R; Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.  
 Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989  
 A; Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows simila  
 A; Reference number: A33260; MUID:89392030  
 A; Accession: A33260  
 A; Molecule type: DNA  
 A; Residues: 656-737 <JOH>  
 A; Cross-references: GB:M29270; NID:9178863; PIDN:AAA51768.1; PID:9178865  
 R; Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B  
 Biochem. Biophys. Res. Commun. 170, 301-307, 1990  
 A; Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid  
 A; Reference number: A35486; MUID:9032244  
 A; Accession: A35486  
 A; Molecule type: DNA  
 A; Residues: 672-710 <PREI>  
 A; Note: 693-Gln was found in DNA isolated from HCHWA-D patients  
 R; Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.  
 Gene 87, 257-263, 1990  
 A; Title: Genomic organization of the human amyloid beta-protein precursor gene  
 A; Reference number: I39451; MUID:9023318  
 A; Accession: I39452  
 A; Status: nucleic acid sequence not shown; translation not shown; translated from GB/  
 A; Molecule type: DNA  
 A; Residues: 1-770 <YOS1>  
 A; Cross-references: GB:M33112; NID:9178613; PIDN:AA859502.1; PID:9178615  
 A; Status: nucleic acid sequence not shown; translation not shown; translated from GB/  
 A; Residues: 1-530, 'QWLMVPVPAWEAKVGR', <YOS2>  
 A; Cross-references: GB:M34875; NID:9178608; PIDN:AA859501.1; PID:9178616  
 A; Status: nucleic acid sequence not shown; translation not shown; translated from GB/  
 A; Molecule type: DNA  
 A; Residues: 1-770 <YOS3>  
 A; Cross-references: GB:M33112; NID:9178613; PIDN:AA859502.1; PID:9178615  
 A; Status: mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemo  
 A; Molecule type: DNA  
 A; Residues: 656-737 <LEV>  
 A; Cross-references: GB:M37866; NID:9178618; PIDN:AAA51727.1; PID:9178620  
 A; Note: a mutation with 693-Gln is presented  
 R; Murray, J.; Farlow, M.; Ghetti, B.; Benson, M.D.  
 Science 254, 97-99, 1991  
 A; Title: A mutation in the amyloid precursor protein associated with hereditary Alzhe  
 A; Accession: I39452  
 A; Status: translated from GB/EMBL/DDJB  
 A; Molecule type: DNA  
 A; Residues: 689-716, 'F', 718-737 <MUR>  
 A; Cross-references: GB:S57665; NID:9236721  
 R; Ramino, K.; Orr, H.T.; Payami, H.; Wijman, E.M.; Alonso, M.E.; Puist, S.M.; Anders  
 arkis, S.E.; Korenberg, J.R.; Sharma, V.; Larsson, E.; Heston, L.L.; Mart  
 Am J Hum. Genet. 51, 998-1014, 1992



Qy 10 YEVHHQ 16  
 Db 658 YEVHHQ 664

**RESULT 12**  
 S54715 probable aspartate transaminase (EC 2.6.1.1) - *Streptomyces coelicolor* (fragment)  
 C;Species: *Streptomyces coelicolor*  
 C;Date: 23-Aug-1995 #sequence\_revision 12-Dec-1997 #text\_change 13-Sep-1998  
 C;Accession: S54715  
 R;Partikkun, C.; Nihira, T.; Yamada, Y.  
*Mol. Gen. Genet.* 247, 118-122, 1995  
 A;Title: Cloning, nucleotide sequence, and transcriptional analysis of the nusG gene of  
 A;Reference number: S54715; MUID:95231511  
 A;Molecule type: DNA  
 A;Cross-references: EMBL:D32254  
 A;Experimental source: strain A3(2), substrate SC  
 C;Superfamily: aspartate transaminase  
 C;Keywords: aminotransferase

Query Match 37.5%; Score 6; DB 2; Length 313;  
 Best Local Similarity 100.0%; Pred. No. 7.6;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 YEVHHQ 15  
 Db 41 YEVHHQ 46

**RESULT 15**  
 S11435 genome polyprotein - potato virus Y (fragment)  
 N;Contains: coat protein; NIB protein  
 C;Species: potato virus Y, PVY  
 C;Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 20-Sep-1999  
 C;Accession: S11435; S11549; JC1526  
 R;Zhou, X.R.; Fang, R.X.; Wang, C.Q.; Mang, K.Q.  
*Nucleic Acids Res.* 18, 5554, 1990  
 A;Title: cDNA sequence of the 3'-coding region of PVY genome (the Chinese isolate).  
 A;Reference number: S11435; MUID:91016851  
 A;Molecule type: mRNA  
 A;Cross-references: 1-327 <ZH01>  
 A;Residues: 1-327 <ZH01>  
 R;Zhou, X.R.  
 submitted to the EMBL Data Library, July 1990  
 A;Reference number: S11435  
 A;Molecule type: mRNA  
 A;Cross-references: EMBL:X54058; NID:961219; PIDN:CAA37993.1; PID:9833159  
 R;Oshima, K.; Hayata, T.; Sano, T.; Inoue, A.K.; Shikata, E.  
*Ann. Phytopathol. Soc. Jpn.* 57, 615-622, 1991  
 A;Title: Comparison of biological properties, serological characteristics and amino acid sequence of the 3'-terminal region of the genome of PVY.  
 A;Reference number: JC1526  
 A;Accession: JC1526  
 A;Molecule type: genomic RNA  
 A;Residues: 61-687<EI>,71-737<ES>,76-111,<S>,113-201,<E>,203-327 <OHS>  
 C;Genetics:  
 A;Start codon: CGA  
 C;Superfamily: tobacco etch virus genome polyprotein; DEAD/H box helicase homology  
 C;Keywords: coat protein; polyprotein  
 F;61-327/Product: coat protein #status predicted <COP>

**RESULT 13**  
 S04723 genome polyprotein - potato virus Y (strain o) (fragment)  
 N;Contains: coat protein; replicase  
 C;Species: potato virus Y, PVV  
 C;Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 20-Sep-1999  
 C;Accession: S04723  
 R;Bravo-Almonacid, F.; Mentaberri, A.N.  
*Nucleic Acids Res.* 17, 4401, 1989  
 A;Title: Nucleotide cDNA sequence coding for the PVYO coat protein.  
 A;Reference number: S04723; MUID:89296509  
 A;Accession: S04723  
 A;Status: translation not shown  
 A;Molecule type: genomic RNA  
 A;Residues: 1-204 <BR>  
 A;Cross-references: EMBL:X14136; NID:g61445; PIDN:CAA32356.1; PID:g61446  
 C;Superfamily: tobacco etch virus genome polyprotein; DEAD/H box helicase homology  
 C;Keywords: polyprotein

Query Match 37.5%; Score 6; DB 2; Length 284;  
 Best Local Similarity 100.0%; Pred. No. 6.9;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 YEVHHQ 15  
 Db 12 YEVHHQ 17

**RESULT 14**  
 JT0960 polyprotein - potato virus Y  
 N;Contains: coat protein  
 C;Species: potato virus Y, PVY  
 C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 29-May-1998  
 C;Accession: JT0960  
 R;Hidaka, M.  
 Submitted to JIPID, November 1991  
 A;Reference number: JT0959

Search completed: September 13, 2000, 02:25:56  
 Job time: 139 sec



| SUMMARIES  |       |             |        |            |                            |  |  |
|------------|-------|-------------|--------|------------|----------------------------|--|--|
| Result No. | Score | Query Match | Length | DB ID      | Description                |  |  |
| 1          | 16    | 100.0       | 57     | A4_PIG     | Q29023 sus scrofa          |  |  |
| 2          | 16    | 100.0       | 57     | A4_DRMSA   | Q29149 ursus marit         |  |  |
| 3          | 16    | 100.0       | 58     | A4_CANFA   | Q28240 canis famili        |  |  |
| 4          | 16    | 100.0       | 58     | A4_CANFA   | Q28748 oryctoferus         |  |  |
| 5          | 16    | 100.0       | 58     | A4_SHEEP   | Q28757 ovis aries          |  |  |
| 6          | 16    | 100.0       | 59     | A4_BOVIN   | Q28053 bos taurus          |  |  |
| 7          | 16    | 100.0       | 751    | A4_SAISC   | Q95241 saimiri sci         |  |  |
| 8          | 16    | 100.0       | 770    | A4_HUMAN   | P05067 homo sapien         |  |  |
| 9          | 6     | 37.5        | 213    | AAT_STKRY  | P36652 streptomyces        |  |  |
| 10         | 6     | 37.5        | 284    | POLG_PVYXY | P11837 potato virus        |  |  |
| 11         | 6     | 37.5        | 327    | POLG_PVYCH | P21394 potato virus        |  |  |
| 12         | 6     | 37.5        | 330    | COAT_PMV   | P07933 pepper mott         |  |  |
| 13         | 6     | 37.5        | 397    | AAT_STKRG  | Q60013 streptomyces        |  |  |
| 14         | 6     | 37.5        | 3061   | POLG_PVYHU | Q22653 genome po           |  |  |
| 15         | 6     | 37.5        | 3063   | POLG_PVYHU | Q9904 aeropyrum p          |  |  |
| 16         | 5     | 31.2        | 90     | EF1B_AERPE | P21172 micrococcus         |  |  |
| 17         | 5     | 31.2        | 132    | RNP4_MICLU | P11293 thermus aqu         |  |  |
| 18         | 5     | 31.2        | 135    | RS12_THE7  | P28161 branchniostoma      |  |  |
| 19         | 5     | 31.2        | 144    | SODM_BRAFL | Q09858 schizosaccharomyces |  |  |
| 20         | 5     | 31.2        | 145    | YAF4_SCCHO | Q46331 miophiteicus        |  |  |
| 21         | 5     | 31.2        | 150    | RNK6_MIOTA | P11291 escherichia         |  |  |
| 22         | 5     | 31.2        | 161    | YZCX_ECOLI | P08576 escherichia         |  |  |
| 23         | 5     | 31.2        | 203    | RUV4_ECOLI | P30066 bacillus su         |  |  |
| 24         | 5     | 31.2        | 214    | ACUB_BACSL | P29151 satellite m         |  |  |
| 25         | 5     | 31.2        | 218    | COAT_SMWLM | P32478 bacillus su         |  |  |
| 26         | 5     | 31.2        | 235    | YYCF_BACSU | P08662 homo sapien         |  |  |
| 27         | 5     | 31.2        | 237    | CD63_HUMAN | P44731 mus musculus        |  |  |
| 28         | 5     | 31.2        | 237    | CD63_MOUSE | P268709 oryctolagus        |  |  |
| 29         | 5     | 31.2        | 237    | CD63_RABIT | P26648 rattus norvegicus   |  |  |
| 30         | 5     | 31.2        | 258    | FABL_SYN3  | P73016 synechocystis       |  |  |
| 31         | 5     | 31.2        | 285    | PNMT_RAT   | P10937 rattus norvegicus   |  |  |
| 32         | 5     | 31.2        | 285    | ATHB_MOUSE | P50992 mus musculus        |  |  |

| ALIGNMENTS   |                 |                   |      |        |      |                       |   |
|--|-----------------|-------------------|------|--------|------|-----------------------|---|
| Scoring table:                                     | OLIGO           | Gapop             | 60.0 | Gapext | 60.0 | RESULT                | 1   |
| Searched:  | 85661 seqs,     | 30989116 residues |      |        |      | A4_PIG                |   |
| Word size :  | 0               |                   |      |        |      | ID                    | A4_PIG  |
| Total number of hits satisfying chosen parameters: | 85661           |                   |      |        |      | AC                    | Q29023;   |
| Minimum DB seq length:                             | 0               |                   |      |        |      | DT                    | 01-Nov-1997 (Rel. 35, created)  |
| Maximum DB seq length:                             | 1000000         |                   |      |        |      | DT                    | 01-Nov-1997 (Rel. 35, last sequence update)   |
| Post-processing: Listing first 45 summaries        |                 |                   |      |        |      | DT                    | 15-Jul-1999 (Rel. 38, last annotation update)   |
| Database :   | SwissProt_38.2* |                   |      |        |      | DE                    | ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID PROTEIN (BETA-APP) (FRAGMENT)].  |
| Scoring table:                                     | OLIGO           | Gapop             | 60.0 | Gapext | 60.0 | GN                    | APP.  |
|  |                 |                   |      |        |      | OS                    | Sus scrofa (pig).   |
|  |                 |                   |      |        |      | OC                    | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.   |
|  |                 |                   |      |        |      | RN                    | SEQUENCE FROM N.A.  |
|  |                 |                   |      |        |      | RC                    | TISSUE-BRAIN.   |
|  |                 |                   |      |        |      | MDLINE                | ; 92017079.   |
|  |                 |                   |      |        |      | RA                    | "Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.; "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis."  |
|  |                 |                   |      |        |      | RL                    | Brain Res. Mol. Brain Res. 10:299-305 (1991).   |
|  |                 |                   |      |        |      | CC                    | -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN (GO) (BY SIMILARITY).   |
|  |                 |                   |      |        |      | CC                    | -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  |
|  |                 |                   |      |        |      | CC                    | -1- SIMILARITY: BELONGS TO THE APP FAMILY.  |
|  |                 |                   |      |        |      | CC                    | This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch). |
|  |                 |                   |      |        |      | CC                    | CC  |
|  |                 |                   |      |        |      | CC                    | CC  |
|  |                 |                   |      |        |      | CC                    | CC  |
|  |                 |                   |      |        |      | CC                    | CC  |
|  |                 |                   |      |        |      | DR                    | X56127; CAA39592.1; -.  |
|  |                 |                   |      |        |      | DR                    | HSSP: P05067; IAML.   |
|  |                 |                   |      |        |      | DR                    | PROSITE: PS00319; A4_EXTRA; PARTIAL.  |
|  |                 |                   |      |        |      | DR                    | PROSITE: PS00320; A4_INTRNA; PARTIAL.   |
|  |                 |                   |      |        |      | FT                    | GLYCcoprotein; Amyloid; Neurone; Transmembrane.   |
|  |                 |                   |      |        |      | FT                    | NON-TER   |
|  |                 |                   |      |        |      | FT                    | 1 1   |
|  |                 |                   |      |        |      | FT                    | CHAIN   |
|  |                 |                   |      |        |      | FT                    | 6 48  |
|  |                 |                   |      |        |      | FT                    | BETA-AMYLOID PROTEIN (POTENTIAL).   |
|  |                 |                   |      |        |      | FT                    | DOMAIN  |
|  |                 |                   |      |        |      | FT                    | <1 33   |
|  |                 |                   |      |        |      | FT                    | EXTRACELLULAR (POTENTIAL).  |
|  |                 |                   |      |        |      | FT                    | POTENTIAL.  |
|  |                 |                   |      |        |      | FT                    | NON-TER   |
|  |                 |                   |      |        |      | FT                    | 57 57   |
|  |                 |                   |      |        |      | SQ                    | SEQUENCE 57 AA: 6172 MW; 84203D88PEBA82DFEA CRC64;  |
|  |                 |                   |      |        |      | Query                 | Match   |
|  |                 |                   |      |        |      | Best Local Similarity | 100.0%; Score 16; DB 1; Length 57;  |
|  |                 |                   |      |        |      | Matches               | 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;   |
|  |                 |                   |      |        |      | Db                    | 1 DAEFRHDSGYEVHHQK 16<br>1                  <br>6 DAEFRHDSGYEVHHQK 21   |

RESULT 2

|   |                                   |      |        |
|---|-----------------------------------|------|--------|
| A4_URSMA  | STANDARD;                         | PRT; | 57 AA. |
| ID Q29149;  |                                   |      |        |
| AC DT 01-NOV-1997   | (Rel. 35, Created)                |      |        |
| DT 01-NOV-1997  | (Rel. 35, Last sequence update)   |      |        |
| DT 15-JUL-1999  | (Rel. 38, Last annotation update) |      |        |
| DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID PROTEIN (BETA-APP) (FRAGMENT)].   |                                   |      |        |
| GN APP.   |                                   |      |        |
| OS Ursus maritimus (Polar bear) (Thalarctos maritimus).   |                                   |      |        |
| OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Tharactros.  |                                   |      |        |
| RN [1] SEQUENCE FROM N.A.   |                                   |      |        |
| RP TISSUE-KIDNEY; TISSUE-BRAIN;   |                                   |      |        |
| RC MEDLINE; 92017079.   |                                   |      |        |
| RX  |                                   |      |        |
| RA Johnston E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;  |                                   |      |        |
| PT "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis." |                                   |      |        |
| RT Brain Res. Mol. Brain Res. 10:299-305(1991).   |                                   |      |        |
| RT -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN (G(O)) (BY SIMILARITY).                      |                                   |      |        |
| CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.   |                                   |      |        |
| CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.   |                                   |      |        |

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RESULT 3

|   |                                   |      |        |
|---|-----------------------------------|------|--------|
| A4_CANFA  | STANDARD;                         | PRT; | 58 AA. |
| ID Q28280;  |                                   |      |        |
| AC DT 01-NOV-1997   | (Rel. 35, Created)                |      |        |
| DT 01-NOV-1997  | (Rel. 35, Last sequence update)   |      |        |
| DT 15-JUL-1999  | (Rel. 38, Last annotation update) |      |        |
| DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID PROTEIN (BETA-APP) (FRAGMENT)].   |                                   |      |        |
| GN APP.   |                                   |      |        |
| OS Canis familiaris (Dog).  |                                   |      |        |
| OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.   |                                   |      |        |
| RN [1] SEQUENCE FROM N.A.   |                                   |      |        |
| RP TISSUE-BRAIN;  |                                   |      |        |
| RC MEDLINE; 92017079.   |                                   |      |        |
| RX  |                                   |      |        |
| RA Johnston E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;  |                                   |      |        |
| PT "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis." |                                   |      |        |
| RT Brain Res. Mol. Brain Res. 10:299-305(1991).   |                                   |      |        |
| RT -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN (G(O)) (BY SIMILARITY).                      |                                   |      |        |
| CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.   |                                   |      |        |
| CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.   |                                   |      |        |

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CC EMBL; X56129; CAA39594.1; -.

DR HSSP; P05067; 1AML.  
DR PROSITE; PS00319; A4\_EXTRA; PARTIAL.  
DR PROSITE; PS00320; A4\_INTRA; PARTIAL.

KW Glycoprotein; Amyloid; Neurone; Transmembrane.

FT NON\_TER 1 1 BETA-AMYLOID PROTEIN (POTENTIAL).

FT CHAIN 6 1 EXTRACELLULAR (POTENTIAL).

FT DOMAIN <1 33 POTENTIAL.

FT DOMAIN 34 57 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 58 >58

FT NON\_TER 58 58 MW; F434209D88EBA82D CRC64;

SQ 58 AA; 6300 MW;

RESULT 5

A4\_SHEEP STANDARD; PRT; 58 AA.

AC Q28757; Score 16; DB 1; Length 58;

Best Local Similarity 100.0%; Pred. No. 9.9e-12;

Matches 16; Conservative 0; Mismatches 0; Gaps 0;

QY 1 DAEFRHDSGYEVHK 16

Db 6 DAEFRHDSGYEVHK 21

RESULT 5

A4\_BOVIN STANDARD; PRT; 59 AA.

AC Q28033; Score 16; DB 1; Length 58;

Best Local Similarity 100.0%; Pred. No. 9.9e-12;

Matches 16; Conservative 0; Mismatches 0; Gaps 0;

QY 1 DAEFRHDSGYEVHK 16

Db 6 DAEFRHDSGYEVHK 21

RESULT 5

A4\_BOVIN STANDARD; PRT; 59 AA.

AC Q28033; Score 16; DB 1; Length 58;

Best Local Similarity 100.0%; Pred. No. 9.9e-12;

Matches 16; Conservative 0; Mismatches 0; Gaps 0;

QY 1 DAEFRHDSGYEVHK 16

Db 6 DAEFRHDSGYEVHK 21

RESULT 5

A4\_BOVIN STANDARD; PRT; 59 AA.

AC Q28033; Score 16; DB 1; Length 58;

Best Local Similarity 100.0%; Pred. No. 9.9e-12;

Matches 16; Conservative 0; Mismatches 0; Gaps 0;

QY 1 DAEFRHDSGYEVHK 16

Db 6 DAEFRHDSGYEVHK 21

RESULT 5

A4\_BOVIN STANDARD; PRT; 59 AA.

AC Q28033; Score 16; DB 1; Length 58;

Best Local Similarity 100.0%; Pred. No. 9.9e-12;

Matches 16; Conservative 0; Mismatches 0; Gaps 0;

QY 1 DAEFRHDSGYEVHK 16

Db 6 DAEFRHDSGYEVHK 21

RESULT 5

A4\_BOVIN STANDARD; PRT; 59 AA.

AC Q28033; Score 16; DB 1; Length 58;

Best Local Similarity 100.0%; Pred. No. 9.9e-12;

Matches 16; Conservative 0; Mismatches 0; Gaps 0;

QY 1 DAEFRHDSGYEVHK 16

Db 6 DAEFRHDSGYEVHK 21

RESULT 5

A4\_BOVIN STANDARD; PRT; 59 AA.

AC Q28033; Score 16; DB 1; Length 58;

Best Local Similarity 100.0%; Pred. No. 9.9e-12;

Matches 16; Conservative 0; Mismatches 0; Gaps 0;

QY 1 DAEFRHDSGYEVHK 16

Db 6 DAEFRHDSGYEVHK 21

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CC EMBL; X56129; CAA39595.1; -.

DR HSSP; P05067; 1AHL.

DR PROSITE; PS00319; A4\_EXTRA; PARTIAL.

DR PROSITE; PS00320; A4\_INTRA; PARTIAL.

KW Glycoprotein; Amyloid; Neurone; Transmembrane.

FT NON\_TER 1 1 BETA-AMYLOID PROTEIN (POTENTIAL).

FT CHAIN 7 49 EXTRACELLULAR (POTENTIAL).

FT DOMAIN <1 34 POTENTIAL.

FT DOMAIN 35 58 CYTOPLASMIC (POTENTIAL).

FT DOMAIN >59 >59

FT NON\_TER 59 59 MW; F43469D488A2E12D CRC64;

SQ 59 AA; 6414 MW;

RESULT 5

A4\_BOVIN STANDARD; PRT; 6414 AA.

AC X56124; CAA39595.1; -.

DR X56126; CAA39595.1; -.

DR PROSITE; PS00319; A4\_EXTRA; PARTIAL.

DR PROSITE; PS00320; A4\_INTRA; PARTIAL.

KW Glycoprotein; Amyloid; Neurone; Transmembrane.

FT NON\_TER 1 1 BETA-AMYLOID PROTEIN (POTENTIAL).

FT CHAIN 7 49 EXTRACELLULAR (POTENTIAL).

FT DOMAIN <1 34 POTENTIAL.

FT DOMAIN 35 58 CYTOPLASMIC (POTENTIAL).

FT DOMAIN >59 >59

FT NON\_TER 59 59 MW; F43469D488A2E12D CRC64;

SQ 59 AA; 6414 MW;

RESULT 5

A4\_BOVIN STANDARD; PRT; 6414 AA.

AC X56124; CAA39595.1; -.

DR X56126; CAA39595.1; -.

DR PROSITE; PS00319; A4\_EXTRA; PARTIAL.

DR PROSITE; PS00320; A4\_INTRA; PARTIAL.

KW Glycoprotein; Amyloid; Neurone; Transmembrane.

FT NON\_TER 1 1 BETA-AMYLOID PROTEIN (POTENTIAL).

FT CHAIN 7 49 EXTRACELLULAR (POTENTIAL).

FT DOMAIN <1 34 POTENTIAL.

FT DOMAIN 35 58 CYTOPLASMIC (POTENTIAL).

FT DOMAIN >59 >59

FT NON\_TER 59 59 MW; F43469D488A2E12D CRC64;

SQ 59 AA; 6414 MW;

RESULT 5

A4\_BOVIN STANDARD; PRT; 6414 AA.

AC X56124; CAA39595.1; -.

DR X56126; CAA39595.1; -.

DR PROSITE; PS00319; A4\_EXTRA; PARTIAL.

DR PROSITE; PS00320; A4\_INTRA; PARTIAL.

KW Glycoprotein; Amyloid; Neurone; Transmembrane.

FT NON\_TER 1 1 BETA-AMYLOID PROTEIN (POTENTIAL).

FT CHAIN 7 49 EXTRACELLULAR (POTENTIAL).

FT DOMAIN <1 34 POTENTIAL.

FT DOMAIN 35 58 CYTOPLASMIC (POTENTIAL).

FT DOMAIN >59 >59

FT NON\_TER 59 59 MW; F43469D488A2E12D CRC64;

SQ 59 AA; 6414 MW;

RESULT 5

A4\_BOVIN STANDARD; PRT; 6414 AA.

AC X56124; CAA39595.1; -.

DR X56126; CAA39595.1; -.

DR PROSITE; PS00319; A4\_EXTRA; PARTIAL.

DR PROSITE; PS00320; A4\_INTRA; PARTIAL.

KW Glycoprotein; Amyloid; Neurone; Transmembrane.

FT NON\_TER 1 1 BETA-AMYLOID PROTEIN (POTENTIAL).

FT CHAIN 7 49 EXTRACELLULAR (POTENTIAL).

FT DOMAIN <1 34 POTENTIAL.

FT DOMAIN 35 58 CYTOPLASMIC (POTENTIAL).

FT DOMAIN >59 >59

FT NON\_TER 59 59 MW; F43469D488A2E12D CRC64;

SQ 59 AA; 6414 MW;

RESULT 5

A4\_BOVIN STANDARD; PRT; 6414 AA.

AC X56124; CAA39595.1; -.

DR X56126; CAA39595.1; -.

DR PROSITE; PS00319; A4\_EXTRA; PARTIAL.

DR PROSITE; PS00320; A4\_INTRA; PARTIAL.

KW Glycoprotein; Amyloid; Neurone; Transmembrane.

FT NON\_TER 1 1 BETA-AMYLOID PROTEIN (POTENTIAL).

FT CHAIN 7 49 EXTRACELLULAR (POTENTIAL).

FT DOMAIN <1 34 POTENTIAL.

FT DOMAIN 35 58 CYTOPLASMIC (POTENTIAL).

FT DOMAIN >59 >59

FT NON\_TER 59 59 MW; F43469D488A2E12D CRC64;

SQ 59 AA; 6414 MW;

RESULT 5

A4\_BOVIN STANDARD; PRT; 6414 AA.

AC X56124; CAA39595.1; -.

DR X56126; CAA39595.1; -.

DR PROSITE; PS00319; A4\_EXTRA; PARTIAL.

DR PROSITE; PS00320; A4\_INTRA; PARTIAL.

KW Glycoprotein; Amyloid; Neurone; Transmembrane.

FT NON\_TER 1 1 BETA-AMYLOID PROTEIN (POTENTIAL).

FT CHAIN 7 49 EXTRACELLULAR (POTENTIAL).

FT DOMAIN <1 34 POTENTIAL.

FT DOMAIN 35 58 CYTOPLASMIC (POTENTIAL).

FT DOMAIN >59 >59

FT NON\_TER 59 59 MW; F43469D488A2E12D CRC64;

SQ 59 AA; 6414 MW;

RESULT 5

A4\_BOVIN STANDARD; PRT; 6414 AA.

AC X56124; CAA39595.1; -.

DR X56126; CAA39595.1; -.

DR PROSITE; PS00319; A4\_EXTRA; PARTIAL.

DR PROSITE; PS00320; A4\_INTRA; PARTIAL.

KW Glycoprotein; Amyloid; Neurone; Transmembrane.

FT NON\_TER 1 1 BETA-AMYLOID PROTEIN (POTENTIAL).

FT CHAIN 7 49 EXTRACELLULAR (POTENTIAL).

FT DOMAIN <1 34 POTENTIAL.

FT DOMAIN 35 58 CYTOPLASMIC (POTENTIAL).

FT DOMAIN >59 >59

FT NON\_TER 59 59 MW; F43469D488A2E12D CRC64;

SQ 59 AA; 6414 MW;

RESULT 5

A4\_BOVIN STANDARD; PRT; 6414 AA.

AC X56124; CAA39595.1; -.

DR X56126; CAA39595.1; -.

DR PROSITE; PS00319; A4\_EXTRA; PARTIAL.

DR PROSITE; PS00320; A4\_INTRA; PARTIAL.

KW Glycoprotein; Amyloid; Neurone; Transmembrane.

FT NON\_TER 1 1 BETA-AMYLOID PROTEIN (POTENTIAL).

FT CHAIN 7 49 EXTRACELLULAR (POTENTIAL).

FT DOMAIN <1 34 POTENTIAL.

FT DOMAIN 35 58 CYTOPLASMIC (POTENTIAL).

FT DOMAIN >59 >59

FT NON\_TER 59 59 MW; F43469D488A2E12D CRC64;

SQ 59 AA; 6414 MW;

RESULT 5

A4\_BOVIN STANDARD; PRT; 6414 AA.

AC X56124; CAA39595.1; -.

DR X56126; CAA39595.1; -.

DR PROSITE; PS00319; A4\_EXTRA; PARTIAL.

DR PROSITE; PS00320; A4\_INTRA; PARTIAL.

KW Glycoprotein; Amyloid; Neurone; Transmembrane.

FT NON\_TER 1 1 BETA-AMYLOID PROTEIN (POTENTIAL).

FT CHAIN 7 49 EXTRACELLULAR (POTENTIAL).

FT DOMAIN <1 34 POTENTIAL.

FT DOMAIN 35 58 CYTOPLASMIC (POTENTIAL).

FT DOMAIN >59 >59

FT NON\_TER 59 59 MW; F43469D488A2E12D CRC64;

SQ 59 AA; 6414 MW;

RESULT 5

A4\_BOVIN STANDARD; PRT; 6414 AA.

AC X56124; CAA39595.1; -.

DR X56126; CAA39595.1; -.

DR PROSITE; PS00319; A4\_EXTRA; PARTIAL.

DR PROSITE; PS00320; A4\_INTRA; PARTIAL.

KW Glycoprotein; Amyloid; Neurone; Transmembrane.

FT NON\_TER 1 1 BETA-AMYLOID PROTEIN (POTENTIAL).

FT CHAIN 7 49 EXTRACELLULAR (POTENTIAL).

FT DOMAIN <1 34 POTENTIAL.

FT DOMAIN 35 58 CYTOPLASMIC (POTENTIAL).

FT DOMAIN >59 >59

FT NON\_TER 59 59 MW; F43469D488A2E12D CRC64;

SQ 59 AA; 6414 MW;

RESULT 5

A4\_BOVIN STANDARD; PRT; 6414 AA.

AC X56124; CAA39595.1; -.

DR X56126; CAA39595.1; -.

|                       |  |  |   |
|-----------------------|--|--|---|
| QY                    | 1 DAEFRHDSGYEVHHQK 16<br>1        <br>7 DAEFRHDSGYEVHHQK 22  | RESULT 7<br>A4_SAISC STANDARD; PRT; 751 AA.  | Db 653 DAEFRHDSGYEVHHQK 668<br>RESULT 8<br>A4_HUMAN STANDARD; PRT; 770 AA.  |
| AC                    | Q52411; AC_052411  | ID A4_SAISC; STANDARD; PRT; 751 AA.  | ID A4_HUMAN; STANDARD; PRT; 770 AA.   |
| DT                    | 15-DEC-1998 (Rel. 37, Created)<br>DT 37. Last sequence update)   | ID P05077; P09000; Q16071;<br>AC DT 13-AUG-1987 (Rel. 05, Created)<br>DT 01-NOV-1991 (Rel. 20, Last sequence update)                         |   |
| DT                    | 15-DEC-1998 (Rel. 37, Last sequence update)<br>DT 39. Last annotation update)  | DE 15-FEB-2000 (Rel. 39, Last annotation update)   |   |
| DE                    | ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN PRECURSOR [CONTAINS: BETA-AMYLOID PROTEIN (BETA-APP)].  | DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN PRECURSOR (PROTEASE NEXIN-II) (PNI-II) (APPI). [CONTAINS: BETA-AMYLOID PROTEIN (BETA-APP)].        |   |
| GN                    | APP.   | GN APP OR A4 OR CVAL OR ADL.   |   |
| OS                    | Saimiri sciureus (Common squirrel monkey).   | OS Homo sapiens (Human).   |   |
| OC                    | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.   | OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.              |   |
| RN                    | [1]  | RN [1]   | RN [1]  |
| RP                    | SEQUENCE FROM N.A.<br>RC TISSUE=LIVER, AND KIDNEY;   | RP SEQUENCE FROM N.A.<br>RC TISSUE=BRAIN; MEDLINE: 87144572.   | RP SEQUENCE FROM N.A.<br>RC TISSUE=BRAIN; MEDLINE: 88122339.  |
| CC                    | MEDLINE: 9610892.  | RP Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D., Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.; Cordell B.; | RP Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L., Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.; Cordell B.   |
| CC                    | "Beta-amyloid precursor protein in squirrel monkeys with cerebral amyloid angiopathy".   | RP "The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface receptor." RT RT  | RA "A new A4 amyloid mRNA contains a domain homologous to serine protease inhibitors." RT RT  |
| CC                    | Neurobiol. Aging 16:805-808(1995).   | RP Nature 331:525-527(1998).   | RA Nature 331:525-527(1998).  |
| CC                    | -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O).  | RP SEQUENCE FROM N.A.  | RA RN [3]   |
| CC                    | -- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  | RP MEDLINE: 89128437.  | RA Lemaire H.G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M., Unterbeck A., Beyreuther K., Mueller-Hill B.;   |
| CC                    | -- SIMILARITY: BELONGS TO THE APP FAMILY.  | RP "The PreA(695) precursor protein of Alzheimer's disease A4 amyloid is encoded by 16 exons." RT RT   | RA RA "The PreA(695) precursor protein of Alzheimer's disease A4 amyloid is encoded by 16 exons." RT RT   |
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| CC                    | -----  | RP SEQUENCE FROM N.A.  | RA RN [4]   |
| DR                    | EMBL: S81024; Aad14347.1; PFAM: PF00014; Kunitez_BPT1; 1.  | RP MEDLINE: 97263807.  | RA Hattori M., Tsukahara F., Furuhata Y., Tanahashi H., Hirose M., Saito M., Tsukuni S., Sakai Y.;  |
| DR                    | PRINTS: PRO0203; AMYLOID.  | RP MEDLINE: 88122640.  | RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L., Gusella J.F., Neve R.J.   |
| DR                    | PRINTS: PR00204; BEPARTYLID.   | RP "A novel method for making nested deletions and its application for sequencing of a 300 kb region of human APP locus." RT RT              | RA "Protease inhibitor domain encoded by an amyloid protein precursor mRNA associated with Alzheimer's disease." RT RT  |
| DR                    | PRINTS: PR00759; BASICPTSE.  | RP Nucleic Acids Res. 25:1802-1808(1997).  | RA RN [5]   |
| DR                    | PS01280; BPT1_KONTZ; 1.  | RP SEQUENCE OF 286-345 AND 365-366 FROM N.A.   | RA Hattori M., Tsukahara F., Furuhata Y., Tanahashi H., Villa-Komaroff L., Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L., Gusella J.F., Neve R.J.   |
| DR                    | PROSITE: PS00319; A4_EXTRA; 1.   | RP MEDLINE: 88122641.  | RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.; RT RT "Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitory activity." RT RT  |
| DR                    | PROSITE: PS00320; A4_INTRA; 1.   | RP NATURE 331:520-532(1998).   | RA Nature 331:520-532(1998).  |
| DR                    | Glycoprotein; Amyloid; Neuron; Transmembrane; Alternative splicing; KW signal; Serine Protease inhibitor.  | RP SEQUENCE OF 284-289 AND 365-770 FROM N.A.   | RA RN [6]   |
| FT                    | SIGNAL 1 17 BY SIMILARITY.   | RP SEQUENCE OF 287-367 FROM N.A.   | RA Robak N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.; RT RT "Molecular cloning and characterization of a cDNA encoding the cerebrovascular and the neuritic plaque amyloid peptides." RT RT Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987). |
| FT                    | A4 PROTEIN.  | RP MEDLINE: 88122641.  | RA RN [7]   |
| FT                    | BETA-AMYLOID PROTEIN (POTENTIAL).  | RP SEQUENCE OF 287-367 FROM N.A.   | RA Robak N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.; RT RT "Molecular cloning and characterization of a cDNA encoding the cerebrovascular and the neuritic plaque amyloid peptides." RT RT Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987). |
| FT                    | EXTRACELLULAR (POTENTIAL).   | RP MEDLINE: 88122641.  | RA RN [7]   |
| FT                    | POTENTIAL.   | RP SEQUENCE OF 287-367 FROM N.A.   | RA Robak N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.; RT RT "Molecular cloning and characterization of a cDNA encoding the cerebrovascular and the neuritic plaque amyloid peptides." RT RT Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987). |
| FT                    | CYTOSMATIC (POTENTIAL).  | RP MEDLINE: 88122641.  | RA RN [7]   |
| FT                    | CLATHRIN-BINDING (BY SIMILARITY).  | RP SEQUENCE OF 284-289 AND 365-770 FROM N.A.   | RA Robak N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.; RT RT "Molecular cloning and characterization of a cDNA encoding the cerebrovascular and the neuritic plaque amyloid peptides." RT RT Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987). |
| FT                    | PROBABLE.  | RP MEDLINE: 88122641.  | RA RN [7]   |
| FT                    | CARBOHYD 523 523 BY SIMILARITY.  | RP SEQUENCE OF 287-367 FROM N.A.   | RA Robak N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.; RT RT "Molecular cloning and characterization of a cDNA encoding the cerebrovascular and the neuritic plaque amyloid peptides." RT RT Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987). |
| FT                    | CARBOHYD 552 552 PROBABLE.   | RP MEDLINE: 88122641.  | RA RN [7]   |
| FT                    | DOMAIN 653 695 REACTIVE BOND.  | RP SEQUENCE OF 287-367 FROM N.A.   | RA Robak N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.; RT RT "Molecular cloning and characterization of a cDNA encoding the cerebrovascular and the neuritic plaque amyloid peptides." RT RT Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987). |
| FT                    | DOMAIN 18 680 BY SIMILARITY.   | RP MEDLINE: 88122641.  | RA RN [7]   |
| FT                    | ACT_SITE 681 704 BY SIMILARITY.  | RP SEQUENCE OF 287-367 FROM N.A.   | RA Robak N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.; RT RT "Molecular cloning and characterization of a cDNA encoding the cerebrovascular and the neuritic plaque amyloid peptides." RT RT Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987). |
| FT                    | DISULFID 705 751 BY SIMILARITY.  | RP MEDLINE: 88122641.  | RA RN [7]   |
| FT                    | SITE 740 743 BY SIMILARITY.  | RP SEQUENCE OF 287-367 FROM N.A.   | RA Robak N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.; RT RT "Molecular cloning and characterization of a cDNA encoding the cerebrovascular and the neuritic plaque amyloid peptides." RT RT Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987). |
| FT                    | CARBOHYD 523 523 PROBABLE.   | RP MEDLINE: 88122641.  | RA RN [7]   |
| FT                    | CARBOHYD 552 552 PROBABLE.   | RP SEQUENCE OF 287-367 FROM N.A.   | RA Robak N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.; RT RT "Molecular cloning and characterization of a cDNA encoding the cerebrovascular and the neuritic plaque amyloid peptides." RT RT Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987). |
| FT                    | DOMAIN 287 345 REACTIVE BOND.  | RP MEDLINE: 88122641.  | RA RN [7]   |
| FT                    | ACT_SITE 301 302 BY SIMILARITY.  | RP SEQUENCE OF 287-367 FROM N.A.   | RA Robak N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.; RT RT "Molecular cloning and characterization of a cDNA encoding the cerebrovascular and the neuritic plaque amyloid peptides." RT RT Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987). |
| FT                    | DISULFID 300 324 BY SIMILARITY.  | RP MEDLINE: 88122641.  | RA RN [7]   |
| FT                    | DISULFID 316 337 BY SIMILARITY.  | RP SEQUENCE OF 287-367 FROM N.A.   | RA Robak N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.; RT RT "Molecular cloning and characterization of a cDNA encoding the cerebrovascular and the neuritic plaque amyloid peptides." RT RT Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987). |
| SQ                    | SEQUENCE 751 AA: 84893 MW: 6C3E431089569049 CRC64;   | RP MEDLINE: 88122641.  | RA RN [7]   |
| Query Match           | 100.0%   | Score 16; DB 1; Length 751;  | RA Robak N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.; RT RT "Molecular cloning and characterization of a cDNA encoding the cerebrovascular and the neuritic plaque amyloid peptides." RT RT Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987). |
| Best Local Similarity | 100.0%   | Pred. No. 8.2e-11; Indels 0; Gaps 0;   | RA Robak N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.; RT RT "Molecular cloning and characterization of a cDNA encoding the cerebrovascular and the neuritic plaque amyloid peptides." RT RT Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987). |
| Matches               | 16;  | Conservative 0; Mismatches 0;  | RA Robak N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.; RT RT "Molecular cloning and characterization of a cDNA encoding the cerebrovascular and the neuritic plaque amyloid peptides." RT RT Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987). |
| Matches               | 16;  | Indels 0; Gaps 0;  | RA Robak N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.; RT RT "Molecular cloning and characterization of a cDNA encoding the cerebrovascular and the neuritic plaque amyloid peptides." RT RT Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987). |

- [8] RN SEQUENCE OF 507-770 FROM N.A.  
RP RX MEDLINE; 88124954.  
RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,  
RA Marotta C.A.;  
RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer  
disease brain: coding and noncoding regions of the fetal precursor";  
RN mRNA are expressed in the cortex.";  
PROC. NATL. ACAD. SCI. U.S.A. 85:929-933(1988).  
[9] RN SEQUENCE OF 672-681.  
RP RX MEDLINE; 98035004.  
RA Pardridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,  
RA Tourtellote W.W., Huebner V., Shirely J.E.;  
RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition  
and partial sequence of a 4,200-dalton peptide isolated from cortical  
microvessels.";  
RT J. Neurochem. 49:1394-1401(1987).  
RN SEQUENCE OF 739-770 FROM N.A.  
RP RX MEDLINE; 90236518.  
RA Schon E.A., Matsui S., Doh-Ura K., Furuya H., Sakaki Y.;  
RT "Genomic organization of the human amyloid beta-protein precursor  
gene";  
RN Gene 87:257-265(1990).  
[11] RN SEQUENCE OF 1-10 FROM N.A.  
RP RX TISSUE-LIVER;  
RC MEDLINE; 89016647.  
RA Schon E.A., Matsui S., Sadlock J., Herbert J.,  
RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)  
encodes a 95-kDa polypeptide.";  
RN Nucleic Acids Res. 16:9331-9351(1988).  
[12] RN SEQUENCE OF 18-50.  
RP RX MEDLINE; 87250462.  
RA van Nostrand W.B., Cunningham D.D.;  
RT "Purification of protease nexin II from human fibroblasts.";  
RL J. Biol. Chem. 262:8508-8514(1987).  
RN IDENTITY OF APP WITH NEXIN-II.  
RP RX MEDLINE; 89380866.  
RA Oltersdorf T., Fritz L.C., Schenk D.B., Lieberburg I.,  
Johnson Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F.,  
Sinha S.;  
RA RT "The secreted form of the Alzheimer's amyloid precursor protein with  
the Kunitz domain is protease nexin-II.";  
RN Nature 341:144-147(1989).  
[14] RN PROTEASE-SPECIFICITY OF INHIBITOR DOMAIN.  
RP RX MEDLINE; 90211252.  
RA Kido H., Fukutomi A., Schilling J., Wang Y., Cordell B., Katunuma N.;  
RT "Protease-specificity of Kunitz inhibitor domain of Alzheimer's  
disease amyloid protein precursor.";  
RL Biochem. Biophys. Res. Commun. 167:716-721(1990).  
RN COMPLEX WITH G(O).  
RP RX MEDLINE; 93188965.  
RA Murayama Y., Ogata E., Matsuura Y., Takahashi S., Okamoto T.,  
RT "Alzheimer amyloid protein precursor complexes with brain GTP-binding  
protein G(O)." ;  
RN Nature 362:75-79(1993).  
[16] X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.  
RP RX MEDLINE; 99215582.  
RA Rossjohn J., Cappa R., Feil S.C., Henry A., McKinstry W.J.,  
Galatis D., Hesse L., Multaup G., Beyreuther K., Masters C.L.,  
Parker M.W.;  
RT "Crystal structure of the N-terminal, growth factor-like domain of  
Alzheimer amyloid precursor protein.";  
RN Nat. Struct. Biol. 6:327-331(1999).  
[17]

AC P36692; 29, Created  
DT 01-JUN-1994 (Rel. 35, Last sequence update)  
DT 01-NOV-1997 (Rel. 39, Last annotation update)  
DT 15-FEB-2000 (Rel. 39, Last annotation update)  
DE PROBABLE ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1) (TRANSAMINASE A)  
DE (ASPART) (FRAGMENT).  
DE (FRAGMENT).  
GN OS Streptomyces griseus.  
OS Bacteria; Firmicutes; Actinobacteria; Actinomycetaceae; Streptomyces.  
OC Actinomycetales; Streptomyceae; Streptomyces; Streptomyces.  
RN [1] RP SEQUENCE FROM N.A.  
RN [1] RP SEQUENCE FROM N.A.  
RN [1] RP STRAININFO 13350; MEDLINE; 94114580.  
RN [1] RP Miyake K., Onaka H., Horinouchi S., Beppu T.; "Organization and nucleotide sequence of the secE-nusG region of Streptomyces griseus: cloning of the gene and analysis of the A-factor binding properties of the gene product.";  
RN [1] RP Biochim. Biophys. Acta 1217:97-100(1994).  
RN [1] RP CATALYTIC ACTIVITY: L-ASPARTATE + 2-OXOGLUTARATE = OXALOACETATE + L-GLUTAMATE.  
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.  
CC -1- SUBSTRATE: HOMODIMER (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.  
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CC EMBL; Y72787; CAP51294; 1; NOT\_ANNOTATED\_CDS.  
DR PIR; SA1059; S41059.  
DR PROTEIN; PS00105; AA\_TRANSFER\_CLASS\_1; PARTIAL.  
KW Transferase; Aminotransferase; Pyridoxal phosphate.  
FT NON\_TER 213 213 AA; 22693 MW; C380BF59DA55A429 CRC64;  
SQ SEQUENCE [1]

RP SEQUENCE FROM N.A.  
RX MEDLINE; 89296509.  
RA Bravo-Almonacid F.F., Martaberry A.N.; "Nucleotide cDNA sequence coding for the PVY coat protein."  
RT "Nucleotide cDNA sequence coding for the PVY coat protein." (Rel. 17:4401-4401(1989)).  
RL Nucleic Acids Res. 17:4401-4401(1989).  
PIM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE POLYPEPTIDE WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT INDIVIDUAL PROTEINS.  
SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.  
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CC EMBL; X14156; CAA32356; 1; -.  
DR PIR; S04723; S04723.  
DR PFAM; PF00767; Poty\_coat; 1.  
KW Transferase; RNA-directed RNA polymerase; Coat protein; Polyprotein.  
FT NON\_TER 1 1 NUCLEAR INCLUSION PROTEIN B.  
FT CHAIN <1 17 COAT PROTEIN.  
FT CHAIN 18 284 AA; 31971 MW; E98335C45078982 CRC64;  
SQ SEQUENCE 284 AA; 31971 MW; E98335C45078982 CRC64;

Query Match 37.5%; Score 6; DB 1; Length 284;  
Best Local Similarity 100.0%; Pred. No. 4.5;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 YEVHQ 15  
Db 12 YEVHQ 17

RESULT 11  
POLG\_PVYCH STANDARD; PRT; 327 AA.  
ID POLG\_PVYCH  
AC P21294;  
DT 01-MAY-1991 (Rel. 18, Last sequence update)  
DT 01-MAY-1991 (Rel. 18, Last annotation update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE GENOME POLYPEPTIDE (CONTAINS: NUCLEAR INCLUSION PROTEIN B (NI-B) (NIB) (RNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.48); COAT PROTEIN (CP))  
DE (FRAGMENT).  
DE Potato virus Y (strain Chinese isolate) (PVY).  
OS Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;  
OC Potyvirus.

RN [1] RP SEQUENCE FROM N.A.  
RX MEDLINE; 91016851.  
RA Zhou X.R., Fang R.X., Wang C.Q., Meng K.Q.; "cDNA sequence of the 3'-coding region of PVY genome (the Chinese isolate)." Nucleic Acids Res. 18: 5554-5554(1990).  
RT "cDNA sequence of the 3'-coding region of PVY genome (the Chinese isolate)." (Rel. 18:5554-5554(1990)).  
RL Nucleic Acids Res. 18: 5554-5554(1990).  
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CC EMBL; X54058; CAA37993; 1; -.  
DR DR

Query Match 37.5%; Score 6; DB 1; Length 213;  
Best Local Similarity 100.0%; Pred. No. 3.6;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DSGYEV 12  
Db 92 DSGYEV 97

RESULT 10  
POLG\_PVYD STANDARD; PRT; 284 AA.  
ID POLG\_PVYD  
AC P11897;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE GENOME POLYPEPTIDE (CONTAINS: NUCLEAR INCLUSION PROTEIN B (NI-B) (NIB) (RNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.48); COAT PROTEIN (CP)).  
DE (FRAGMENT).  
OS Potato virus Y (strain Yo) (PVY).  
OS Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;  
OC Potyvirus.  
RN [1]

DR PIR; S11549; S11549.  
 DR HSSP; P03067; 1 AMB.  
 DR Transferase; RNA-directed RNA polymerase; Coat protein; Polyprotein.  
 KW NUCLEAR INCLUSION PROTEIN B.

FT CHAIN <1 60  
 FT CHAIN 1 61  
 FT CHAIN 61 327 COAT PROTEIN.  
 SEQUENCE 327 AA; 36868 MW; 8F83552DE6F2F18 CRC64;

Query Match 37.5%; Score 6; DB 1; Length 327;  
 Best Local Similarity 100.0%; Pred. No. 5.1;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 YEVHQ 15  
 Db 55 YEVHQ 60

**RESULT 12**

COAT\_PENNY STANDARD; PRT; 330 AA.

ID COAT\_PENNY STANDARD; PRT; 330 AA.  
 AC P01933;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 DT 01-OCT-1994 (Rel. 34, Last annotation update)  
 DE COAT PROTEIN.  
 OS Pepper mottle virus (PeMV).  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;  
 Potyvirus.  
 [1]  
 RN SEQUENCE FROM N.A.  
 RA Doughtery W.G., Allison R.F., Parks T.D., Johnston R.E., Feild M.J.,  
 Armstrong F.B.;  
 RT "Nucleotide sequence at the 3' terminus of pepper mottle virus  
 genomic RNA: evidence for an alternative mode of Potyvirus capsid  
 protein gene organization";  
 RL Virology 146:282-291(1985).  
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to license@isb-sib.ch).

Query Match 37.5%; Score 6; DB 1; Length 397;  
 Best Local Similarity 100.0%; Pred. No. 6;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DSGYEV 12  
 Db 82 DSGYEV 87

**RESULT 14**

POLG\_PVYHU STANDARD; PRT; 3061 AA.

ID POLG\_PVYHU STANDARD; PRT; 3061 AA.  
 AC Q02963;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER  
 COMPONENT PROTEINASE (BC 3.4.22.-) (HC-PRO); PROTEIN P3; 6 KDA PROTEIN  
 1 (KL1); CYTOPLASMIC INCLUSION PROTEIN (C1); 6 KDA PROTEIN 2 (6K2);  
 DE GENOME-LINKED PROTEIN (VPG); NUCLEAR INCLUSION PROTEIN A (NI-A) (NIA)  
 DE (EC 3.4.22.-) (49 KDA-PRO); NUCLEAR INCLUSION PROTEIN B (NI-B) (NIB) (RNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.48);  
 DE COAT PROTEIN (CP);  
 DE POTATO VIRUS Y (strain Hungarian) (PVY).  
 OS Potato virus Y (strain Hungarian) (PVY).  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;  
 Potyvirus.  
 [1]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE; 93134578.  
 RA Thöle V., Dalmau T., Burgyan J., Balazs E.; (Hungarian isolate) genomic  
 RNA.";  
 RT Gene 123:149-156(1993).  
 RL -1- FUNCTION: HELPER COMPONENT-PROTEINASE IS REQUIRED FOR APHID  
 CC TRANSMISSION AND ALSO HAS PROTEOLYTIC ACTIVITY.  
 CC -1- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY. IT  
 CC MAY BE INVOLVED IN REPLICATION.  
 CC -1- FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.  
 CC -1- PTM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.  
 CC ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1) (TRANSAMINASE A) (ASPAT).  
 GN ASPC OR AAT.  
 OC Streptomyces virginiae.

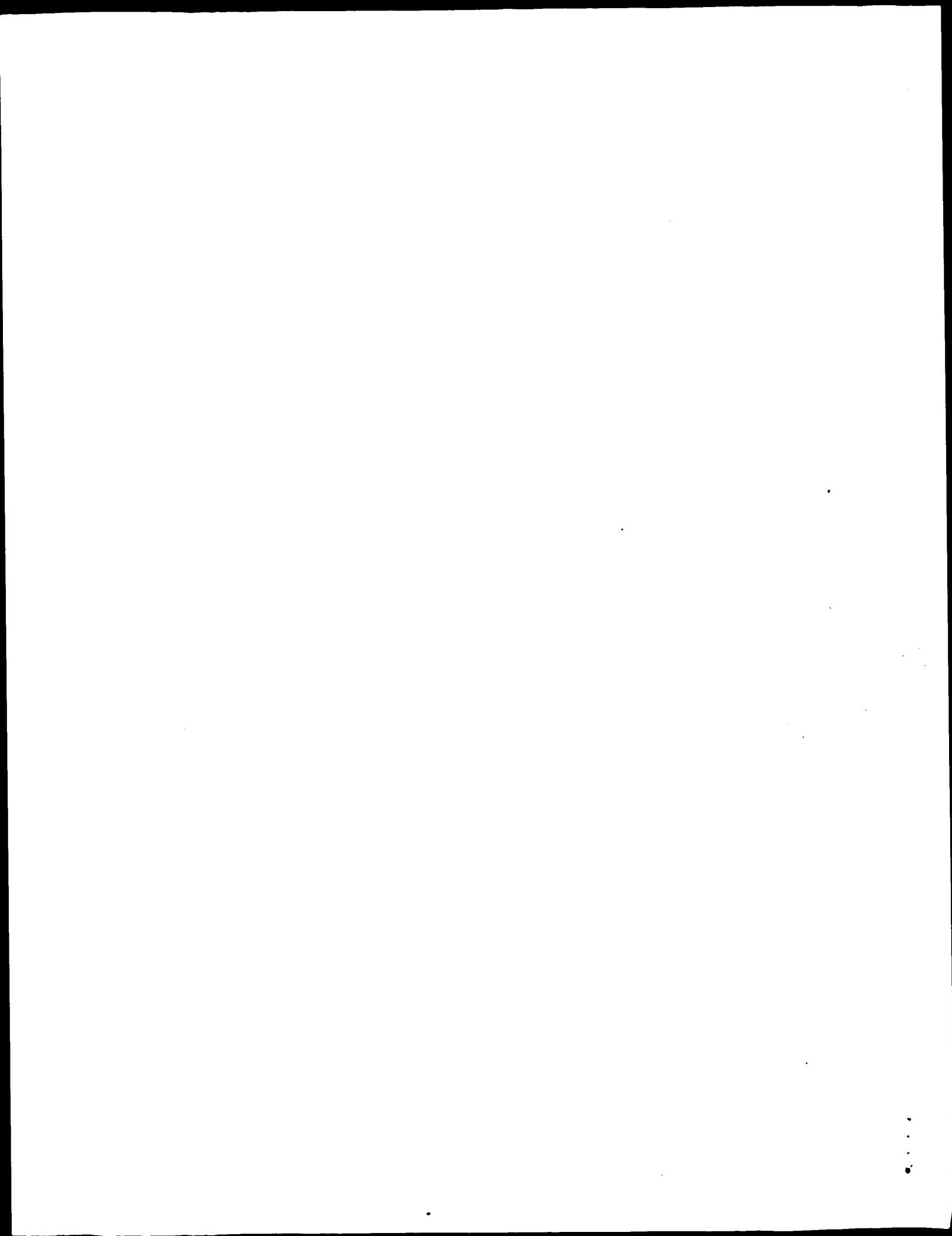
**RESULT 13**

AAAT\_STRYVG STANDARD; PRT; 397 AA.

ID AAAT\_STRYVG STANDARD; PRT; 397 AA.  
 AC Q60013;  
 DT 15-FEB-2000 (Rel. 39, Created)  
 DT 15-FEB-2000 (Rel. 39, Last sequence update)  
 DE ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1) (TRANSAMINASE A) (ASPAT).  
 GN ASPC OR AAT.









OS Homo sapiens (Human). Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 MEDLINE: 93236601.  
 RX DENMAN R. B., ROSENZWAIG R., MILLER D.L.;  
 RT "A system for studying the effect(s) of familial Alzheimer disease  
 mutations on the processing of the beta-amyloid peptide precursor.";  
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).  
 EMBL: S61380; CAB32007.1; -.  
 DR HSSP; P05067; 1AML.  
 FT NON\_TER 1 1  
 FT NON\_TER 82 82  
 SQ SEQUENCE 82 AA; 8938 MW; 4C8B0E6E CRC32;

Query Match 3  
 ID Q16014 PRELIMINARY; PRT; 82 AA.  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
 DE BETA-AMYLOID PEPTIDE (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX DENMAN R. B., ROSENZWAIG R., MILLER D.L.;  
 RT "A system for studying the effect(s) of familial Alzheimer disease  
 mutations on the processing of the beta-amyloid peptide precursor.";  
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).  
 EMBL: S60721; CAB31988.1; -.  
 DR HSSP; P05067; 1AML.  
 FT NON\_TER 1 1  
 FT NON\_TER 82 82  
 SQ SEQUENCE 82 AA; 8972 MW; 30147E4F CRC32;

Query Match 4  
 ID P78438 PRELIMINARY; PRT; 82 AA.  
 DT 01-MAY-1997 (TREMBLrel. 03, Created)  
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
 DE AMYLOID PROTEIN (BETA-AMYLOID PROTEIN) (FRAGMENT).  
 GN APP.  
 OS Homo sapiens (Human). Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE: 89392030.  
 RA JOHNSTONE E.M., CHANEY M.O., MOORE R.E., WARD K.E., NORRIS F.H.,  
 RA LITTLE S.P.;  
 RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows  
 similarity to soybean trypsin inhibitor.";  
 RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).  
 RN [2]  
 RP SEQUENCE OF 1948 FROM N.A.  
 RX MEDLINE: 87120329.  
 RA TANZI R.E., GUSELLA J.F., WATKINS P.C., BRUNS G.A., GEORGE-HYSLOP P.,  
 RA VAN KEUREN M.L., PATTERSON D., PAGAN S., KURNIT D.M., NEVE R.L.;  
 RT "Amyloid beta protein gene: cDNA, mRNA distribution, and genetic  
 linkage near the Alzheimer locus.";  
 RL Science 235:880-884(1987).  
 RN [3]  
 RP SEQUENCE OF 32-63 FROM N.A.  
 RX MEDLINE: 93053397.  
 RA KAMINO K., ORR H.T., PAYAMI H., WIJSMAN E.M., ALONSO M.E., PULST S.M.,  
 RA ANDERSON L., O'DAHL S., NEMENS E., WHITE J.A.;  
 RT "Linkage and mutational analysis of familial Alzheimer disease  
 kindreds for the APP gene region.";  
 RL Am. J. Hum. Genet. 51:98-104(1992).  
 DR EMBL: M9270; AAA51768.1;  
 DR EMBL: M29269; AAA51768.1; JOINED.  
 DR EMBL: M15532; AAA51564.1; -.  
 DR EMBL: S45136; AAB23646.1; -.  
 DR HSSP; P05067; 1AML.  
 DB NON\_TER 1 1  
 SQ SEQUENCE 82 AA; 8994 MW; 5399FFA4 CRC32;

Query Match 5  
 ID Q16014 PRELIMINARY; PRT; 82 AA.  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
 DE BETA-AMYLOID PEPTIDE (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX DENMAN R. B., ROSENZWAIG R., MILLER D.L.;  
 RT "A system for studying the effect(s) of familial Alzheimer disease  
 mutations on the processing of the beta-amyloid peptide precursor.";  
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).  
 EMBL: S60721; CAB31988.1; -.  
 DR HSSP; P05067; 1AML.  
 FT NON\_TER 1 1  
 FT NON\_TER 82 82  
 SQ SEQUENCE 82 AA; 8972 MW; 30147E4F CRC32;

Query Match 6  
 ID P78438 PRELIMINARY; PRT; 82 AA.  
 DT 01-MAY-1997 (TREMBLrel. 03, Created)  
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
 DE AMYLOID PROTEIN (BETA-AMYLOID PROTEIN) (FRAGMENT).  
 GN APP.  
 OS Homo sapiens (Human). Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 RN [1]

Db 436 DAEFRHDSGYEVHHQK 451

|          |  |                                       |      |         |             |  |   |      |         |
|----------|--|---------------------------------------|------|---------|-------------|--|---|------|---------|
| RESULT   | 6  |                                       |      |         | RESULT      | 8  |   |      |         |
| ID       | 060496   | PRELIMINARY;                          | PRT; | 695 AA. | ID          | 057394   | PRELIMINARY;                            | PRT; | 699 AA. |
| ID       | 060496   |                                       |      |         | AC          | 057394;  |   |      |         |
| AC       | Q60496;  |                                       |      |         | DT          | 01-JUN-1998  | (TREMBLrel. 06, Created)                |      |         |
| DT       | 01-NOV-1996  | (TREMBLrel. 01, Last sequence update) |      |         | DT          | 01-JUN-1998  | (TREMBLrel. 06, Last sequence update)   |      |         |
| DT       | 01-NOV-1996  | (TREMBLrel. 01, Last sequence update) |      |         | DT          | 01-NOV-1999  | (TREMBLrel. 12, Last annotation update) |      |         |
| DE       | ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN.  |                                       |      |         | DE          | EL AMYLOID PRECURSOR PROTEIN 699   |   |      |         |
| OS       | Cavia porcellus (Guinea pig).  |                                       |      |         | GN          | EL APP699.   |   |      |         |
| OC       | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  |                                       |      |         | OS          | Narke japonica (Electric ray).   |   |      |         |
| OC       | Eumetabranchia; Rajiformes; Narke.   |                                       |      |         | OC          | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  |   |      |         |
| RN       | [1]  |                                       |      |         | RN          | [1]  |   |      |         |
| RP       | SEQUENCE FROM N.A.   |                                       |      |         | RP          | SEQUENCE FROM N.A.   |   |      |         |
| RC       | TISSUE-ELECTRIC LOBE;  |                                       |      |         | RC          | TISSUE-ELECTRIC LOBE;  |   |      |         |
| RA       | TIJUTMA K., LEE D., OKUTSU J., TOMITA S., HIRASHIMA N., KIRINO Y.,   |                                       |      |         | RA          | TIJUTMA K., LEE D., OKUTSU J., TOMITA S., HIRASHIMA N., KIRINO Y.,   |   |      |         |
| RA       | SUZUKI T.  |                                       |      |         | RA          | SUZUKI T.  |   |      |         |
| RL       | BECK M., MULLER D., BIGL V.  |                                       |      |         | RL          | Biochem. J. 0-0-0(1998).   |   |      |         |
| RL       | Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.   |                                       |      |         | DR          | EMBL; AB055414; BRA2430.1;   |   |      |         |
| CC       | -1: FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN  |                                       |      |         | DR          | PROSITE; PS00319; A4_EXTRA; 1.   |   |      |         |
| CC       | G(O).  |                                       |      |         | DR          | PROSITE; PS00320; A4_INTRAA; 1.  |   |      |         |
| CC       | -1: SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.   |                                       |      |         | DR          | PRINTS; PRO003; AMYLOIDA4.   |   |      |         |
| CC       | -1: SIMILARITY: TO OTHER SPECIES APP ANALOGUES.  |                                       |      |         | DR          | PRINTS; PRO004; BETAAMYLOID.   |   |      |         |
| DR       | EMBL; X97631; CA66230.1; -.  |                                       |      |         | SQ          | SEQUENCE 699 AA; 11604C05 CRC32;   |   |      |         |
| DR       | HSSP; P05067; IAML.  |                                       |      |         | Query Match | 62.5%; Score 10; DB 13; Length 699;  |   |      |         |
| DR       | PRINTS; PRO0203; AMYLOIDA4.  |                                       |      |         | Query Match | Best Local Similarity 100.0%; Pred. No. 0.0007; Mismatches 0; Indels 0; Gaps 0;  |   |      |         |
| DR       | PR00204; BETAAMYLOID.  |                                       |      |         | Query Match | Best Local Similarity 100.0%; Pred. No. 0.0007; Mismatches 0; Indels 0; Gaps 0;  |   |      |         |
| SEQUENCE | 695 AA; 78701 MW; CE05C651 CRC32;  |                                       |      |         | Query Match | Best Local Similarity 100.0%; Pred. No. 0.0007; Mismatches 0; Indels 0; Gaps 0;  |   |      |         |
| •        | •  |                                       |      |         | Query Match | Best Local Similarity 100.0%; Pred. No. 0.0007; Mismatches 0; Indels 0; Gaps 0;  |   |      |         |
| Oy       | 1 DAEFRHDSGYEVHHQK 16  |                                       |      |         | Query Match | 7 DSSEYEVHHQK 16   |   |      |         |
| Matches  | 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  |                                       |      |         | Query Match | Best Local Similarity 100.0%; Pred. No. 0.0007; Mismatches 0; Indels 0; Gaps 0;  |   |      |         |
| Db       | 597 DAEFRHDSGYEVHHQK 612   |                                       |      |         | Query Match | 7 DSSEYEVHHQK 16   |   |      |         |
| RESULT   | 7  |                                       |      |         | Query Match | 607 DSSEYEVHHQK 616  |   |      |         |
| ID       | Q13778   | PRELIMINARY;                          | PRT; | 97 AA.  | Query Match | 7 DSSEYEVHHQK 16   |   |      |         |
| AC       | Q13778;  |                                       |      |         | Query Match | 607 DSSEYEVHHQK 616  |   |      |         |
| DT       | 01-NOV-1996  | (TREMBLrel. 01, Created)              |      |         | RESULT      | 9  |   |      |         |
| DT       | 01-NOV-1999  | (TREMBLrel. 01, Last sequence update) |      |         | ID          | Q91963   | PRELIMINARY;                            | PRT; | 747 AA. |
| DE       | AMYLOID PROTEIN (AD-AP) (FRAGMENT).  |                                       |      |         | AC          | Q91963;  |   |      |         |
| OS       | Homo sapiens (Human).  |                                       |      |         | DT          | 01-NOV-1996  | (TREMBLrel. 01, Created)                |      |         |
| OC       | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  |                                       |      |         | DT          | 01-NOV-1999  | (TREMBLrel. 01, Last sequence update)   |      |         |
| RN       | Eutheria; Primates; Catarrhini; Hominidae; Homo.   |                                       |      |         | DE          | APP747.  |   |      |         |
| RX       | SEQUENCE FROM N.A.   |                                       |      |         | OS          | Xenopus laevis (African clawed frog).  |   |      |         |
| RX       | MEDLINE; 87120328.   |                                       |      |         | OC          | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae. |   |      |         |
| RA       | GOLDGABER D., LERMAN M.I., MCBRIDE O.W., SAFFIOTTI U., GAJDUSEK D.C.; "Characterization and chromosomal localization of a cDNA encoding brain amyloid of Alzheimer's disease." |                                       |      |         | RN          | [1]  |   |      |         |
| RT       | EMBL; M15533; AAA35540.1; -.   |                                       |      |         | RP          | SEQUENCE FROM N.A.   |   |      |         |
| DR       | HSSP; P05067; IAML.  |                                       |      |         | RX          | MEDLINE; 93129227.   |   |      |         |
| FT       | NON_TER 1 10884 MW; C4D32AA2 CRC32;  |                                       |      |         | RA          | OKADO H., OKAMOTO H.:  |   |      |         |
| SQ       | SEQUENCE 97 AA; 10884 MW; C4D32AA2 CRC32;  |                                       |      |         | RT          | "A Xenopus homologue of the human beta-amyloid precursor protein: Developmental regulation of its gene expression."            |   |      |         |
| •        | •  |                                       |      |         | RL          | Biochim. Biophys. Res. Commun. 189:1561-1568(1992).  |   |      |         |
| Oy       | Query Match 87.5%; Score 14; DB 4; Length 97;  |                                       |      |         | DR          | EMBL; S52417; RAB24853.1;  |   |      |         |
| Matches  | 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  |                                       |      |         | DR          | PROSITE; PS00320; A4_INTRAA; 1.  |   |      |         |
| Db       | 1 EFRHDSGYEVHHQK 16  |                                       |      |         | DR          | PROSITE; PS00280; BPT1_KUNITZ; 1.  |   |      |         |
| Qy       | 3 EFRHDSGYEVHHQK 16  |                                       |      |         | DR          | PFAM; P00014; Kunitz_BPT1; 1.  |   |      |         |
| Db       | 1 EFRHDSGYEVHHQK 14  |                                       |      |         | DR          | PRINTS; PRO0203; AMYLOIDA4.  |   |      |         |
| Qy       | 10 YEVEHQK 16  |                                       |      |         | DR          | PRINTS; PRO0204; BETAAMYLOID.  |   |      |         |
| Db       | 658 YEVEHQK 664  |                                       |      |         | DR          | PROT59; BASICCPASE.  |   |      |         |
| Qy       | Query Match 43.8%; Score 7; DB 13; Length 747;   |                                       |      |         | KW          | Serine protease inhibitor.   |   |      |         |
| Matches  | 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;   |                                       |      |         | SQ          | SEQUENCE 747 AA; 84892 MW; A7580143 CRC32;   |   |      |         |

RESULT 10  
 Q85276 PRELIMINARY; PRT; 292 AA.  
 ID Q85276; PRELIMINARY;  
 AC Q85276; PRELIMINARY;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TREMBLrel. 07, Last annotation update)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
 AMBID: PRECURSOR PROTEIN  
 OS Tetraodon fluviatilis (Puffer fish).  
 Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Actinopterygii:  
 Retrodontiformes; Tetraodontidae; Tetraodon.  
 OC Retrodontiformes; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;  
 OC Tetraodontiformes; Tetraodontidae; Tetraodon.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RP GRIFFIN J.D., SHIEL, P.S., BERGER P.H., THORNBURY D.W.;  
 RL Submitted (DEC-1991) to the EMBL/GenBank/DDBJ databases.  
 DR M81435; AAA47185.1;  
 DR PF00767; Poty\_coat; 1.  
 RT "Analysis of Pufferfish homologues of the At-rich human APP gene.";  
 RL Gene 210:17-24 (1998);  
 DR EMBL: AF018165; AAC1275.1;  
 DR PROSITE: PS00319; A4\_EXTRA; 1.  
 DR PROSITE: PS00320; A4\_INTRAA; 1.  
 DR PFAM: PF00014; Kunitz\_BPTI; 1.  
 DR PRINTS: PR00203; ANKYL0IDA4.  
 DR PRINTS: PR00204; BETAMYLOID.  
 DR PRINTS: PR00759; BASICPIASE.  
 SQ SEQUENCE 780 AA; 88238 MW; 99DD89A8 CRC32;

Query Match Score 7; DB 13; Length 780;  
 Best Local Similarity 100.0%; Pred. No. 1,5;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 11  
 Q85108 PRELIMINARY; PRT; 298 AA.  
 ID Q85108; PRELIMINARY;  
 AC Q85108; PRELIMINARY;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
 DE ASPARATE AMINOTRANSFERASE (FRAGMENT).  
 OS Streptomyces coelicolor.  
 OC Bacteria: Firmicutes; Actinobacteria; Streptomyces; Streptomycetales; Streptomyces; Streptomyceae; Streptomyces.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAINNNP;  
 RMIDLINE: 95231511.  
 RX PUTTIKHUNT C., NIHIRA T., YAMADA Y.;  
 RA "Cloning, nucleotide sequence, and transcriptional analysis of the RTNUSG gene of Streptomyces coelicolor A3(2), which encodes a putative transcriptional antiterminator.";  
 RL Mol. Gen. Genet. 247:118-122 (1995).  
 DR EMBL: D32254; BAA2105.1; -.  
 KW Transf erase; Aminotransferase.  
 FT NON\_TER 123  
 SQ SEQUENCE 123 AA; 12765 MW; 5394477B CRC32;

Query Match Score 6; DB 2; Length 123;  
 Best Local Similarity 100.0%; Pred. No. 4,3;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12  
 Q85276 PRELIMINARY; PRT; 292 AA.  
 ID Q85276; PRELIMINARY;  
 AC Q85276; PRELIMINARY;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
 DE POLYPEPTIDE (FRAGMENT).  
 OS Potato virus Y.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae; Potyvirus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RP GRIFFIN J.D., SHIEL, P.S., BERGER P.H., THORNBURY D.W.;  
 RL Submitted (DEC-1991) to the EMBL/GenBank/DDBJ databases.  
 DR M81435; AAA47185.1;  
 DR PFAM: PF00767; Poty\_coat; 1.  
 RT "Analysis of Pufferfish homologues of the At-rich human APP gene.";  
 RL Gene 210:17-24 (1998);  
 DR EMBL: AF018165; AAC1275.1;  
 DR PROSITE: PS00319; A4\_EXTRA; 1.  
 DR PROSITE: PS00320; A4\_INTRAA; 1.  
 DR PFAM: PF00014; Kunitz\_BPTI; 1.  
 DR PRINTS: PR00203; ANKYL0IDA4.  
 DR PRINTS: PR00204; BETAMYLOID.  
 DR PRINTS: PR00759; BASICPIASE.  
 SQ SEQUENCE 292 AA; 32945 MW; 8CB34E72 CRC32;

Query Match Score 6; DB 12; Length 292;  
 Best Local Similarity 100.0%; Pred. No. 9;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 YEVHHQ 15  
 DR 20 YEVHHQ 25

RESULT 13  
 Q85108 PRELIMINARY; PRT; 298 AA.  
 ID Q85108; PRELIMINARY;  
 AC Q85108; PRELIMINARY;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
 DE CAPSID PROTEIN (FRAGMENT).  
 OS Potato virus Y.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae; Potyvirus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAINNNP;  
 RMIDLINE: 95231511.  
 RX DAQUINO L., DALMAY T., BURGYAN J., RAGOZZINO A., SCALA F.;  
 RA D'AQUINO L., DALMAY T., BURGYAN J., RAGOZZINO A., SCALA F.;  
 RL Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL: U10378; AAA19172.1; -.  
 DR PFAM: PF00767; Poty\_coat; 1.  
 FT NON\_TER 298  
 FT NON\_TER 298  
 SQ SEQUENCE 298 AA; 33459 MW; 93324303 CRC32;

Query Match Score 6; DB 12; Length 298;  
 Best Local Similarity 100.0%; Pred. No. 9,1;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 YEVHHQ 15  
 DR 27 YEVHHQ 32

RESULT 14  
 Q85259 PRELIMINARY; PRT; 313 AA.  
 ID Q85259; PRELIMINARY;  
 AC Q85259; PRELIMINARY;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-JAN-1999 (TREMBLrel. 09, Last annotation update)

QY 7 DSGYEV 12  
 DR 93 DSGYEV 98

DE ORF (FRAGMENT).  
 OS Potato virus Y.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;  
 OC Potyvirus.  
 RN [1]

SEQUENCE FROM N.A.

RC STRAIN=NECROTIC (PVY-T);

RA HIDAKA M.;

RL Submitted (NOV-1991) to the EMBL/GenBank/DDBJ databases.

DR EMBL: D12570; BAA02120.1; -.

DR PFAM; PFO0767; poty\_coat; 1.

KW Coat protein.

FT NON\_TER 1

FT CHAIN 47 1 COAT PROTEIN.

SEQUENCE 313 AA; 313 MW; 453E75C2 CRC32;

Query Match 37.5%; Score 6; DB 12; Length 313;  
 Best Local Similarity 100.0%; Pred. No. 9.5;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 YEYHQ 15

Db 41 YEYHQ 46

RESULT 15

O9WG05 ID Q9WG05 PRELIMINARY; PRT; 365 AA.

AC Q9WG05;

DT 01-NOV-1999 (TREMBLrel. 12, Created)

DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)

DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)

DE POLYPROTEIN (FRAGMENT).

OS Potato virus Y.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;

OC Potyvirus.

RN [1]

SEQUENCE FROM N.A.

RC STRAIGHT, O.

RA BHAT A.I., VARMA A., PAPPU H.R., RAJAMANNAR M., JAIN R.K., PRAVEEN S.;

RT "N-terminal serology and sequence relationships indicate that a

RT potyvirus from eggplant, Solanum melongena L., is a strain of potato

RT virus Y.";

RL Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.

DR EMBL: AF118153; RAD24563.1; -.

KW Polyprotein.

FT NON\_TER 1

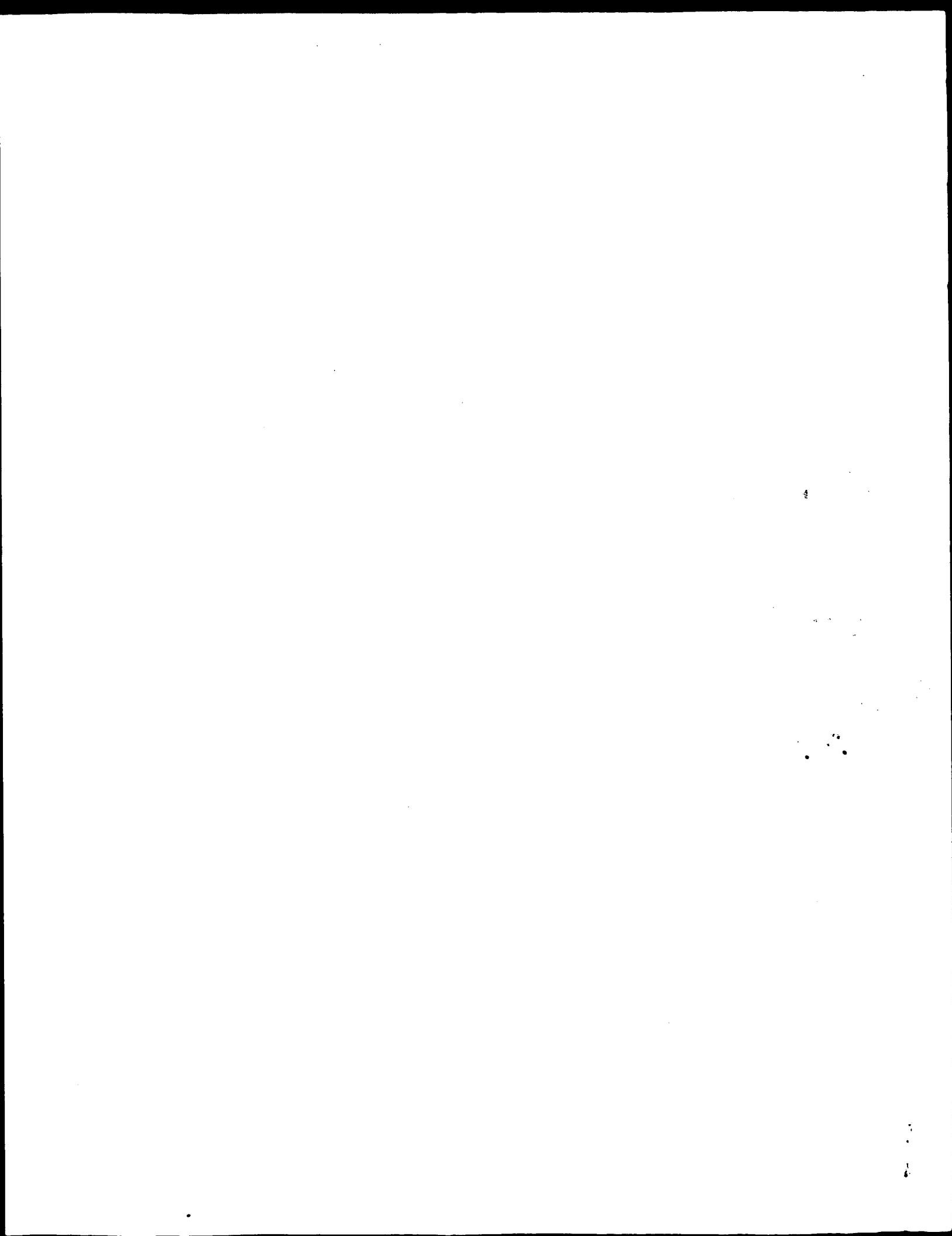
FT CHAIN 365 AA; 41418 MW; F3CF9EBD CRC32;

Query Match 37.5%; Score 6; DB 12; Length 365;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 YEYHQ 15

Db 93 YEYHQ 98

Search completed: September 13, 2000, 02:27:32  
 Job time: 174 sec



OM of: US-09-155-076-2 to: EST:\* out\_format : pfs  
 Date: Sep 13, 2000 3:35 AM  
 About: Results were produced by the GenCore software, version 4.5,  
 Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:  
 -MODEL=frame=p2n.modele -DEV=xip  
 -Q=cgn2.1/DSTPO.spool/US09155076/runat\_29082000\_092538\_16898/app\_query.fasta\_1.144  
 -DB=EST\_QMFT=fastap -SUFFIX=\_first -GAPEXT=5.00 -LOOPEXT=0.000 -QGAPOP=4.500  
 -MINMATCH=0.100 -LOOPL=0.000 -LOOPR=0.000 -QGAPOP=4.500  
 -QGAPEXT=0.050 -XGAPOP=60.000 -XGAPEXT=60.000 -FGAPOP=6.000  
 -GAPEXT=7.000 -YGAPOP=60.000 -YGAPEXT=60.000 -DELOP=6.000  
 -DELEXT=7.000 -START=1 -MATRIX=oligo -TRANS=human0.cdf -LIST=45  
 -MODE=LOCAL -OUTFMT=PIS -NORM=EXT -MINLEN=0 -MAXLEN=1000000  
 -USER=US09155076 -CGNI\_1..1327 -NCPU=6 -ICPU=3 -LONGLOG -NO\_XLPXY  
 -WAIT -THREADS=1

## Search information block:

Query: US-09-155-076-2  
 Query length: 16  
 Database: EST:  
 Database sequences: 5247842  
 Database length: -2090053206  
 Search time (sec): 889.020000  
  
 WARNING: XGAPOP and YGAPOP must be equal. Assuming YGAPOP=XGAPOP=60.000  
 WARNING: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.000

## score\_list:

| Sequence           | Strd | Orig  | Zscore | Escore  | Len | Documentation                         |
|--------------------|------|-------|--------|---------|-----|---------------------------------------|
| gb.est;AA385402    | +    | 16.00 | 339.90 | 4.2e-10 | 246 | A3385402 EST999018 Thyroid Homo       |
| gb.est;1:AN79017   | -    | 16.00 | 339.24 | 4.6e-10 | 277 | AN79017 RC3-HR030-241099-012-         |
| gb.est;5:AN02976   | -    | 16.00 | 339.22 | 4.6e-10 | 278 | AN02976 OV-BT203-070599-188 BT        |
| gb.est;5:AA303751  | +    | 16.00 | 338.85 | 4.8e-10 | 297 | AA303751 ESP16434 Aorta endotho       |
| gb.est;7:FG0018    | +    | 16.00 | 338.70 | 4.9e-10 | 305 | FG0018 HSC0A101 normalized inq        |
| gb.est;14:AN80695  | -    | 16.00 | 338.68 | 4.9e-10 | 306 | AW80695 RCV-LT001-0012-               |
| gb.est;16:AN20528  | +    | 16.00 | 338.17 | 5.2e-10 | 335 | AI902528 OVB-T009-101198-075 BT       |
| gb.est;22:AN902074 | +    | 16.00 | 338.12 | 5.3e-10 | 338 | AI322074 EST21653 Cerebellum II       |
| gb.est;26:AN902529 | -    | 16.00 | 338.12 | 5.3e-10 | 338 | AI902529 OVB-T009-101198-074 BT       |
| gb.est;5:AA04003   | +    | 16.00 | 337.86 | 5.4e-10 | 354 | AA3040003 EST16883 Aorta endotho      |
| gb.est;52:TA9906   | +    | 16.00 | 337.42 | 5.8e-10 | 383 | T49906 Y92B06_E1 Stratagene pl        |
| gb.est;51:RA9709   | +    | 16.00 | 337.09 | 5.9e-10 | 399 | R19709 Y935104_E1 Soares infant       |
| gb.est;2:AA134479  | +    | 16.00 | 336.95 | 6.1e-10 | 417 | AI134479 2010904_r1 Stratagene        |
| gb.est;16:AN124771 | -    | 16.00 | 336.39 | 6.6e-10 | 461 | AI124771 am11a12_x1 Johnston F1       |
| gb.est;4:AN601576  | +    | 16.00 | 336.29 | 6.7e-10 | 469 | AI601576 QV3-BT381-270100-073-        |
| gb.est;51:RS5913   | +    | 16.00 | 336.10 | 6.8e-10 | 485 | R25913 Y956C07_r1 Soares infant       |
| gb.est;3:AA18652   | +    | 16.00 | 335.81 | 7.1e-10 | 511 | AA218652 z314d12_s1 Stratagene        |
| gb.est;4:AN602133  | +    | 16.00 | 335.48 | 7.4e-10 | 542 | AW602193 ba54e09_Y3 NIH_NGC_10        |
| gb.est;5:AN673480  | +    | 16.00 | 334.86 | 8.0e-10 | 606 | AW673480 z203g07_r1 Stratagene        |
| gb.est;2:AN02598   | +    | 16.00 | 334.81 | 8.1e-10 | 611 | AA028298 AA01869 z23g07_r1 Stratagene |
| gb.est;2:AN01869   | +    | 16.00 | 334.72 | 8.2e-10 | 621 | AA01869 pat_ph0033_f8_f chick         |
| gb.est;8:AN980795  | +    | 16.00 | 334.45 | 8.4e-10 | 652 | AI980795 RC0-IP0070-070100-011        |
| gb.est;4:AN58103   | +    | 15.00 | 313.48 | 1.2e-08 | 647 | AW58103 AA299326 EST1104 Uterus tumor |
| gb.est;4:AN602133  | +    | 14.00 | 297.93 | 1.0e-07 | 286 | AW602190 RC0-IP0050-180100-011-       |
| gb.est;1:AN029792  | +    | 14.00 | 295.98 | 1.0e-07 | 289 | AA029792 zK07c09_r1 Soares_preg       |
| gb.est;1:AN034297  | +    | 14.00 | 294.62 | 1.4e-07 | 440 | AA034297 zk20ad6_r1 Soares_preg       |
| gb.est;4:AN608486  | -    | 14.00 | 292.54 | 1.8e-07 | 639 | AW608486 RC0-LT0070-170100-031-       |
| gb.est;4:AN362005  | -    | 13.00 | 276.47 | 1.4e-06 | 264 | AW362005 PM2-CM0265-281059-004-       |
| gb.est;5:W26339    | +    | 13.00 | 270.83 | 3.0e-06 | 724 | W26339_26b3_Human retina CDNA         |
| gb.est;4:AN602133  | +    | 12.00 | 253.41 | 2.8e-05 | 381 | AA299326 EST1104 Uterus tumor         |
| gb.est;4:AN581394  | -    | 12.00 | 250.42 | 4.0e-05 | 650 | AW581394 RC0-LT0070-070100-011-       |
| gb.est;4:AN608488  | +    | 12.00 | 230.10 | 4.2e-05 | 688 | AW608488 RC0-LT0070-170100-031-       |
| gb.est;5:W26191    | +    | 11.00 | 231.22 | 0.0005  | 470 | W26191_26b1_Human retina CDNA         |
| gb.est;4:AN608455  | +    | 11.00 | 229.84 | 0.0006  | 602 | AW608455 RC0-LT0070-170100-031-       |
| gb.est;5:DS1546    | +    | 10.00 | 210.57 | 0.0067  | 441 | T644202 yc0906_r1 Stratagene          |
| gb.est;5:AN64402   | +    | 10.00 | 210.15 | 0.0071  | 475 | AW393653 RC5-SF0317-161299-011-       |
| gb.est;4:AN93653   | +    | 10.00 | 209.64 | 0.0076  | 520 | W27250_24d5_Human retina CDNA         |
| gb.est;5:W26650    | -    | 10.00 | 206.48 | 0.0113  | 915 | W26650_34c4_Human retina CDNA         |

|  |   |                      |         |                         |             |                                |
|--|---|----------------------|---------|-------------------------|-------------|--------------------------------|
| gb.est28:AI046001  | +   | 9.00                 | 188.53  | 0.1133                  | 530         | AL046001 DKFZP434P016_r1 434   |
| gb.est54:W26178  | +   | 9.00                 | 187.83  | 0.1239                  | 600         | W26178 2496 Human retina cDNA  |
| gb.est54:W27265  | +   | 9.00                 | 187.71  | 0.1258                  | 613         | W27265 2411 Human retina cDNA  |
| gb.est54:W27702  | +   | 9.00                 | 187.59  | 0.1277                  | 626         | W27702 36611 Human retina cDNA |
| gb.est44:AW607850  | +   | 9.00                 | 187.58  | 0.1280                  | 628         | AW607850 RC0-HT0505-010500-0   |
| gb.est44:AW581394  | -   | 9.00                 | 187.45  | 0.1301                  | 642         | AW581394 RC0-LT0070-070100-0   |
| seq_name: gb_est6:AA385402                                 |   |                      |         |                         |             |                                |
| seq_documentation_block:                                   |   |                      |         |                         |             |                                |
| LOCUS  | A3385402  | 246 bp               | tRNA    | EST                     | 21-APR-1997 |                                |
| DEFINITION   | EST999018   | Thyroid Homo sapiens | CDNA 5' | end similar to amyloid, | A4          |                                |
| beta subunit   |   | mrna sequence.       |         |                         |             |                                |
| ACCESSION  | AA385402  |                      |         |                         |             |                                |
| VERSION  | AA385402.1  |                      |         |                         |             |                                |
| KEYWORDS   |   |                      |         |                         |             |                                |
| SOURCE   |   |                      |         |                         |             |                                |
| ORGANISM   | Homo sapiens  |                      |         |                         |             |                                |
| Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. |   |                      |         |                         |             |                                |
| REFERENCE  | 1 (bases 1 to 246)  |                      |         |                         |             |                                |
| AUTHORS  | Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldhauer,R.A.,   |                      |         |                         |             |                                |
|  | White,C.J., Lee,N.H., Kirchner,E.F., Weinstock,G., Gocayne,J.D.,  |                      |         |                         |             |                                |
|  | Clayton,R.A., Sutton,G., Blakes,J.A., Brandon,R.C., Man-Wai,C.,   |                      |         |                         |             |                                |
|  | Fitzgerald,I.M., Fitchugh,W.M.D., Earle,Hughes,J., Fine,L.D.,   |                      |         |                         |             |                                |
|  | Globe,K.A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinckle,P.S.Jr.,  |                      |         |                         |             |                                |
|  | Kelley,J.M., Kelley,J.C., Liu,L.-I., Marinaro,S.M., Merrick,J.M.,   |                      |         |                         |             |                                |
|  | Moreno-Palauque,R.F., McDonald,D.T., Pellegrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., |                      |         |                         |             |                                |
|  | Bednarcik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,  |                      |         |                         |             |                                |
|  | Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,   |                      |         |                         |             |                                |
|  | He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,  |                      |         |                         |             |                                |
|  | Kozak,D.L., Kunsch,C., Hungjung,J., Li,B., Meissner,P.S., Olsen,H.,   |                      |         |                         |             |                                |
|  | Raymond,L., Wei,Y.F., Wang,J., Xu,G.L., Ruben,S.M.,   |                      |         |                         |             |                                |
|  | Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,   |                      |         |                         |             |                                |
| TITLE  | Initial assessment of human gene diversity and expression patterns  |                      |         |                         |             |                                |
| JOURNAL  | Nature 377 (6547 Suppl), 3-174 (1995)   |                      |         |                         |             |                                |
| MEDLINE  |   |                      |         |                         |             |                                |
| COMMENT  | Other ESTs: THCL72078   |                      |         |                         |             |                                |
|  | Contact: Kerlavage, AR  |                      |         |                         |             |                                |
|  | Bioinformatics  |                      |         |                         |             |                                |
|  | The Institute for Genomic Research  |                      |         |                         |             |                                |
|  | 9712 Medical Center Drive, Rockville, MD 20850 USA  |                      |         |                         |             |                                |
|  | Tel: 301869056  |                      |         |                         |             |                                |
|  | Fax: 3018699423   |                      |         |                         |             |                                |
|  | Email: arkerlav@tigr.org  |                      |         |                         |             |                                |
|  | For clone availability, additional sequence and expression  |                      |         |                         |             |                                |
|  | information related to this EST, please check the TIGR Human Gene   |                      |         |                         |             |                                |
|  | Index ( <a href="http://www.tigr.org/tedb/tgi/gi.html">http://www.tigr.org/tedb/tgi/gi.html</a> )                     |                      |         |                         |             |                                |
|  | Seq primer: M13 Reverse   |                      |         |                         |             |                                |
| FEATURES   | source  |                      |         |                         |             |                                |
|  | 1. 246  |                      |         |                         |             |                                |
|  | /organism="Homo sapiens"  |                      |         |                         |             |                                |
|  | /db_xref="ITCC (inhost):189572"   |                      |         |                         |             |                                |
|  | /db_xref="taxon:9606"   |                      |         |                         |             |                                |
|  | /clone_id="Thyroid"   |                      |         |                         |             |                                |
|  | /dev_stage="adult"  |                      |         |                         |             |                                |
|  | /note="Organ: thyroid gland; Vector: pBluescript SK+;   |                      |         |                         |             |                                |
|  | Site_1: ECoRI; Site_2: XbaI"  |                      |         |                         |             |                                |
|  | 1. 70 a   | 48 c                 | 68 g    | 58 t                    | 2 others    |                                |
| ORIGIN   |   |                      |         |                         |             |                                |

US-09-155-076-2 x AA385402 .. LOCUS AI909276 278 bp mRNA EST 30-MAR-2000  
 DEFINITION QV-BT02-070599-188 BT202 Homo sapiens cDNA, mRNA sequence.  
 ACCESSION AI909216  
 VERSION AI909276.1 GI:6499956  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Chordata; Vertebrata; Buteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 278)  
 REFERENCE Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
 AUTHORS Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,  
 Brunsstein,A., de Oliveira,P.S., Bucher,P., Jongeneel,C.V.,  
 O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
 Simpson,A.J.  
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 COMMENT On Jan 19, 1998 this sequence version replaced gi:2284565.  
 CONTACT: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
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 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (<http://www.ludwig.org.br/seq/gethtml.pl?tl=qv&t2=QV-BT202-188.html&t3=070599-188&t4=1>)  
 Seq primer: puc 18 forward.

FEATURES Location/Qualifiers  
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 /db\_xref="taxon:9606"  
 /clone\_lib="PRT202"  
 /sex="Female"  
 /dev\_stage="Adult"  
 /note="Organ: breast; Vector: puc18; Site\_1: SmaI; Site\_2:  
 Smal; A mini-library was made by cloning products derived  
 from ORESTES PCR (U.S. Letters Patent application No.  
 196,716 - Ludwig Institute for Cancer Research) profiles  
 into the PUC 18 vector. Reverse transcription of tissue  
 mRNA and cDNA amplification were performed under low  
 stringency conditions."  
 BASE COUNT 71 a 79 c 54 g 74 t  
 ORIGIN alignment\_scores:  
 Quality: 16.00 Length: 16  
 Ratio: 1.000 Gaps: 0  
 Percent Identity: 100.000 Percent Identity: 100.000  
 alignment\_block:  
 US-09-155-076-2 x AA379017/rev ..  
 Align seg 1/1 to reverse of: AA379017 from: 1 to: 277  
 1 AspAlaGluPheArgHisAspSerGlyTyrgluvalHisHisGlnLys 16  
 220 GATGCCAGATTCCGACATGACTGGATTGAGTCATCATCAAAA 173  
 seq\_name: gb\_est27:AI909276  
 seq\_documentation\_block:

seq\_documentation\_block:  
 LOCUS AA303751 297 bp mRNA EST 18-APR-1997  
 DEFINITION EST16434 Aorta endothelial cells, TNF alpha-treated Homo sapiens  
 cDNA 5' end similar to amyloid, A4 beta subunit, mRNA sequence.  
 ACCESSION AA303751  
 VERSION AA303751.1 GI:1956103

**KEYWORDS** EST.  
**SOURCE** Homo sapiens  
**ORGANISM** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 ("bases 1 to 297")

**REFERENCE** Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fulmer, R.A., White, O., Sutton, G., Blakes, J.A., Brandon, R.C., Mar-wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle, Hughes, J., Fine, L.D., Fitzgerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghegan, N., S., Glodek, A., Gneim, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palauques, R.P., McDonald, D.T., Nguyen, D.T., Pelliigrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Sauudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednark, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Koza, D.L., Kunsch, C., Hungjun, J., Li, H., Weissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wang, J., Xu, G.L., Rubin, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.

**TITLE** Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence  
Nature 377 (6547 Suppl), 3-174 (1995)

**JOURNAL** 12140200  
**COMMENT** On Sep 29, 1997 this sequence version replaced g1:1520591.

Contact: Kerlavage, AR  
Bioinformatics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850 USA  
Tel: 301899056  
Fax: 3018999423  
Email: arterialav@tigr.org  
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)

**FEATURES**  
**SOURCE** 1..297  
Seq primer: M13 Reverse.  
Location/Qualifiers  
1..297  
Organism: "Homo sapiens"  
/db\_xref="ATCC (inhost):115367"  
/db\_xref="taxon:9606"  
/clone\_lib="Aorta endothelial cells, TNF alpha-treated"  
/cell\_type="endothelial cell"  
/dev\_stage="adult"  
/note="Organ: aorta; Vector: pBluescript SK-; Site\_1:  
ECORI; Site\_2: XbaI"  
Align seg 1/1 to: AA303751 from: 1 to: 297  
BASE COUNT 79 a 71 c 79 g 67 t 1 others  
ORIGIN

alignment\_scores:  
Quality: 16.00 Length: 16  
Ratio: 1.000 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignments:  
US-09-155-076-2 x F06018 ..  
Align seg 1/1 to: F06018 from: 1 to: 305  
1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16  
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3 GATGCAGAAATTGCCACATGACTCAGGATATGAAGTCATCATCAAAA 264 DEFINITION RC4-LT00011-100100-012-c11 LT0011 Homo sapiens CDNA, mRNA sequence.  
ACCESSION AW510695  
VERSION AW510695.1  
KEYWORDS EST  
SOURCE human  
ORGANISM Homo sapiens

seq\_name: gb\_est44:AW580695  
seq\_documentation\_block:  
1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16  
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| LOCUS AW510695 306 bp mRNA EST 16-MAR-2000  
3 GATGCAGAAATTGCCACATGACTCAGGATATGAAGTCATCATCAAAA 264 DEFINITION RC4-LT00011-100100-012-c11 LT0011 Homo sapiens CDNA, mRNA sequence.  
ACCESSION AW510695  
VERSION AW510695.1  
KEYWORDS EST  
SOURCE human  
ORGANISM Homo sapiens

seq\_name: gb\_est47:F06018  
seq\_documentation\_block:  
1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16  
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| LOCUS F06018 305 bp mRNA EST 19-FEB-1995  
217 GATGCAGAAATTGCCACATGACTCAGGATATGAAGTCATCATCAAAA 264 DEFINITION HSC001A101 normalized infant brain cDNA Homo sapiens CDNA clone

REFERENCE 1 (bases 1 to 306)  
 AUTHORS HCGP  
 TITLE The FAPESP/LICR Human Cancer Genome Project  
 JOURNAL Unpublished (1999)  
 COMMENT On Jan 6, 2000 this sequence version replaced gi:6676947.  
 Contact: Simpson A.J.G.

FEATURES source  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (<http://www.ludwig.org.br/scripts/gethtml1.pl?pt1=RC4&t2=RC4-LT0011-100100-012-c11&t3=2000-01-10&t4=1>)  
 Seq primer: puc 18 forward

High quality sequence start: 6  
 High quality sequence stop: 306.

FEATURES source  
 1. Location/Qualifiers  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="L7001"  
 /dev\_stage="Adult"  
 /note="Organ: leiomios; Vector: puc18; Site\_1: SmaI;  
 Site\_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) Profiles profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT ORIGIN  
 72 a 80 c 65 g 89 t

alignment\_scores:  
 Quality: 16.00 Length: 16  
 Ratio: 1.000 Gaps: 0  
 Percent Identity: 100.000

alignment\_block:  
 US-09-155-076-2 x AW580695/rev ..

Align seg 1/1 to reverse of: AW580695 from: 1 to: 306

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16  
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 188 GATGCCGAGTTCGGCATGCTCAGGATATGAGTTCTCATCAAAA 141

seq\_name: qb\_est26:AI902528

seq\_documentation\_block:  
 LOCUS AI902528 335 bp mRNA Homo sapiens cDNA, mRNA sequence.  
 DEFINITION EST 30-MAR-2000  
 ACCESSION AI902528.1 GI:6492915  
 VERSION EST.  
 KEYWORDS human.  
 SOURCE Homo sapiens  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 335)  
 REFERENCE Dias, Nero, E., Garcia Correa, R., Verioski-Almeida, S., Briones, M. R., Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F., Goldman, G. H., Carvalho, A. F., de Oliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and Simpson, A. J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags  
 proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 On May 18, 1998 this sequence version replaced gi:3138510.  
 JOURNAL COMMENT  
 Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rue Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (<http://www.ludwig.org.br/seq/gethtml1.pl?pt1=QV-BT009-075.html&t3=101198at4-1>)  
 Seq primer: puc 18 forward.  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="BT009"  
 /sex="Female"  
 /dev\_stage="Adult"  
 /note="Organ: breast; Vector: puc18; Site\_1: SmaI; Site\_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) Profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."  
 BASE COUNT ORIGIN  
 77 a 89 c 76 g 93 t  
 alignment\_scores:  
 Quality: 16.00 Length: 16  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000  
 Percent Identity: 100.000  
 alignment\_block:  
 US-09-155-076-2 x AI902528/rev ..  
 Align seg 1/1 to reverse of: AI902528 from: 1 to: 335  
 1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 312 GATGCCGAGTTCGGCATGCTCAGGATATGAGTTCTCATCAAAA 265  
 seq\_name: qb\_est5:AA322074

seq\_documentation\_block:  
 LOCUS AA322074 338 bp mRNA Homo sapiens cDNA 5', end similar to amyloid, A4 beta subunit, mRNA sequence.  
 DEFINITION AA322074  
 ACCESSION AA322074.1 GI:1974399  
 VERSION EST.  
 KEYWORDS human.  
 SOURCE Homo sapiens  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 338)  
 REFERENCE Adams, M. D., Kerlavage, A. R., Fleischmann, R. D., Fulndner, R. A., Bult, C. J., Kirkness, E. F., Weinstock, R. G., Gocayne, J. G., White, O., Sutton, G., Blake, J. A., Brandon, R. C., Man, Wai, C., Clayton, R. A., Cline, T. R., Cotton, M. D., Earle, Hughes, J., Fine, L. D., Fitzgerald, L. M., Fitzhugh, W. M., Fritchman, J. L., Geoghegan, N. S., Glodek, B., Gnehm, C. L., Hannan, M. C., Hebdom, E., Hinkle, P. S. Jr., Kelley, J. M., Kelley, J. C., Liu, L.-I., Marmaro, S. M., Pellegrino, S. M., Moreira-Palauque, R. F., McDonald, J. A., Nguyen, D. T., Saudek, D. M., Shirley, R., Phillips, C. A., Ryder, S. E., Scott, J. L., Utterback, T. R., Weidman, J. F., Li, Y., Small, K. V., Spriggs, T. A., Brentani, R. R., Reis, L. F., de Souza, S. J., and Bednarik, D. P., Cao, L., Cepeda, M. A., Coleman, T. A., Collins, E. J.,

**JOURNAL** Dimke,D., Feng,D.-F., Ferrie,A., Fischer,A., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.J., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,R., Raymond,L., Wei,Y.F., Weng,J., Xu,C., Yu,G.L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.

**TITLE** Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

**NATURE** 377 (6547 Suppl.), 3-14 (1995)

**MEDLINE** 12140300

**COMMENT** Other ESTs: THC172078

Contact: Kerlavage, AR

Bioinformatics

The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850 USA  
tel: 301869056  
Fax: 301869423  
Email: arteria@tigr.org

For clone availability, additional sequence and expression index (<http://www.tigr.org/tigr/hg1/hg1.html>)

Seq primer: M13 Reverse

1. .338

/organism="Homo sapiens"

/db\_xref="ARCC (Innate):122569"

/clone\_id="Cerebellum II"

/tissue\_type="cerebellum"

/dev\_stage="adult"

/note="Organ: brain; Vector: pBluescript SK-; Site\_1:

Site\_2: XhoI"

BASE COUNT 86 a 78 c 95 g 79 t

ORIGIN

alignment\_scores:

Quality: 16.00

Ratio: 1.000

Percent Similarity: 100.000

Length: 16

Gaps: 0

Percent Identity: 100.000

align\_block:

US-09-155-076-2 x AA322074 ..

Align seg 1/1 to: AA322074 from: 1 to: 338

1 AsPALaGluPheArgHisAsPSPGlyTyroGluValHisGlnLys 16

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210 GATGCAGAATTCGAAATGACTCAGGATATAAGTTCATCATCAAAA 257

seq\_name: 9b\_est26:AI902529

LOCUS AI902529 338 bp mRNA EST 30-MAR-2000

DEFINITION QV-BT009-101198-074 BT009 Homo sapiens cDNA, mRNA sequence.

ACCESSION AI902529

VERSION AI902529.1 GI:6492916

KEYWORDS EST

ORGANISM Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 354)

AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fulndier,R.A.,

Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,

White,O., Sutton,G., Blake,J.A., Branden,R.C., Man,Wai,C.,

Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,

Fitzgerald,L.M., FitzHugh,W.M., Fritchman,J.L., Geoghegan,N.S.,

Glodek,A., Gnehm,C.L., Hana,C., Hedblom,E., Hinkle,F.S.Jr.,

Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaro,S.M., Merrick,J.M.,

Morano-Palangues,R.F., McDonald,L.A., Nguyen,D.T., Pelliigrino,S.M.,

Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,

Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,

Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,

Dinke,D., Feng,D.-F., Ferrie,A., Fisher,C., Hastings,G.A.,

He,W.W., Hu,J.S., Greene,J.M., Gruber,P., Hudson,P., Kim,A.K.,

Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,

Shoemaker,D., Smith,J., Stoffel,W., Tatusov,R., Tatusova,V.,

Taylor,J., Tatusova,V., Tatusov,R., Tatusova,V., Tatusova,V.,

Tatusova,V., Tatusova,V., Tatusova,V., Tatusova,V., Tatusova,V.,

Tatusova,V., Tatusova,V., Tatusova

Raymond,L., Wei,Y.F., Wind,J., Xu,C., Yu,G.L., Ruben,S.M./  
 Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseitine,W.A., Fields,C.,  
 Fraser,C.M. and Venter,J.C.  
 Initial assessment of human gene diversity and expression patterns  
 based upon 83 million nucleotides of cDNA sequence  
 Nature 377 (6547 Suppl.), 3-174 (1995).  
 On Jan 17, 1998 this sequence version replaced gi:1900069.  
 Other ESTs: THC12078  
 Contact: Kerlavage, AR  
 Bioinformatics  
 The Institute for Genomic Research  
 9712 Medical Center Drive, Rockville, MD 20850 USA  
 Tel: 3018699056  
 Fax: 3018699123  
 Email: kerlavag@tigr.org  
 For clone availability, additional sequence and expression  
 information related to this EST, please check the TIGR Human Gene  
 Index (<http://www.tigr.org/cdb/hgi/ngi.html>)  
 Seq. Primer: M13 Reverse.  
**SATURNS**  
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 ECORI; Site\_2: XbaI"  
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 1 AspalagiuphearghisaspSerglytrgluvalhishisGlnLys 16  
 10 GATCGAGATTCCGACATGACICAGGATAGAAGTTCATCATCAAAA 57  
 eq\_name: gb\_est52:T49306  
 eq\_documentation\_block: 383 bp mRNA EST 06-FEB-1995  
 OCUS T49906 r1 Stratagene placenta (#937225) Homo sapiens cDNA clone  
 DEFINITION IMAGE:69779 5' similar to similar to qb:x0989\_rna1 ALZHEIMER'S  
 DISEASE AMYLOID A4 PROTEIN PRECURSOR (HUMAN), mRNA sequence.  
 ACCESSION T49906  
 VERSION T49906.1 GI:651766  
 EST.  
 EYWORDS  
 ORGANISM Homo sapiens  
 SOURCE human.  
 Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 383)  
**REFERENCE**  
**AUTHORS**  
 Chissoe,S., Dietrich,N., Dubugre,T., Favello,A., Gish,W.,  
 Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,N.,  
 Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Raffkin,L.,  
 Rohlfing,T., Scheibenbogen,K., Soares,M.B., Tan,P., Thierry-Mieg,J.,  
 Trevastis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.,  
 and Marra,M.  
**TITLE** Generation and analysis of 280,000 human expressed sequence tags  
**JOURNAL** Genome Res. 6 (9), 807-828 (1996)  
**ISSN** 0897-3129

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| This clone is available royalty-free through LLNL ; contact the IMAGE Consortium ( <a href="http://infoimage.llnl.gov">infoimage.llnl.gov</a> ) for further information. |        |   |                        |        |           |
| Insert Length:   | 1369   | Std Error:  | 0.00                   |        |           |
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|  |        | /sex="female"   |                        |        |           |
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|  |        | /note="Organ: whole brain; Vector: Lafmid BA; Site: 1: Hind III; Site 2: Hind III; 1st strand cDNA was primed with a Not I - Oligo(dT) primer [5'-ACTGGAAATTGGCCGCCAGAAATTTTTTTTTTTTTTTTTT 3'];   |                        |        |           |
|  |        | double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Lafmid BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Patima Bonaldo." |                        |        |           |
| 104  | a      | 85 c  | 106 g                  | 94 t   | 10 others |
|  |        | BASE COUNT  |                        |        |           |
|  |        | DIGITIN   |                        |        |           |

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    Ratio: 1.000           Gaps: 0
  Percent Similarity: 100.000      Percent Identity: 100.000

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DEFINITION 2010g4.r1 Straenomepithelium 937234 Homo sapiens
CDS  clone IMAGE:567318 5' similar to gb:X06989 rnal ALZHEIMER'S
DISEASE AMYLOID A4 PROTEIN PRECURSOR (HUMAN); mRNA sequence.
ACCESSION AA134479
VERSION AA134479.1
SOURCE GI:1692245
ORGANISM Homo sapiens
KEYWORDS human
REFERENCE
AUTHORS
  Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
  Chissoe,S., Dietrich,N., Dubuge,T., Favello,A., Gish,W.,
  Hawkins,M., Hullman,M., Kucaba,T., Lacy,M., Le,N., Le,M.,
  Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Riekin,L.,
  Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry,Meg,J.,
  Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.,
  and Marra,M.
  Generation and analysis of 280,000 human expressed sequence tags
  Genome Res. 6 (9). 807-820 (1996)
  TITLE
  JOURNAL

```

Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway,  
Box 8501, St. Louis, MO 63108  
314-286-1800

Fax: 314 286 1810  
 Email: est@wustl.edu  
**WARNING:** There is evidence that suggests that the 384-well parent plate of this clone contains both human and mouse derived clones. Thus, the origin of this clone is uncertain. This caution should be kept in mind should you use this clone.

This clone is available royalty-free through LInL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
 Insert Length: 1384 Std Error: 0.00  
 Seq primer: -28NL3 rev2 from Amersham  
 High Quality sequence stop: 394.

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| adaptor sequence: 5' CTCGAGTTTCTTCTTCTTCTTCTTCTT 3'_n   |        |
| BASE COUNT  |        |
| 110 a 93 c 117 g 95 t 2 others  |        |
| ORIGIN  |        |

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Seq Primer: -40m13 fwd. Et from Amersham

High quality sequence stop: 423.

Location/Qualifiers

1..461

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/note="Organ: breast; Vector: puc18; Site: 1: SmaI; Site: 2:

SmaI; A mini-library was made by cloning products derived

from ORESTES PCR (U.S. Letters Patent Application No.

196,716 - Ludwig Institute for Cancer Research) profiles

into the PUC 18 vector. Reverse transcription of tissue

mRNA and cDNA amplification were performed under low

tissue conditions."

/sex="male"

/tissue\_type="pooled frontal lobe"

/dev\_stage="adult"

/lab\_host="SOLR (kanamycin resistant)"

/note="Organ: brain; Vector: Bluescript SK; Site: 1:

EcoRI; Stanley Neuropathology Consortium

(www.stanleylab.org) brains S-58, S-65, S-67, S-78,

Random + oligo-dT primed into EcoRI site of ZAP II Vector.

Mass excised. Avg insert length 1.9kb. Custom library

provided by Dr. Nancy Johnston (410) 614-3918,

njl@welchlink.welch.jhu.edu".

101 a 123 C 110 g 126 t 1 others

BASE COUNT

ORIGIN

alignment\_scores;

Quality: 16.00

Length: 16

Ratio: 1.000

Gaps: 0

Percent Similarity: 100.000

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1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisHisGlnLys 16

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314 GATGCCAGATTCCGACATGACTCAGGGATATGAACTCATCATCAAAA 267

seq\_name: gb\_est4:AW001576

seq\_documentation\_block:

LOCUS AW601576 469 bp mRNA

DEFINITION BT0381-270100-073-f06 BT0381 Homo sapiens CDNA, mRNA sequence.

ACCESSION AW601576

VERSION AW601576.1 GI:7306315

EST

KEYWORDS

human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 469)

AUTHORS HCGP http://www.ludwig.org.br/ORESTES.

TITLE The FAPESP/LICR Human Cancer Genome Project

JOURNAL Unpublished (1999)

COMMENT On Jan 6, 2000 this sequence version replaced gi:6677550.

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

<http://www.ludwig.org.br/scripts/gethtml2.pl?1=QY3&t2=BT0381-270100-073-f06&t3=200-01-27&t4=1>

Seq primer: puc 18 forward

High quality sequence start: 111

High quality sequence stop: 469.

Location/Qualifiers

1..469

FEATURES

source

|  |  |                                       |
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| Total number of hits satisfying chosen parameters: | 188963   |                                       |
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| Post-processing:                                   | Maximum Match 10%  |                                       |
|  | Listing first 45 summaries   |                                       |
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|  | SUMMARIES  |                                       |
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| 1  | 92   | 100.0 16 1 R60371 Beta-amyloid (1-16  |
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| 3  | 92   | 100.0 21 1 W08361 Beta-secretase sub  |
| 4  | 92   | 100.0 22 1 R07753 Beta amyloid Protri |
| 5  | 92   | 100.0 28 1 P90381 Synthetic A4 amylo  |
| 6  | 92   | 100.0 28 1 R54702 Beta-amyloid fragm  |
| 7  | 92   | 100.0 28 1 R60368 Beta-amyloid (1-28  |
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| 9  | 92   | 100.0 28 1 W01414 Beta/A4 amyloid pe  |
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| 11   | 92   | 100.0 28 1 R64172 A4-B(1-28) a parti  |
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| 13   | 92   | 100.0 30 1 W81468 Synthetic amyloid   |
| 14   | 92   | 100.0 33 1 W08359 Beta-secretase sub  |
| 15   | 92   | 100.0 33 1 W81469 Synthetic amyloid   |
| 16   | 92   | 100.0 33 1 W80002 Amyloid precursor   |
| 17   | 92   | 100.0 35 1 W02335 Beta-amyloid Pepti  |
| 18   | 92   | 100.0 35 1 W47228 Beta-amyloid Pepti  |
| 19   | 92   | 100.0 35 1 W89355 Beta-amyloid Pepti  |
| 20   | 92   | 100.0 35 1 W89359 Synthetic amyloid   |
| 21   | 92   | 100.0 36 1 W81471 Beta-amyloid (1-38  |
| 22   | 92   | 100.0 38 1 R60362 Human tachykinin a  |
| 23   | 92   | 100.0 38 1 W92722 Beta-amyloid (1-39  |
| 24   | 92   | 100.0 39 1 R60363 Synthetic amyloid   |
| 25   | 92   | 100.0 39 1 W81472 Beta-amyloid Pepti  |
| 26   | 92   | 100.0 40 1 R33191 Beta-amyloid (1-40  |
| 27   | 92   | 100.0 40 1 R60364 Amyloid beta Pepti  |
| 28   | 92   | 100.0 40 1 W23335 Amyloid beta Prote  |
| 29   | 92   | 100.0 40 1 W37507 Beta-amyloid Pepti  |
| 30   | 92   | 100.0 40 1 W47222 Beta-amyloid Pepti  |
| 31   | 92   | 100.0 40 1 W47226 Synthetic amyloid   |
| 32   | 92   | 100.0 40 1 W81473 Human tachykinin a  |
| 33   | 92   | 100.0 40 1 W92723                     |

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| 4  | 92   | 100.0 22 1 R07753 Beta amyloid Protri |
| 5  | 92   | 100.0 28 1 P90381 Synthetic A4 amylo  |
| 6  | 92   | 100.0 28 1 R54702 Beta-amyloid fragm  |
| 7  | 92   | 100.0 28 1 R60368 Beta-amyloid (1-28  |
| 8  | 92   | 100.0 28 1 W01413 Beta/A4 amyloid pe  |
| 9  | 92   | 100.0 28 1 W01414 Beta/A4 amyloid pe  |
| 10   | 92   | 100.0 28 1 R64170 A4-(1-28) a parti   |
| 11   | 92   | 100.0 28 1 R64172 A4-B(1-28) a parti  |
| 12   | 92   | 100.0 28 1 W81467 Synthetic amyloid   |
| 13   | 92   | 100.0 30 1 W81468 Synthetic amyloid   |
| 14   | 92   | 100.0 33 1 W08359 Beta-secretase sub  |
| 15   | 92   | 100.0 33 1 W81469 Synthetic amyloid   |
| 16   | 92   | 100.0 33 1 W80002 Amyloid precursor   |
| 17   | 92   | 100.0 35 1 W02335 Beta-amyloid Pepti  |
| 18   | 92   | 100.0 35 1 W47228 Beta-amyloid Pepti  |
| 19   | 92   | 100.0 35 1 W89355 Beta-amyloid Pepti  |
| 20   | 92   | 100.0 35 1 W89359 Synthetic amyloid   |
| 21   | 92   | 100.0 36 1 W81471 Beta-amyloid (1-38  |
| 22   | 92   | 100.0 38 1 R60362 Human tachykinin a  |
| 23   | 92   | 100.0 38 1 W92722 Beta-amyloid (1-39  |
| 24   | 92   | 100.0 39 1 R60363 Synthetic amyloid   |
| 25   | 92   | 100.0 39 1 W81472 Beta-amyloid Pepti  |
| 26   | 92   | 100.0 40 1 R33191 Beta-amyloid (1-40  |
| 27   | 92   | 100.0 40 1 R60364 Amyloid beta Pepti  |
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| 30   | 92   | 100.0 40 1 W47222 Beta-amyloid Pepti  |
| 31   | 92   | 100.0 40 1 W47226 Synthetic amyloid   |
| 32   | 92   | 100.0 40 1 W81473 Human tachykinin a  |
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PA (ISIS-) ISIS INNOVATION LTD.  
 PI Greenfield SA, Vaux DJ;  
 DR WPI; 97-4896245.  
 PT Peptide(s) from acetylcholine esterase which open calcium channels -  
 PT used for treating disorders of the central nervous system, cancer  
 and stroke  
 PS Claim 3; Page 20; 27PP; English.  
 This 16-mer peptide is present in a region of the beta-amyloid precursor polypeptide. This region lies at the amino acid terminus of the 42 residue peptide which accumulates in Alzheimer's disease. The 16-mer has at least 70% homology with the beta-amyloid precursor. This peptide is known to act alone or in synergism with a fragment of acetylcholinesterase (W5340-W5353) to contribute to neuronal degeneration. Compounds that inhibit the biological activity of the novel peptides, and antibodies, can be used to control cytoplasmic calcium ion currents *in vivo*, and are useful for treating disorders of the central nervous system (e.g. Parkinson's and Alzheimer's diseases), stroke and cancer.

Sequence 16 AA;

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 Best Local Similarity 100.0%; Pred. No. 5.e-09;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQK 16  
 Db 1 DAEFRHDSGYEVHHQK 16

RESULT 3  
 ID W08361 standard; peptide; 21 AA.  
 AC W08361;  
 DT 05-SEP-1997 (first entry)  
 DE Beta-secretase substrate #3.  
 KW Beta-cleavage site; beta amyloid precursor protein; APP; beta-secretase; inhibitor; Alzheimer's disease;  
 alpha-secretase; proteolytic cleavage; inhibitor; Alzheimer's disease.  
 SYNTETIC  
 OS Synthetic.

PN W0864085-A2.  
 PD 19-DEC-1996.  
 PF 07-JUN-1996; US-099851.  
 PR 07-JUN-1995; US-485152.  
 PR 07-JUN-1995; US-480498.

PA (ATHE-) ATHENA NEUROSCIENCES INC.  
 PI Anderson JP, Chrysier SMS, Jacobson-oroak KL, Kelim PS;  
 PI Mcconlogue LC, Sinha S, Tan H;

DR WPI; 97-02304/05  
 PT Beta-secretase which specifically cleaves beta-amyloid precursor protein - useful to screen for inhibitors useful in treatment of Alzheimer's disease

PS Disclosure: Page 45; 92PP; English.  
 CC W08362 represents substrates for the enzyme of the invention. The enzyme of the invention is beta-secretase, and specifically cleaves beta-amyloid precursor protein (beta-APP). Normal processing of beta-APP is thought to occur via cleavage between residues 16 and 17 of the beta-amyloid peptide region by an alpha-secretase. Pathogenic processing is thought to occur by beta-secretase cleavage of beta-APP.  
 CC Beta-secretase activity can be detected and measured using a method of the invention, which detects at least one of the beta-secretase cleavage products formed on cleavage. The method can be used to determine whether a test substance inhibits proteolytic cleavage, by beta-secretase, of beta-APP. Compounds effective to at least partially inhibit beta-secretase activity can be used to inhibit cleavage of beta-APP in cells or mammalian hosts. Isolation and purification of beta-secretase will permit chemical modelling of a critical event in the pathology of Alzheimer's disease.  
 Sequence 21 AA;

Qy 1 DAEFRHDSGYEVHHQK 16  
 Db 6 DAEFRHDSGYEVHHQK 21

RESULT 4

ID R07753 standard; protein; 22 AA.  
 AC R07753  
 PT 22-FEB-1991 (first entry)  
 DE Bta-amyloid protein, SCYAP2.  
 KW Monoclonal antibody SV17-6E10; Down's syndrome; Alzheimer's disease; beta-amyloid precursor; amyloid plaques.  
 OS synthetic.  
 PN WO912871-A.  
 PD 01-NOV-1990.  
 PR 14-APR-1999; US-3339983.

PA (REME ) RES FOUND MENTAL HY.  
 PI Kim KS, Wisniewski HM, Wen GY, Chen CMJ, Sapienza VJ;  
 DR WPI; 90-348474/46.  
 PT Cerebrovascular amyloid protein-specific monoclonal antibody SV17-6E10 - for immunoassay of peptide whose levels are raised in Down's syndrome or Alzheimer's disease patients  
 PT This Peptide is used in a "Double Ab Sandwich Immunoassay" to detect beta-amyloid protein. SV17-6E10 MAb (capture Ab) is used to coat microtitre plate wells. The plate is then washed (distilled water), coated with PBS(TGB) and this (scvAP2) protein is added. The plate is washed and a 2nd Ab (detection Ab), MAb 4G8-CC added. This double Ab sandwich ELISA test is a highly sensitive and accurate detection system for the beta-amyloid protein.  
 CC See also R07752.  
 SQ Sequence 22 AA;

Query Match 100.0%; Score 92; DB 1; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 8e-09;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQK 16  
 Db 1 DAEFRHDSGYEVHHQK 16

RESULT 5

ID P90381 standard; protein; 28 AA.  
 AC P90381;  
 DT 1-NOV-1989 (first entry)  
 DE Synthetic A4 amyloid polypeptide  
 KW Synthetic; A4 amyloid polypeptide; Alzheimer's disease;  
 KW Immunassays; antibodies  
 OS Synthetic  
 PN W08905242-A.  
 PD 13-JUL-1989.  
 PR 08-OCT-1987; US-105751.  
 PA (MCLE) McLean Hospital Corp; (UYRO) University of Rochester.  
 PI Majocha R, Marotta CA, Zain S;  
 DR WPI; 89-220551/30.  
 PT Antibodies to A4 amyloid polypeptide  
 CC used in immunassays and for imaging of A4 amyloid  
 CC in Alzheimer's disease patients.  
 CC Claim 1; page 27; 30PP; English.  
 CC Synthetic A4 amyloid polypeptide (see also P90382, P90383). Used in  
 CC as immunogen, (un)coupled, or to produce antibodies. Used in  
 CC immunassays and for imaging of A4 amyloid in Alzheimer's disease.  
 SQ Sequence 28 AA;

Query Match 100.0%; Score 92; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 7.6e-09;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match

100.0%; Score 92; DB 1; Length 28;

| Best Local Similarity 100.0%; Pred. No. 1e-08; Mismatches 0; Indels 0; Gaps 0; Sequence 28 AA; |                     |                                     |   |                     |   |   |   |                  |   |
|--|---------------------|-------------------------------------|---|---------------------|---|---|---|------------------|---|
| <b>RESULT 6</b>  |                     |                                     |   |                     |   |   |   |                  |   |
| R54702   | 1 DAEFRHDSGYEVHK 16 | ID R54702 standard; peptide; 28 AA. | Qy  | 1 DAEFRHDSGYEVHK 16 | AC R54702; 15-DEC-1994 (first entry)  | DE Beta-amyloid fragment (1-28).                | KW Beta-amyloid protein; BAP; Alzheimer's disease; diagnosis; Homo sapiens.   | OS WO9409364-A.  | SQ PN 28-APR-1994.                        |
| AC   | R54702              |                                     | PF 13-OCT-1993; 009772.   |                     | DE  | (UYDP-) UNIV DUKE.                              |   |                  | PD 13-OCT-1992; US-959251.                |
| DE   |                     |                                     | PA Strittmatter WJ;   |                     | PI  | PI: 94-11484-18.                                |   |                  | PS Page 28; 40pp; English.                |
| KW   |                     |                                     | DR Immobilised beta-amyloid protein or fragments - used in assays for obtaining prods for use in the diagnosis and treatment of Alzheimer's disease.  |                     | CC A construct comprising a beta-amyloid protein (BAP) or fragment (esp. the peptides given in R54702-03) immobilised on a solid support can be used to detect cdps which bind to BAP. Binding of proteins in human cerebrospinal fluid protiens were shown to bind to beta-amyloid peptides 1-28 and 12-28. Hydropathic mimic peptide (12-28) was used as control. | CC  | CC  | CC               | CC  |
| OS   |                     |                                     | PT  |                     | CC  | CC  | CC  | CC               | CC  |
| SQ   |                     |                                     | PT  |                     | CC  | CC  | CC  | CC               | CC  |
| <b>RESULT 7</b>  |                     |                                     |   |                     |   |   |   |                  |   |
| R60368   | 1 DAEFRHDSGYEVHK 16 | ID R60368 standard; peptide; 28 AA. | Qy  | 1 DAEFRHDSGYEVHK 16 | AC 15-MAR-1995 (first entry)  | DE Beta-amyloid (1-28).                         | KW Amyloid precursor protein; APP; Alzheimer's disease; beta-amyloid; anti-beta amyloid antibody; diagnosis; immunogen; antigen; epitope. Homo sapiens.   | OS WO9417197-A.  | SQ PN 04-AUG-1994.                        |
| AC   | R60368              |                                     | PF 24-JAN-1994; J00089  |                     | DE  | DE  |   |                  | PD 05-JAN-1993; JP-01032.                 |
| DE   |                     |                                     | PR 05-FEB-1993; JP-01933.   |                     | KW  | PR 16-NOV-1993; JP-286385.                      |   |                  | PR 28-DEC-1993; JP-33473.                 |
| KW   |                     |                                     | PA (TAKE ) TAKEDA CHEM IND LTD.   |                     | CC  | PA Kitada C, Odaka A, Suzuki N.                 |   |                  | PT WO94-26410/32.                         |
| OS   |                     |                                     | PT Antibodies recognising specific parts of beta-amyloid - can be used for diagnosis of diseases implicating beta-amyloid, such as Alzheimer's disease  |                     | CC  | CC  | CC  | CC               | PT PS Claim 7; Page 84; 116pp; Japanese.  |
| SQ   |                     |                                     | CC Antibodies which recognise specific subfragments of the beta-amyloid protein are claimed. Specifically, the antibodies (which are pref. monoclonal) recognise residues 1-16 and/or 1-28 from the N-terminal portion of beta-amyloid or they recognise residues 25-35 or 43 from the C-terminal portion. The antibodies are useful for assaying |                     | CC  | CC  | CC  | CC               | PT PS Claim 7; Page 84; 116pp; Japanese.  |
| <b>RESULT 8</b>  |                     |                                     |   |                     |   |   |   |                  |   |
| R01413   | 1 DAEFRHDSGYEVHK 16 | ID WO1413 standard; Protein; 28 AA. | Qy  | 1 DAEFRHDSGYEVHK 16 | AC WO1413; 20-JAN-1997 (first entry)  | DE Beta/A4 amyloid peptide residues 1-28.       | KW Alzheimer's disease; stimulation; investigation; pathogenesis; hereditary cerebral haemorrhage with amyloidosis Dutch type; control; cerebral amyloid angiopathy; cerebral; haemorrhage; Homo sapiens.   | OS WO9615799-A1. | SQ PN 28-APR-1994.                        |
| AC   | R01413              |                                     | PF 30-MAY-1996; U15007.   |                     | DE  | CC  | CC  | CC               | PD 22-NOV-1995; U15007.                   |
| DE   |                     |                                     | PR 22-NOV-1994; US-347144.  |                     | KW  | CC  | CC  | CC               | PA (RUTF ) UNIV RUTGERS STATE NEW JERSEY. |
| KW   |                     |                                     | PA Anderson S.  |                     | CC  | CC  | CC  | CC               | PI WPI; 96-268332/27.                     |
| OS   |                     |                                     | DR  |                     | CC  | CC  | CC  | CC               | CC  |
| SQ   |                     |                                     | PT Use of agents which bind beta-amyloid peptide - for diagnosis, prevention and treatment of vascular damage caused by amyloid deposits, partic. in haemorrhaging and Alzheimer's disease  |                     | PT  | PT  | PT  | PT               | PT  |
| <b>RESULT 9</b>  |                     |                                     |   |                     |   |   |   |                  |   |
| R01414   | 1 DAEFRHDSGYEVHK 16 | ID WO1414 standard; Protein; 28 AA. | Qy  | 1 DAEFRHDSGYEVHK 16 | AC WO1414; 20-JAN-1997 (first entry)  | DE Beta/A4 amyloid peptide residues 1-28 Dutch. | KW Beta/A4 amyloid peptide; tissue plasminogen activator; Dutch; Alzheimer's disease; stimulation; investigation; pathogenesis; hereditary cerebral haemorrhage with amyloidosis Dutch type; control; cerebral amyloid angiopathy; cerebral; haemorrhage. | OS WO9615799-A1. | SQ PN 28-APR-1994.                        |
| AC   | R01414              |                                     | PF 1 DAEFRHDSGYEVHK 16  |                     | DE  | CC  | CC  | CC               | PD 1 DAEFRHDSGYEVHK 16                    |
| DE   |                     |                                     | PR 1 DAEFRHDSGYEVHK 16  |                     | KW  | CC  | CC  | CC               | PA 1 DAEFRHDSGYEVHK 16                    |

KW control; cerebral amyloid angiopathy; cerebral; haemorrhage;  
 KW hemorrhage.  
 OS Homo sapiens. Location/Qualifiers  
 FH Key misc\_difference 22  
 FT /note= "wild type Glu substd. with Gln"  
 PN W09615799-A1.  
 PD 30-MAY-1996.  
 PR 22-NOV-1995; US-15007.  
 PR 22-NOV-1994; US-347144.  
 PA (RUTF ) UNIV RUTGERS STATE NEW JERSEY.  
 PI Anderson, S;  
 WP; 96-268332/27.  
 DR ;  
 PT use of agents which bind beta-amyloid peptide - for diagnosis,  
 PT prevention and treatment of vascular damage caused by amyloid  
 deposits, partic. in haemorrhaging and Alzheimer's disease  
 Example 1; Fig 1; 52pp; English.  
 PS To investigate the effects of beta-amyloid peptide (BAP) on  
 CC tissue plasminogen activator (t-PA) 3 synthetic peptides were used.  
 One peptide contained 42 amino acids and corresponds to the full  
 CC length BAP (R95248). The other 2 peptides (R95249 and 50) contained  
 the 28 N-terminal residues of the BAP found in Alzheimer's disease  
 and hexapeptide cerebral haemorrhage with amyloidosis-Dutch type  
 (HCHWA-D), respectively. In an assay to determine the effect of  
 the peptides on t-PA activation, each peptide (R95248, 49 and 50)  
 CC gave 1st order rate constant of activation ( $k_{app}$ ) values of  
 13, 4, 13, 9 and 14, 5, respectively, compared to 1, 7, and 7, 8 for nill  
 CC and fibrinogen controls. The results demonstrate that the BAP are  
 able to stimulate t-PA activity in vitro, which is significant in  
 CC that it provides a means for investigating and controlling the  
 CC pathogenesis of Alzheimer's disease, HCHWA-D and cerebral amyloid  
 angiopathy related cerebral haemorrhage.  
 Sequence 28 AA;

Query Match 100.0%; Score 92; DB 1; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 1e-08;  
 Matches 16; Conservative 0; Mismatches 0; Gaps 0;  
 Indels 0;

QY 1 DAEFRHDSGYEVHK 16  
 Db 1 DAEFRHDSGYEVHK 16

RESULT 10  
 R64170 ID R64170 standard; peptide: 28 AA.  
 AC R64170;  
 DT 03-AUG-1995 (first entry)

DE A4-(1-28) a partial beta amyloid peptide.  
 KW beta amyloid protein; mutant; variant; detection; amyloid deposition;  
 KW diagnosis; amyloidosis associated disease; Alzheimer's disease;  
 KW Down's syndrome; A4-(1-28).  
 OS Synthetic.  
 PD 08-DEC-1994; 005809.  
 PR 27-MAY-1993; US-05809.

(MIRI-) MIRIAM HOSPITAL.

PI Majocha RE, Marotta CA;

WP; 95-023013/03.

PT Amyloid binding composition comprising labelled amyloid protein  
 and carrier - useful for *in vivo* imaging of amyloid deposits, for  
 diagnosing Alzheimer's disease and Down's Syndrome.  
 Example 1; Page 23; 58pp; English.  
 R64170, the A4-(1-28) polypeptide is the first 28 amino acids of the  
 4.2 kd peptide derived from senile plaque cores of an AD (Alzheimer's  
 disease) brain. Known as beta amyloid A4-O has strong aggregation  
 properties, and binds to itself strongly. This peptide is used to obtain  
 and select beta amyloid proteins that can be used for *in vivo* imaging  
 of amyloid deposits and hence diagnosis of an amyloidosis-associated  
 disease, such as AD or Down's syndrome. R64165 shows the generic sequence  
 of the amyloid protein for generation of variants.

SQ Sequence 28 AA;  
 Query Match 100.0%; Score 92; DB 1; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 1e-08;  
 Matches 16; Conservative 0; Mismatches 0; Gaps 0;  
 Indels 0;

QY 1 DAEFRHDSGYEVHK 16  
 Db 1 DAEFRHDSGYEVHK 16

RESULT 11  
 R64172 ID R64172 standard; peptide: 28 AA.

AC R64172;  
 DT 03-AUG-1995 (first entry)

DE A4-B-(1-28) a partial beta amyloid peptide.  
 KW beta amyloid protein; mutant; variant; detection; amyloid deposition;  
 KW diagnosis; amyloidosis associated disease; Alzheimer's disease;  
 KW Down's syndrome; A4-B(1-28).  
 OS Synthetic.  
 PD 08-DEC-1994; 005809.  
 PR 27-MAY-1994; U05809.  
 PR 28-MAY-1993; US-06910.  
 PR (MIRI-) MIRIAM HOSPITAL.  
 PI Majocha RE, Marotta CA;  
 DR WP; 95-023013/03.  
 PT Amyloid binding composition comprising labelled amyloid protein  
 and carrier - useful for *in vivo* imaging of amyloid deposits, for  
 diagnosing Alzheimer's disease and Down's Syndrome.  
 Example 3; Page 23; 58pp; English.

CC R64172, the A4-B(1-28) polypeptide is deriv. from vascular amyloid of the  
 CC AD (Alzheimer's disease) brain and a Down Syndrome brain. Three of the  
 CC 28 amino acids are different from the A4-(1-28) peptide shown in R64170.  
 CC A4-O has strong aggregation properties, and binds to itself strongly. It  
 CC is used to obtain and select beta amyloid proteins that can be used for  
 CC *in vivo* imaging of amyloid deposits and hence diagnosis of an  
 CC amyloidosis-associated disease, such as AD or Down's syndrome. R64165  
 CC shows the generic sequence of the amyloid protein for generation of  
 CC variants.  
 SQ Sequence 28 AA;

Query Match 100.0%; Score 92; DB 1; Length 28;

Best Local Similarity 100.0%; Pred. No. 1e-08;  
 Matches 16; Conservative 0; Mismatches 0; Gaps 0;

QY 1 DAEFRHDSGYEVHK 16  
 Db 1 DAEFRHDSGYEVHK 16

RESULT 12

W81467

ID W81467 standard; peptide: 28 AA.

AC W81467;

DT 28-JAN-1999 (first entry)

DE Synthetic amyloid beta (Abeta) peptide 2 (residues 1-28).  
 KW Amyloid beta; Abeta; deoxyriinated solvent; evaporative deposition;  
 KW research; neurotoxicity; free-radical; glutamine synthetase.

OS Synthetic.

PD 24-NOV-1998.

PS Page 23; 58pp; English.

CC R64170, the A4-O(1-28) polypeptide is the first 28 amino acids of the

CC 4.2 kd peptide derived from senile plaque cores of an AD (Alzheimer's

CC disease) brain. Known as beta amyloid A4-O has strong aggregation

CC properties, and binds to itself strongly. This peptide is used to obtain

CC and select beta amyloid proteins that can be used for *in vivo* imaging

CC of amyloid deposits and hence diagnosis of an amyloidosis-associated

CC disease, such as AD or Down's syndrome. R64165 shows the generic sequence

CC of the amyloid protein for generation of variants.

PS

CC Sequences W81466 to W81476 represent synthetic amyloid beta (Abeta) peptides. The invention provides a process for treating a synthetic Abeta peptide that comprises dissolving the peptide in a deoxygenated solvent selected from trifluoroethanol, hexafluorocyclohexane, dimethyl sulphoxide, morpholinopropanesulphonic acid, dimethylformamide and acetonitrile to a concentration of 0.01-10 mg/ml, incubating the solution at 20-65 deg. C for 0.5-4 hour, and removing the solvent by 'evaporative deposition', in 5-10 minutes. Synthetic amyloid beta peptides are useful as research tools for studying neurotoxicity resulting from Abeta peptide -enhanced free-radical production. The treatment increases the activity of the synthetic Abeta peptides in tests to determine free-radical generating capacity and glutamine synthetase inactivation. Sequence 28 AA;

Query Match 100.0%; Score 92; DB 1; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1e-08; Gaps 0;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 DAEFRHDSGYEVHHQK 16  
Db 1 DAEFRHDSGYEVHHQK 16

RESULT 13  
W81468 ID W81468 standard; Peptide; 30 AA.  
AC W81468;  
DT 28-JAN-1999 (first entry)  
DE Synthetic amyloid beta (Abeta) peptide 3 (residues 1-30).  
KW Anyloid beta; Abeta; deoxygenated solvent; evaporative deposition;  
KW research; neurotoxicity; free-radical; glutamine synthetase.  
OS Synthetic.  
PN US5840538-A.  
PD 24-NOV-1998.  
PF 29-FEB-1998; 603090.  
PA (KENT ) UNIV KENTUCKY RES FOUND.  
PI Aksenen M, Butterfield DA, Carney JM, Hensley K;  
DR WPI; 99-03120/03.  
PT Process for treating synthetic amyloid beta peptides - by organic solvent treatment, useful for studying neurotoxicity  
PS Claim 5; Columns 9-10; 14P; English.  
CC Sequences W81466 to W81476 represent synthetic amyloid beta (Abeta) peptides. The invention provides a process for treating a synthetic Abeta peptide that comprises dissolving the peptide in a deoxygenated solvent selected from trifluoroethanol, hexafluorocyclohexane, dimethyl sulphoxide, morpholinopropanesulphonic acid, dimethylformamide and acetonitrile to a concentration of 0.01-10 mg/ml, incubating the solution at 20-65 deg. C for 0.5-4 hour, and removing the solvent by 'evaporative deposition', in 5-10 minutes. Synthetic amyloid beta peptides are useful as research tools for studying neurotoxicity resulting from Abeta peptide -enhanced free-radical production. The treatment increases the activity of the synthetic Abeta peptides in tests to determine free-radical generating capacity and glutamine synthetase inactivation. Sequence 30 AA;

Query Match 100.0%; Score 92; DB 1; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1e-08; Gaps 0;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 DAEFRHDSGYEVHHQK 16  
Db 1 DAEFRHDSGYEVHHQK 16

RESULT 14  
W08359 ID W08359 standard; Peptide; 33 AA.  
AC W08359;  
DT 05-SEP-1997 (first entry)  
DE Beta-secretase substrate #1.

Beta-cleavage site; beta amyloid precursor protein; APP; beta-secretase; alpha-secretase; proteolytic cleavage; inhibitor; Alzheimer's disease. Synthetic.  
KW KW  
CC PN W09610885-A2.  
CC PD 19-DEC-1996  
CC PF 07-JUN-1996; 009985.  
CC PR 07-JUN-1995; US-485152.  
CC PR 07-JUN-1995; US-480498.  
(ATHENE ) ATHENA NEUROSCIENCES INC  
PA Anderson JP, Chrysler SMS, Jacobson croak KL, Keim PS;  
PI McConlogue LC, Sinha S, Tan H;  
WP; 97-052304/05.  
PR Beta-secretase which specifically cleaves beta-amyloid precursor protein - useful to screen for inhibitors useful in treatment of Alzheimer's disease  
PT Disclosure; Page 44; 92PP; English.  
PS W08359-W08362 represent substrates for the enzyme of the invention. The enzyme of the invention is beta-secretase, and specifically cleaves beta-amyloid precursor protein (beta-APP). Normal processing of beta-APP is thought to occur via cleavage between residues 16 and 17 of the beta-amyloid peptide region by an alpha-secretase. Pathogenic processing is thought to occur by beta-secretase cleavage of beta-APP. Beta-secretase activity can be detected and measured using a method of the invention, which detects at least one of the beta-secretase cleavage products formed on cleavage. The method can be used to determine whether a test substance inhibits proteolytic cleavage, by beta-secretase, of beta-APP. Compounds effective to at least partially inhibit beta-secretase activity can be used to inhibit cleavage of beta-APP in cells or mammalian hosts. Isolation and Purification of beta-secretase will permit chemical modelling of a critical event in the pathology of Alzheimer's disease. Sequence 33 AA;

Query Match 100.0%; Score 92; DB 1; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.3e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 DAEFRHDSGYEVHHQK 16  
Db 18 DAEFRHDSGYEVHHQK 33

RESULT 15  
W81469 ID W81469 standard; Peptide; 33 AA.  
AC W81469;  
DT 28-JAN-1999 (first entry)  
DE Synthetic amyloid beta (Abeta) peptide 4 (residues 1-33).  
KW Anyloid beta; Abeta; deoxygenated solvent; evaporative deposition; research; neurotoxicity; free-radical; glutamine synthetase.  
OS Synthetic.  
PN US5840538-A.  
PD 24-NOV-1998.  
PR 29-FEB-1996; 603090.  
PA (KENT ) UNIV KENTUCKY RES FOUND.  
PI Aksenen M, Butterfield DA, Carney JM, Hensley K;  
DR WPI; 99-034120/03.  
PT Process for treating synthetic amyloid beta peptides - by organic solvent treatment, useful for studying neurotoxicity  
PS Claim 5; Columns 9-10; 14P; English.  
CC Sequences W81466 to W81476 represent synthetic amyloid beta (Abeta) peptides. The invention provides a process for treating a synthetic Abeta peptide that comprises dissolving the peptide in a deoxygenated solvent selected from trifluoroethanol, hexafluorocyclohexane, dimethyl sulphoxide, morpholinopropanesulphonic acid, dimethylformamide and acetonitrile to a concentration of 0.01-10 mg/ml, incubating the solution at 20-65 deg. C for 0.5-4 hour, and removing the solvent by 'evaporative deposition', in 5-10 minutes. Synthetic amyloid beta peptides are useful as research tools for studying neurotoxicity resulting from Abeta peptide -enhanced free-radical production. The treatment increases the activity of the synthetic Abeta peptides in tests to determine free-radical generating capacity and glutamine synthetase inactivation. Sequence 30 AA;

Query Match 100.0%; Score 92; DB 1; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.1e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 DAEFRHDSGYEVHHQK 16  
Db 1 DAEFRHDSGYEVHHQK 16

RESULT 14  
W08359 ID W08359 standard; Peptide; 33 AA.  
AC W08359;  
DT 05-SEP-1997 (first entry)  
DE Beta-secretase substrate #1.

Synthetic amyloid beta peptides are useful for studying neurotoxicity as research tools for studying neurotoxicity resulting from Abeta peptide -enhanced free-radical production. The treatment increases the activity of the synthetic Abeta peptides in tests to determine free-radical

CC generating capacity and glutamine synthetase inactivation.  
Sequence 33 AA;

SQ  
Query Match 100.0%; Score 92; DB 1; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.3e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;  
QY 1 DAEFRHDSGYEVHK 16  
| | | | | | | | | | | | | |  
Db 1 DAEFRHDSGYEVHK 16

Search completed: September 13, 2000, 02:21:37  
Job time: 140 sec

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OM protein - protein search, using sw model.

Run on: September 13, 2000, 02:22:01 ; Search time 14.59 Seconds  
(without alignments)  
16.811 Million cell updates/sec

Title: US-09-155-076-2  
Perfect score: 92  
Sequence: 1 DAEFRHDSGYVHQK 16

Scoring table: BloSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 15329161 seqs, 15329161 residues

total number of hits satisfying chosen parameters: 152396

Minimum DB seq length: 0  
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA:  
1: /cgn2\_6/ptodata/2/1aa/5A\_COMBO.pep:  
2: /cgn2\_6/ptodata/2/1aa/5B\_COMBO.pep:  
3: /cgn2\_6/ptodata/2/1aa/6\_COMBO.pep:  
4: /cgn2\_6/ptodata/2/1aa/PCUTUS\_COMBO.pep:  
5: /cgn2\_6/ptodata/2/1aa/backfiller1.pep:  
\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query | Match | Length | DB ID             | Description        |
|------------|-------|-------|-------|--------|-------------------|--------------------|
| 1          | 92    | 100.0 | 16    | 1      | US-09-302-808-10  | Sequence 10, Appli |
| 2          | 92    | 100.0 | 16    | 2      | US-09-986-948-10  | Sequence 10, Appli |
| 3          | 92    | 100.0 | 21    | 2      | US-08-659-984A-18 | Sequence 18, Appli |
| 4          | 92    | 100.0 | 27    | 1      | US-08-141-324-11  | Sequence 11, Appli |
| 5          | 92    | 100.0 | 27    | 1      | US-08-141-324-12  | Sequence 12, Appli |
| 6          | 92    | 100.0 | 27    | 1      | US-08-541-902-11  | Sequence 11, Appli |
| 7          | 92    | 100.0 | 27    | 1      | US-08-541-902-12  | Sequence 12, Appli |
| 8          | 92    | 100.0 | 28    | 1      | US-08-346-849-4   | Sequence 4, Appli  |
| 9          | 92    | 100.0 | 28    | 1      | US-08-302-808-7   | Sequence 7, Appli  |
| 10         | 92    | 100.0 | 28    | 2      | US-08-609-904-2   | Sequence 2, Appli  |
| 11         | 92    | 100.0 | 28    | 2      | US-08-986-948-7   | Sequence 7, Appli  |
| 12         | 92    | 100.0 | 28    | 2      | US-08-293-284A-4  | Sequence 4, Appli  |
| 13         | 92    | 100.0 | 28    | 2      | US-08-461-216-2   | Sequence 2, Appli  |
| 14         | 92    | 100.0 | 30    | 2      | US-08-609-090-3   | Sequence 3, Appli  |
| 15         | 92    | 100.0 | 33    | 2      | US-08-609-090-4   | Sequence 4, Appli  |
| 16         | 92    | 100.0 | 33    | 1      | US-08-659-984A-16 | Sequence 16, Appli |
| 17         | 92    | 100.0 | 35    | 1      | US-08-304-585-6   | Sequence 6, Appli  |
| 18         | 92    | 100.0 | 35    | 2      | US-08-612-785B-15 | Sequence 15, Appli |
| 19         | 92    | 100.0 | 35    | 2      | US-08-612-785B-38 | Sequence 38, Appli |
| 20         | 92    | 100.0 | 36    | 2      | US-08-609-090-6   | Sequence 6, Appli  |
| 21         | 92    | 100.0 | 38    | 1      | US-08-302-008-1   | Sequence 1, Appli  |
| 22         | 92    | 100.0 | 38    | 2      | US-07-737-371E-68 | Sequence 1, Appli  |
| 23         | 92    | 100.0 | 39    | 1      | US-08-986-948-1   | Sequence 1, Appli  |
| 24         | 92    | 100.0 | 39    | 1      | US-08-302-808-2   | Sequence 2, Appli  |
| 25         | 92    | 100.0 | 39    | 2      | US-08-609-090-7   | Sequence 7, Appli  |
| 26         | 92    | 100.0 | 39    | 2      | US-08-682-24A-1   | Sequence 1, Appli  |
| 27         | 92    | 100.0 | 39    | 2      | US-08-986-948-2   | Sequence 2, Appli  |
| 28         | 92    | 100.0 | 40    | 1      | US-07-744-767A-2  | Sequence 1, Appli  |

## ALIGNMENTS

RESULT 1  
US-08-302-808-10  
; Sequence 10, Application US/08302808  
; GENERAL INFORMATION:  
; APPLICANT: SUZUKI, No. 5750349uhiro  
; APPLICANT: ODAKA, Asano  
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR DERIVATIVES AND USE THEREOF  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; STREET: 130 WATER STREET  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02119  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/302, 808  
FILING DATE: 15-SEP-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP94/00089  
FILING DATE: 24-JAN-1994  
APPLICATION NUMBER: 010132/1993  
FILING DATE: 25-JAN-1993  
CLASSIFICATION: 435  
FILING DATE: 05-FEB-1993  
APPLICATION NUMBER: 286985/1993  
FILING DATE: 16-NOV-1993  
APPLICATION NUMBER: 334773/1993  
FILING DATE: 28-DEC-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: DAVID . RESNICK S  
REGISTRATION NUMBER: 34, 235  
REFERENCE/DOCKET NUMBER: 44631  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-522-6440  
TELEFAX: 617-522-6440  
TELEFAX: 200391 STRE  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: single

TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: N-terminal  
 ORIGINAL SOURCE:  
 US-08-302-808-10

Query Match 100.0%; Score 92; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-09;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQK 16  
 Db 1 DAEFRHDSGYEVHHQK 16

RESULT 2  
 US-08-986-948-10  
 Sequence 10, Application US/08986948  
 Patent No. 5955317  
 GENERAL INFORMATION:  
 APPLICANT: SUZUKI, No. 5955317uhiro  
 APPLICANT: ODAKA, Asano  
 APPLICANT: KITADA, Chieko  
 TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR DERIVATIVES AND USE THEREOF  
 NUMBER OF SEQUENCES: 14  
 CURRENT APPLICATION DATA:  
 ADDRESSSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
 STREET: 130 WATER STREET  
 CITY: BOSTON  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02119  
 COMPUTER READABLE FORM:  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: Fastseq Version 1.5  
 APPLICATION NUMBER: US/08/986,948  
 FILING DATE:  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/302,808  
 FILING DATE: 15-SEP-1994  
 APPLICATION NUMBER: PCT/JP94/00089  
 FILING DATE: 24-JAN-1994  
 APPLICATION NUMBER: 010132/1993  
 FILING DATE: 25-JAN-1993  
 APPLICATION NUMBER: 019035/1993  
 FILING DATE: 05-FEB-1993  
 APPLICATION NUMBER: 286385/1993  
 FILING DATE: 16-NOV-1993  
 APPLICATION NUMBER: 334173/1993  
 FILING DATE: 28-DEC-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: DAVID, RESNICK S  
 REGISTRATION NUMBER: 44631  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-523-3400  
 TELEFAX: 617-523-6440  
 TELEX: 20291 STRE  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 16 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide

Query Match 100.0%; Score 92; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-09;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQK 16  
 Db 6 DAEFRHDSGYEVHQK 21

RESULT 4

US-08-141-324-11  
 ; Sequence 11, Application US/08141324  
 ; Patent No. 5475097

GENERAL INFORMATION:  
 ; APPLICANT: Travis, James  
 ; APPLICANT: Potempa, Jan S.  
 ; APPLICANT: Barr, Phillip J.  
 ; APPLICANT: Pavloff, Nadine  
 ; APPLICANT: Pike, Robert N.

TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis  
 TITLE OF INVENTION: Protease  
 NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Greenlee and Winner, P.C.  
 STREET: 5370 Manhattan Circle, Suite 201  
 CITY: Boulder  
 STATE: CO  
 COUNTRY: US  
 ZIP: 80303

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/141-324  
 FILING DATE: 21-OCT-1993  
 CLASSIFICATION: 424  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ferber, Donna M.  
 REGISTRATION NUMBER: 33,878  
 REFERENCE/DOCKET NUMBER: 44-93  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 303-499-8080  
 TELEFAX: 303-499-8089

INFORMATION FOR SEQ ID NO: 11:  
 APPLICATION NUMBER: US/08/141,324  
 FILING DATE: 21-Oct-1993  
 CLASSIFICATION: 424  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ferber, Donna M.  
 REGISTRATION NUMBER: 33,878  
 REFERENCE/DOCKET NUMBER: 44-93  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 303-499-8080  
 TELEFAX: 303-499-8089

SEQUENCE CHARACTERISTICS:  
 LENGTH: 27 amino acids  
 STRANDEDNESS: single  
 TOPOLOGY: Linear  
 MOLECULE TYPE: Peptide  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 US-08-141-324-11

Query Match 100.0% Score 92; DB 1; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-09;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHK 16  
 Db 9 DAEFRHDSGYEVHK 24

RESULT 6  
 US-08-141-902-11  
 ; Sequence 11, Application US/08541902  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Travis, James  
 ; APPLICANT: Potempa, Jan S.  
 ; APPLICANT: Barr, Phillip J.  
 ; APPLICANT: Pavloff, Nadine  
 ; APPLICANT: Pike, Robert N.  
 ; TITLE OF INVENTION: Protease  
 ; NUMBER OF SEQUENCES: 28  
 ; CORRESPONDENCE ADDRESS:  
 ; STREET: 5370 Manhattan Circle, Suite 201  
 ; CITY: Boulder  
 ; STATE: CO  
 ; ZIP: 80303

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/541,902  
 FILING DATE:  
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/141,324  
 FILING DATE: 21-OCT-1993  
 ATTORNEY/AGENT INFORMATION:

NAME: Ferber, Donna M.  
 REFERENCE/DOCKET NUMBER: 33,878  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 303-499-8080  
 TELEX/FAX: 303-499-8089  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 27 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 US-08-541-902-11

RESULT 7  
 US-08-541-902-12  
 Sequence 12, Application US/08541902  
 ; Patent No. 5707620  
 GENERAL INFORMATION:  
 APPLICANT: Travis, James  
 APPLICANT: Potempa, Jan S.  
 APPLICANT: Barr, Phillip J.  
 APPLICANT: Pavloff, Nadine  
 APPLICANT: Pike, Robert N.  
 TITLE OF INVENTION: Lysine specific porphyromonas gingivalis  
 NUMBER OF SEQUENCES: 28  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Greenlee and Winner, P.C.  
 STREET: 5370 Manhattan Circle, Suite 201  
 CITY: Boulder  
 STATE: CO  
 COUNTRY: US  
 ZIP: 80303  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/541,902  
 FILING DATE: 21-OCT-1993  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/141,324  
 FILING DATE: 21-OCT-1993  
 NAME: Ferber, Donna M.  
 REGISTRATION NUMBER: 33,878  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 303-499-8080  
 TELEX/FAX: 303-499-8089  
 INFORMATION FOR SEQ ID NO: 12:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 27 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide

NAME: Ferber, Donna M.  
 REFERENCE/DOCKET NUMBER: 44-93  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 303-499-8080  
 TELEX/FAX: 303-499-8089  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 27 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide

;

HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 US-08-541-902-12

Query Match 100.0%; Score 92; DB 1; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-09;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16  
 Db 9 DAEFRHDSGYEVHHQK 24

RESULT 8  
 US-08-346-849-4  
 Sequence 4, Application US/08346849  
 ; Patent No. 5670483  
 GENERAL INFORMATION:  
 APPLICANT: Zhang, Shuguang  
 APPLICANT: Lockshin, Curtis  
 APPLICANT: Rich, Alexander  
 APPLICANT: Holmes, Todd  
 TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY SELF ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES  
 TITLE OF INVENTION: THEREAFTER  
 NUMBER OF SEQUENCES: 64  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
 STREET: Two Militia Drive  
 CITY: Lexington  
 STATE: Massachusetts  
 COUNTRY: U.S.A.  
 ZIP: 02173-4799  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/346,849  
 FILING DATE:  
 PRIORITY APPLICATION NUMBER: US/08/346,849  
 CLASSIFICATION: 435  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 07/973,326  
 FILING DATE: 28 DECEMBER 1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Brook, David E.  
 REGISTRATION NUMBER: 22,592  
 REFERENCE/DOCKET NUMBER: MIT-6008  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 861-6240  
 TELEX/FAX: (617) 861-6240  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 28 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide

Query Match 100.0%; Score 92; DB 1; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-09;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16  
 Db 1 DAEFRHDSGYEVHHQK 16

RESULT 9  
 US-08-302-808-7

Sequence 7, Application US/08302808  
 Patent No. 5750319  
 GENERAL INFORMATION:  
 APPLICANT: SUZUKI, No. 5750349uhiro  
 ODAKA, Asano  
 APPLICANT: KITADA, Chieko  
 TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR DERIVATIVES AND USE THEREOF  
 NUMBER OF SEQUENCES: 14  
 NUMBER OF SEQUENCES: 14  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
 STREET: 130 WATER STREET  
 CITY: BOSTON  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02119  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patient Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/609 090  
 FILING DATE: 29-FEB-1996  
 CLASSIFICATION: 530  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Kraus, Eric J.  
 REGISTRATION NUMBER: 36,190  
 REFERENCE/DOCKET NUMBER: 434-059  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 03-684-1111  
 TELEFAX: 703-684-1124  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 28 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: Linear  
 MOLECULE TYPE: Peptide  
 US-08-609-090-2

RESULT 11  
 Query Match 100.0% Score 92; DB 1; Length 28;  
 Best Local Similarity 100.0% Pred. No. 5.7e-09; Mismatches 0; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHK 16  
 Db 1 DAEFRHDSGYEVHK 16

RESULT 11  
 US-08-986-948-7  
 Sequence 7, Application US/08986948  
 Patent No. 5955317  
 GENERAL INFORMATION:  
 APPLICANT: SUZUKI, No. 5955317uhiro  
 APPLICANT: ODAKA, Asano  
 APPLICANT: KITADA, Chieko  
 TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR DERIVATIVES AND USE THEREOF  
 NUMBER OF SEQUENCES: 14  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
 STREET: 130 WATER STREET  
 CITY: BOSTON  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02119  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEQ Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/986, 948

RESULT 10  
 US-08-609-090-2  
 Sequence 2, Application US/08609090  
 Patent No. 5840838  
 GENERAL INFORMATION:  
 APPLICANT: HENSLEY, Kenneth

PATENT APPLICATION FORM  
FILING DATE: US/08/293, 284A  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/302, 808  
FILING DATE: 15-SEP-1994  
APPLICATION NUMBER: PCT/JP94/00089  
FILING DATE: 24-JAN-1994  
APPLICATION NUMBER: 010/321/1993  
FILING DATE: 25-JAN-1993  
APPLICATION NUMBER: 019/035/1993  
FILING DATE: 03-FEB-1993  
APPLICATION NUMBER: 286985/1993  
FILING DATE: 16-NOV-1993  
APPLICATION NUMBER: 134773/1993  
FILING DATE: 28-DEC-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: DAVID, RESNICK S  
REGISTRATION NUMBER: 34, 235  
REFERENCE/DOCKET NUMBER: 44631  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-1400  
TELEFAX: 617-523-6440  
TELEX: 200291 STRE  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
US-08-948-7

Query Match 100.0%; Score 92; DB 2; Length 28;  
Best Local Similarity 100.0%; Pred. No. 5.7e-09;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHKQ 16  
Db 1 DAEFRHDSGYEVHKQ 16

RESULT 13  
US-08-461-216-2

Query Match 100.0%; Score 92; DB 2; Length 28;  
Best Local Similarity 100.0%; Pred. No. 5.7e-09;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHKQ 16  
Db 1 DAEFRHDSGYEVHKQ 16

RESULT 12  
US-08-293-284A-4  
Sequence 4, Application US/08293284A  
Patent No. 595343  
GENERAL INFORMATION:  
APPLICANT: Holmes, Todd  
APPLICANT: Zhang, Shuguang  
APPLICANT: Rich, Alexander  
APPLICANT: DiPersio, C. Michael  
APPLICANT: Lockshin, Curtis  
TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES  
TITLE OF INVENTION: THEREFOR  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02173-4799

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/293, 284A  
FILING DATE: 22-AUG-1994  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/973, 326  
FILING DATE: 28-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Brook, David E.  
REGISTRATION NUMBER: 22, 592  
REFERENCE/DOCKET NUMBER: MIT-6008A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 861-6240  
TELEFAX: (617) 861-9540  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-293-284A-4

Query Match 100.0%; Score 92; DB 2; Length 28;  
Best Local Similarity 100.0%; Pred. No. 5.7e-09;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHKQ 16  
Db 1 DAEFRHDSGYEVHKQ 16

RESULT 13  
US-08-461-216-2

Sequence 2, Application US/08461216  
Patent No. 5958833

GENERAL INFORMATION:  
APPLICANT: Show, A.D.  
TITLE OF INVENTION: ANIMAL MODELS OF HUMAN AMYLOIDOSSES  
NUMBER OF SEQUENCES: 8  
COPRISDEE: Christensen, O'Connor, Johnson and Kindness  
ADDRESS: 1420 Fifth Avenue, Suite 2800  
STREET: 1420 Fifth Avenue, Suite 2800  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98101-3347

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage  
COMPUTER: IBM PC/386 Compatible  
OPERATING SYSTEM: MS-DOS 4.01  
SOFTWARE: Word for Windows-t  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461, 216  
FILING DATE:  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/969, 734  
FILING DATE: October 23, 1992  
APPLICATION NUMBER: 0/950, 417  
FILING DATE: September 23, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Broderick, Thomas F.  
REGISTRATION NUMBER: 31, 332  
REFERENCE/DOCKET NUMBER: UOFW-1-6707  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 1-206-682-8100; 1-206-224-0709 (direct)  
TELEFAX: 1-206-224-0779  
TELEX: 493803  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28 amino acids  
TYPE: amino acid  
STRANDEDNESS: single

TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 DESCRIPTION: peptide SYMBOL 98 \f "Symbol" /A4(1-28);  
 ; DESCRIPTION: page 83, line 31  
 US-08-461-216-2

Query Match 100.0%; Score 92; DB 2; Length 28;  
 Best Local Similarity 100.0%; Prod. No. 5.7e-09; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHKQ 16  
 | ||||| ||||| |||||  
 Db 1 DAEFRHDSGYEVHKQ 16

RESULT 14  
 US-08-609-090-3  
 ; Sequence 3, Application US/08509090  
 ; Application No. 08509090  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HENSLEY, Kenneth  
 ; ATTORNEY/AGENT INFORMATION:  
 ; APPLICANT: BUTTERFIELD, D. A.  
 ; ATTORNEY/AGENT INFORMATION:  
 ; APPLICANT: CARNEY, John M.  
 ; ATTORNEY/AGENT INFORMATION:  
 ; APPLICANT: AKSENOV, Michael  
 ; TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF  
 ; TITLE OF INVENTION: AN OLIGOPEPTIDE OR POLYPEPTIDES  
 ; NUMBER OF SEQUENCES: 11  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: LOWE PRICE LEBLANC & BECKER  
 ; STREET: 99 Canal Center Plaza, Suite 300  
 ; CITY: Alexandria  
 ; STATE: Virginia  
 ; COUNTRY: USA  
 ; ZIP: 22314

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/609,090  
 FILING DATE: 29-FEB-1996  
 CLASSIFICATION: 530  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Kraus, Eric J.  
 REGISTRATION NUMBER: 36,190  
 REFERENCE/DOCKET NUMBER: 434-059

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-684-1111  
 TELEFAX: 703-684-1124  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 33 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide  
 US-08-609-090-4

Query Match 100.0%; Score 92; DB 2; Length 33;  
 Best Local Similarity 100.0%; Prod. No. 6.8e-09; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Kraus, Eric J.  
 REGISTRATION NUMBER: 36,190  
 REFERENCE/DOCKET NUMBER: 434-059  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-684-1111  
 TELEFAX: 703-684-1124  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 30 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide  
 US-08-609-090-3

Query Match 100.0%; Score 92; DB 2; Length 30;  
 Best Local Similarity 100.0%; Prod. No. 6.1e-09; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 DAEFRHDSGYEVHKQ 16  
 | ||||| ||||| |||||  
 Db 1 DAEFRHDSGYEVHKQ 16

RESULT 15  
 US-08-609-090-4  
 ; Sequence 4, Application US/08509090



OM of: US-09-155-076-2 to: GenEmbl:\* out\_format : pfs  
 Date: Sep 13, 2000 2:56 AM  
 About: Results were produced by the Gencore software, version 4.5.  
 Copyright (c) 1993-2000 Compugen Ltd.

## Command line parameters:

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-Q/cg2-1/0SP0.spool/US09155076/runat_29082000_092505_15746/app_query.fasta_1.144
-OEMT=fastaP -SUFFIX=xrge -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -OGAPOP=4.500
-QGAPENT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-DEGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=6.000 -DELCP=6.000
-DELET=7.000 -START=1 -MATRIX=bblobsum62 -TRANS=human40.Cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100.0 -THR_MIN=0
-MAXLEN=1000000 -USER=US09155076_eCGNL_1_3119 -NCPU=6 -ICPU=3
-MAXLN=1000000 -USER=US09155076_eCGNL_1_3119 -NCPU=6 -ICPU=3
-LONGLOG -NO_XLXY -WAIT -THREADS=1
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## Search information block:

Query: US-09-155-076-2  
 Query length: 16  
 Database: GenEmbl:  
 Database sequences: 972840  
 Database length: 89248106  
 Search time (sec): 757.400000

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 Sequence Strd Orig ZScore EScore Len | Documentation  
 9b\_pat:AR016774 + 92.00 300.31 1.2e-08 58 | AR016774 Sequence 15 from Patent W  
 9b\_pat:A49228 + 92.00 296.89 1.9e-08 85 | A49528 Sequence 10 from Patent W  
 9b\_pat:A69920 + 92.00 291.45 3.9e-08 156 | A69920 Sequence 15 from Patent W  
 9b\_com:SSAPPMR + 92.00 290.42 4.4e-08 175 | X56127 S.scrofa mRNA for amyloid precursor protein gene  
 9b\_com:UMAPPMR + 92.00 290.42 4.4e-08 175 | X56128 U.maritimus mRNA for amyloid precursor protein gene  
 9b\_com:CEAPPMR + 92.00 290.37 4.5e-08 176 | X56125 C.familiaris mRNA for amyloid precursor protein gene  
 9b\_com:ORAPPMR + 92.00 290.37 4.5e-08 176 | X56129 Oryctoceratulus sp. mRNA for amyloid precursor protein gene  
 9b\_com:BTAPPMR + 92.00 290.32 4.5e-08 177 | X56124 B.taurus mRNA for amyloid precursor protein gene  
 9b\_com:OVAPPMR + 92.00 290.27 4.5e-08 178 | X56130 Ovis sp. mRNA for amyloid precursor protein gene  
 9b\_pat:HUMANMYBBI + 92.00 289.74 4.e-08 189 | M29269 Human amyloid precursor protein gene  
 9b\_pr2:S60721 + 92.00 287.52 6.4e-08 242 | M37895 Human amyloid beta protein prepropeptide  
 9b\_pr2:S61380 + 92.00 287.38 6.6e-08 246 | S61380 beta-amyloid peptide precursor  
 9b\_pr2:S61383 + 92.00 287.38 6.6e-08 246 | S61383 beta-amyloid peptide precursor  
 9b\_pr1:HSPRA414 + 92.00 286.38 7.e-08 275 | X13479 Human Pr44 gene for preprohormone convertase 1  
 9b\_pat:I065131 + 92.00 285.60 8.2e-08 300 | I065131 Sequence 21 from Patent W  
 9b\_pat:I08767 + 92.00 285.60 8.2e-08 300 | I08767 Sequence 14 from Patent W  
 9b\_pat:A69499 + 92.00 284.12 9.9e-08 354 | A69499 Sequence 2 from Patent W  
 9b\_pat:A69501 + 92.00 284.12 9.9e-08 354 | A69501 Sequence 4 from Patent W  
 9b\_pat:A69503 + 92.00 284.12 9.9e-08 354 | A69503 Sequence 6 from Patent W  
 9b\_pat:A69505 + 92.00 284.12 9.9e-08 354 | A69505 Sequence 8 from Patent W  
 9b\_pat:A69507 + 92.00 284.12 9.9e-08 354 | A69507 Sequence 10 from Patent W  
 9b\_pat:A72176 + 92.00 284.12 9.9e-08 354 | A72176 Sequence 2 from Patent W  
 9b\_pat:A72178 + 92.00 284.12 9.9e-08 354 | A72178 Sequence 4 from Patent W  
 9b\_pat:A72180 + 92.00 284.12 9.9e-08 354 | A72180 Sequence 6 from Patent W  
 9b\_pat:A72182 + 92.00 284.12 9.9e-08 354 | A72182 Sequence 8 from Patent W  
 9b\_pat:A72184 + 92.00 284.12 9.9e-08 354 | A72184 Sequence 10 from Patent W  
 9b\_pat:A72186 + 92.00 283.97 1.e-07 360 | A72186 Sequence 12 from Patent W  
 9b\_pat:I06120 + 92.00 281.28 1.e-07 486 | I06120 Sequence 10 from Patent W  
 9b\_pat:I08764 + 92.00 281.28 1.e-07 486 | I08764 Sequence 8 from Patent W  
 9b\_pat:A47565 + 92.00 280.67 1.5e-07 520 | A47565 Sequence 9 from Patent W  
 9b\_pat:AR016224 + 92.00 280.67 1.5e-07 520 | AR016224 Sequence 9 from Patent W  
 9b\_com:OCAPPEx16 + 92.00 271.46 5.0e-07 1455 | X63471 O.cuniculus APP gene for  
 9b\_com:HUMANMYB17 + 92.00 271.17 5.2e-07 1553 | M83538 Rabbit ORF1 and amyloid precursor protein gene  
 9b\_com:RABMPREA + 92.00 271.06 5.3e-07 1552 | AR013651 Sequence 3 from Patent W  
 9b\_pat:AR013651 + 92.00 270.81 5.5e-07 1554 | I09366 Sequence 1 from Patent W  
 9b\_pat:I09366 + 92.00 270.81 5.5e-07 1554 | I09368 Sequence 1 from Patent W

seq\_documentation\_block:  
 LOCUS AR016774 58 bp DNA PAT 05-DEC-1998  
 DEFINITION Sequence 15 from patent US 5777194.  
 ACCESSION AR016774  
 VERSION AR016774.1 GI:3973051  
 KEYWORDS .  
 SOURCE unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 58)  
 AUTHORS Scott,R.W., Reutme,A.G., Truskko,S.P. and Siman,R.  
 TITLE Gene-targeted mice with humanized A.
 JOURNAL Patent: US 5777194-A 15 07-JUL-1998;  
 FEATURES Location/Qualifiers 1 .. 58 /organism="unknown"  
 SOURCE BASE COUNT 23 a 11 c 11 g 13 t  
 ORIGIN seq\_alignment\_scores:  
 Quality: 92.00 Length: 16  
 Percent Similarity: 100.000 Percent Identity: 100.000  
 alignment\_block:  
 US-09-155-076-2 x AR016774 ..  
 Align seg 1/1 to: AR016774 from: 1 to: 58  
 1 ASPAlaGluPheArgHISAspSerGlyGluValHisIglNlys 16  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 8 GATGCAGATTGACATGATTCAGATTGATGAGTCCACCATCAAAA 55  
 seq\_name: gb\_pat:AR49528  
 seq\_documentation\_block:  
 LOCUS A49528 85 bp DNA PAT 07-MAR-1997  
 DEFINITION Sequence 10 from Patent WO9608561.  
 ACCESSION A49528  
 VERSION A49528.1 GI:2302985  
 KEYWORDS unidentified.  
 SOURCE ORGANISM unidentified unclassified.  
 REFERENCE 1 (bases 1 to 85)  
 AUTHORS Chaudhuri,B. and Stephan,C.  
 TITLE METHOD FOR DETECTION OF MAILFOLDED PROTEIN  
 JOURNAL CIBA GENIG AG (CH)  
 COMMENT Other publication AU 3521595 960329.  
 FEATURES Location/Qualifiers 1 .. 85 /organism="unidentified"  
 SOURCE BASE COUNT 22 a 18 c 21 g 24 t  
 ORIGIN alignment\_scores:  
 Quality: 92.00 Length: 16  
 Ratio: 5.750 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000  
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TITLE Little,S.P. Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis  
JOURNAL Brain Res. Mol. Brain Res. 10 (4), 299-305 (1991)  
MEDLINE 92017079  
FEATURES source  
1. >176 /organism="Cavia sp."  
/db\_xref="taxon:1043"  
/tissue\_type="brain"  
<1. >176 /codon\_start=1  
/product="amyloid precursor protein"  
/protein\_id="CAA39591.1"  
/db\_xref="GI:49570"  
/translation="ISEVKMDAEPRHDSGYEVHOKLVFFAEDVGSNKGAIGLMVGG  
VVIATVITVILMK"  
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Quality: 92.00 Length: 16  
Ratio: 5.750 Gaps: 0  
Percent Similarity: 100.000 Identity: 100.000  
alignment\_block:  
US-09-155-076-2 x BTAPMR ..  
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seq\_name: gb\_om:OVAPPMR  
seq\_documentation\_block:  
LOCUS OVAPPMR 178 bp mRNA MAM 14-JUL-1992  
DEFINITION mRNA for amyloid precursor protein (APP) (partial).  
ACCESSION X56130  
VERSION X56130.1 GI:1829  
KEYWORDS amyloid polypeptide.  
ORGANISM Ovis sp.  
SOURCE Ovis sp.  
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
Artiodactyla; Ruminantia; Pecora; Bovidae; Caprinae;  
Ovis.  
REFERENCE 1 (bases 1 to 178)  
AUTHORS Johnstone,E.M.  
TITLE Direct Submission  
JOURNAL Submitted (24-SEP-1990) E.M. Johnstone, ELI LILLY AND COMPANY,  
LILLY CORPORATE CENTER 0424, INDIANAPOLIS IN 46285, USA  
REFERENCE 2 (bases 1 to 178)  
AUTHORS Johnstone,E.M., Chaney,M.O., Norris,F.H., Pascual,R. and  
Little,S.P.  
TITLE Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis  
JOURNAL Mol. Brain Res. 10 (4), 299-305 (1991)  
MEDLINE 92017079  
FEATURES source  
1. >178 /organism="Ovis sp."  
/db\_xref="taxon:9939"  
/tissue\_type="heart"  
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/product="amyloid precursor protein"  
/protein\_id="CAA39595.1"  
/db\_xref="GI:1830"  
/db\_xref="SWISS-PROT:Q28757"  
/translation="SEVKMDAEPRHDSGYEVHOKLVFFAEDVGSNKGAIGLMVGG  
VVIATVITVILMK"  
BASE COUNT 48 a 31 c 49 g 50 t  
ORIGIN  
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Quality: 92.00 Length: 16  
Ratio: 5.750 Gaps: 0  
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US-09-155-076-2 x OVAPPMR ..  
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seq\_documentation\_block:  
LOCUS OVAPPMR 178 bp mRNA MAM 14-JUL-1992  
DEFINITION mRNA for amyloid precursor protein (APP) (partial).  
ACCESSION X56130  
VERSION X56130.1 GI:1829  
KEYWORDS amyloid polypeptide.  
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
Artiodactyla; Ruminantia; Pecora; Bovidae; Caprinae;  
Ovis.  
REFERENCE 1 (bases 1 to 178)  
AUTHORS Johnstone,E.M.  
TITLE Direct Submission  
JOURNAL Submitted (24-SEP-1990) E.M. Johnstone, ELI LILLY AND COMPANY,  
LILLY CORPORATE CENTER 0424, INDIANAPOLIS IN 46285, USA  
MEDLINE 92017079  
FEATURES source  
1. >177 /organism="Bos taurus"  
/db\_xref="taxon:9913"  
/tissue\_type="brain"  
<1. >177 /codon\_start=1  
/product="amyloid precursor protein"  
/protein\_id="CAA39588.1"  
/db\_xref="GI:83"  
/db\_xref="SWISS-PROT:Q28053"  
/translation="ISEVKMDAEPRHDSGYEVHOKLVFFAEDVGSNKGAIGLMVGG  
VVIATVITVILMK"

18 GATCGAGAATTCCSACATGATTCGGATGAAAGTCACTCATCATAAAA 65  
 seq\_name : gb\_pr1:HUMAPR4A1  
 seq\_documentation\_block:  
 LOCUS HUMAPR4A1 189 bp DNA PRI 31-OCT-1994  
 DEFINITION Human amyloid protein gene, exon X.  
 ACCESSION M29269  
 KEYWORD amyloid protein.  
 SEGMENT 1 of 2  
 SOURCE Human DNA (library of T.Maniatis), clone lambda-41.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 Johnstone, E.M., Chaney, M.O., Moore, R.E., Ward, K.E., Norris, F.H. and  
 Little, S.P.  
 TITLE Alzheimer's disease amyloid Peptide is encoded by two exons and  
 shows similarity to soybean trypsin inhibitor  
 JOURNAL Biochem. Biophys. Res. Commun. 163 (3), 1248-1255 (1989)  
 FEATURES Location/Qualifiers  
 source 1..189  
 /organism="Homo sapiens"  
 /map="21q21.2"  
 /db\_xref="taxon:9606"  
 intron <1..42  
 /gene="APP"  
 /note="intron X-1; G00-119-692"  
 exon 43..143  
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 /note="exon X; G00-119-692"  
 BASE COUNT 59 a 32 C 59 g 60 t  
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 Quality: 92.00 Length: 16  
 Ratio: 5.750 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000  
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 1 AspAlaGlupheArgIleAspSerGlyTyrGluValHisHisGlnLys 16  
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 93 GATGCGAAATTCCGACATGACTCAGGATAAGTCATCATCAAAA 140  
 seq\_name : gb\_pr1:HUMANAMYB1  
 seq\_documentation\_block:  
 LOCUS HUMANAMYB1 242 bp DNA PRI 31-OCT-1994  
 DEFINITION Human amyloid-beta protein DNA, exon 14.  
 VERSION M37895  
 KEYWORD amyloid-beta protein.  
 SEGMENT 1 of 2  
 SOURCE Human (Dutch patient with hereditary cerebral hemorrhage with  
 amyloidosis) DNA.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 Levy, E., Carmn, M.D., Fernandez-Madrid, I.J., Power, M.D.,  
 Lieberberg, I., van Duinen, S.G., Bots, G.T., Luyendijk, W. and  
 Frangione, B.  
 TITLE Mutation of the Alzheimer's disease amyloid gene in hereditary  
 cerebral hemorrhage, Dutch type  
 JOURNAL Science 248 (4959), 1124-1126 (1990)

MEDLINE 90260663  
 FEATURES source  
 /organism="Homo sapiens"  
 /isolate="hereditary cerebral hemorrhage with amyloidosis"  
 of Dutch type patient"  
 /db\_xref="taxon:9606"  
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 104..104  
 /gene="APP"  
 /note="G00-119-692"  
 /number=1  
 205..>242  
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 BASE COUNT 75 a 35 c  
 ORIGIN 52 g 80 t  
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 Quality: 92.00 Length: 16  
 Percent Similarity: 100.000 Percent Identity: 100.000  
 alignment\_block: US-09-155-076-2 x HUMANAMYB1 ...  
 Align seg 1/1 to: HUMANAMYB1 from: 1 to: 242  
 1 AspAlaGlupheArgIleAspSerGlyTyrGluValHisHisGlnLys 16  
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 154 GATGAGAATTCCGACATGACTCAGGATAAGTCATCATCAAAA 201  
 seq\_name: gb\_pr2:560721  
 seq\_documentation\_block:  
 LOCUS S60721 246 bp mRNA PRI 23-JUL-1993  
 DEFINITION beta-amyloid peptide precursor [clone 1] [human, mRNA Partial  
 Mutant, 246 nt].  
 ACCESSION S60721  
 VERSION S60721.1 GI:299644  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 246)  
 AUTHORS Denman, R.B., Rosenzwaig, R. and Miller, D.L.  
 TITLE A system for studying the effects of familial Alzheimer disease  
 mutations on the processing of the beta-amyloid peptide Precursor  
 Biochem. Biophys. Res. Commun. 192 (1), 96-103 (1993)  
 JOURNAL 93236601  
 MEDLINE GenBank staff at the National Library of Medicine created this  
 entry [NCBI gibbsq 129915] from the original journal article.  
 REMARK This sequence comes from Fig. 1.  
 Map location: 21.  
 FEATURES source  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 gene  
 /partial  
 /gene="beta-amyloid peptide precursor, beta APP"  
 CDS  
 /partial  
 /gene="beta-amyloid peptide precursor, beta APP"  
 /note="This sequence comes from Fig. 1; Protein sequence  
 is in conflict with the conceptual translation;  
 mismatches(44[K->N], 73[W->Y], 76[L->N]); beta APP"  
 /codon\_start=1  
 /product="beta-amyloid peptide precursor"  
 /protein\_id="PAB2263.1"  
 /db\_xref="GI:299645"

translation="GSGLTNIKTEESEVKMDAEFRHDSGYEVHHQKLVFFAAVDVGSK  
KGAIIGIMyGavVIASVIFTYLMKQNTSIHGVVE"  
BASE COUNT 72 a 40 c 69 g 65 t ORIGIN

alignment\_scores:  
Quality: 92.00 Length: 16  
Ratio: 5.750 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
1 AspAlaGluPheArgHisAspSerGlyTyrGluValIshIshGlnLys 16  
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52 GATGAGAATTCCGACATGACTCAGGATATGAACTCATCACAAAAA 99

seq\_name: qb\_pr2:S61383

seq\_documentation\_block:  
LOCUS S61383 246 bp mRNA PRI 23-JUL-1993  
DEFINITION beta-amyloid peptide precursor [clone 3] [human, mRNA Partial  
Mutant, 246 nt].

ACCESSION S61383  
VERSION GI:299648  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 246)  
REFERENCE Denman,R.B., Rosenzwaig,R. and Miller,D.L.  
AUTHORS A system for studying the effect(s) of familial Alzheimer disease  
TITLE mutations on the processing of the beta-amyloid peptide precursor  
JOURNAL Biochem. Biophys. Res. Commun. 192 (1), 96-103 (1993)  
MEDLINE 9336601  
REMARK GenBank staff at the National Library of Medicine created this  
entry [NCBI gibbsq 132966] from the original journal article.  
This sequence comes from Fig. 1.  
Map location: 21.

FEATURES Location/Qualifiers  
source  
1. .246 /organism="Homo sapiens"  
/db\_xref="taxon:9606"  
1. .246 gene  
/partial  
/gene="beta-amyloid peptide precursor, beta APP"  
CDS  
1. .246 /partial  
/gene="beta-amyloid peptide precursor, beta APP"  
/note="This sequence comes from Fig. 1; protein sequence  
is in conflict with the conceptual translation;  
mismatches (638 [K->N], 727 [W->Y], 730 [I->N]); beta APP"  
/codon\_start=1  
/product="beta-amyloid peptide precursor"  
/protein\_id="PAB26165.1"  
/db\_xref="GI:299649"  
/translation="GSGITNIKTEESEVKMDAEFRHDSGYEVHHQKLVFFAAVDVGSK  
KGATIGLMMGGVVATVIGITLVMKQWTSHHGVV"

BASE COUNT 72 a 40 c 71 g 63 t ORIGIN

alignment\_scores:  
Quality: 92.00 Length: 16  
Ratio: 5.750 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
US-09-155-076-2 x S61383 ..

Align seg 1/1 to: S61383 from: 1 to: 246

1 AspAlaGluPheArgHisAspSerGlyTyrGluValIshIshGlnLys 16  
||||||| ||||| ||||| ||||| ||||| ||||| |||||  
52 GATGCAAGATTCGACATGACTCAGGATATGAACTCATCACAAAAA 99

OM of: US-09-155-076-2 to: N\_Geneseq\_36:\*

out\_format : pfs

Date: Sep 13, 2000 2:58 AM

About: Results were produced by the Gencore software, version 4.5,  
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

-MODEl=framet p2n.model -DEV=x1D  
 -O=/cgn2\_1/USP10\_spool/US09155076/runat\_29082000\_092505\_15779/app\_query.fasta\_1.144  
 -GAPEXT=36 -QFMT=fasta -SUFFIX=-rng -GAPOP=12.000  
 -GAPEXT=4.500 -MINMATCH=0.100 -LOOPCXT=0.000  
 -QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPCXT=0.500  
 -DELPOP=6.000 -DELEXT=7.000 -YGAPOP=10.000 -YGAPCXT=0.500  
 -DELTEXT=7.000 -SPART=1 -MATRIX=GLOSUM62  
 -TRANS:human40\_cdi -LIST=15 -DOALIGN=200 -THR\_SCORE=POt  
 -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
 -NORM=ext -MINLEN=0 -MAXLEN=1000000 -USR=US09155076\_ecGNN1\_1.75  
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Search information block:

Query: US-09-155-076-2  
 Query length: 16  
 Database: N\_Geneseq\_36:\*

Database sequences: 311585  
 Database length: 125096042  
 Search time (sec): 75.680000

score\_list:

| Sequence             | Strd | Orig  | ZScore | Escore  | Len  | Documentation  |
|----------------------|------|-------|--------|---------|------|--|
| N_Geneseq_36:T38687  | +    | 92.00 | 295.99 | 6.9e-09 | 58   | ! Mouse amyloid precursor protein                          |
| N_Geneseq_36:T14516  | +    | 92.00 | 292.49 | 1.1e-08 | 85   | ! Beta-amyloid peptide coding seq                          |
| N_Geneseq_36:N92266  | +    | 92.00 | 285.75 | 2.6e-08 | 177  | ! Region of pre-APP coding sequen                          |
| N_Geneseq_36:Q7192   | +    | 92.00 | 285.15 | 2.8e-08 | 189  | ! cDNA encoding the APP leader se                          |
| N_Geneseq_36:V23754  | +    | 92.00 | 282.15 | 4.1e-08 | 262  | ! Alzasc1 coding sequence. Nucleic                         |
| N_Geneseq_36:Q88696  | +    | 92.00 | 281.00 | 4.7e-08 | 297  | ! Beta-amyloid precursor protein                           |
| N_Geneseq_36:Q88697  | +    | 92.00 | 281.00 | 4.7e-08 | 297  | ! Beta-amyloid precursor protein                           |
| N_Geneseq_36:Q88698  | +    | 92.00 | 280.91 | 4.7e-08 | 297  | ! Beta-amyloid precursor protein                           |
| N_Geneseq_36:Q10017  | +    | 92.00 | 280.91 | 4.8e-08 | 300  | ! Sequence encoding beta-amyloid                           |
| N_Geneseq_36:Q42665  | +    | 92.00 | 280.91 | 4.8e-08 | 300  | ! Full-length beta-amyloid protein                         |
| N_Geneseq_36:Q88699  | +    | 92.00 | 280.64 | 5.0e-08 | 309  | ! Beta-amyloid precursor protein                           |
| N_Geneseq_36:Q88700  | +    | 92.00 | 280.64 | 5.0e-08 | 309  | ! Beta-amyloid precursor protein                           |
| N_Geneseq_36:TI8082  | +    | 92.00 | 279.87 | 5.5e-08 | 336  | ! Familial Alzheimer's disease AP                          |
| N_Geneseq_36:V20377  | +    | 92.00 | 279.39 | 5.8e-08 | 354  | ! DNA for APP C-terminal fragment                          |
| N_Geneseq_36:Y20380  | +    | 92.00 | 279.39 | 5.8e-08 | 354  | ! DNA for APP C-terminal fragment                          |
| N_Geneseq_36:Y20381  | +    | 92.00 | 279.39 | 5.8e-08 | 354  | ! DNA for APP C-terminal fragment                          |
| N_Geneseq_36:Y20379  | +    | 92.00 | 279.39 | 5.8e-08 | 354  | ! DNA for APP C-terminal fragment                          |
| N_Geneseq_36:Y20378  | +    | 92.00 | 279.39 | 5.8e-08 | 354  | ! DNA for APP C-terminal fragment                          |
| N_Geneseq_36:Y07188  | +    | 92.00 | 279.39 | 5.8e-08 | 354  | ! Flag/amyloid protein precursor                           |
| N_Geneseq_36:X08982  | +    | 92.00 | 279.39 | 5.8e-08 | 354  | ! Amyloid precursor protein (APP)                          |
| N_Geneseq_36:Y20382  | +    | 92.00 | 279.24 | 5.9e-08 | 360  | ! DNA for APP C-terminal fragment                          |
| N_Geneseq_36:NB0605  | +    | 92.00 | 276.48 | 8.5e-08 | 486  | ! Lambda clone encoding first 18 am                        |
| N_Geneseq_36:Q10015  | +    | 92.00 | 276.48 | 8.5e-08 | 486  | ! Genomic clone including beta-amy                         |
| N_Geneseq_36:Q42662  | +    | 92.00 | 276.48 | 8.5e-08 | 486  | ! Clone Lambda SH2 encoding beta-amyloid precursor protein |
| N_Geneseq_36:Q82910  | +    | 92.00 | 275.86 | 9.2e-08 | 520  | ! Human beta amyloid fusion prote                          |
| N_Geneseq_36:Q2753   | +    | 92.00 | 275.58 | 9.5e-08 | 536  | ! Alzasc1 coding sequence. Nucleic                         |
| N_Geneseq_36:N90497  | +    | 92.00 | 266.11 | 3.2e-07 | 1504 | ! DNA sequence of clone my37                               |
| N_Geneseq_36:Y36456  | +    | 92.00 | 266.01 | 3.2e-07 | 1521 | ! Maltose binding protein-APP (S                           |
| N_Geneseq_36:N90397  | +    | 92.00 | 265.77 | 3.3e-07 | 1562 | ! cDNA sequence of amy37 clone.                            |
| N_Geneseq_36:Q424257 | +    | 92.00 | 264.88 | 3.7e-07 | 1721 | ! APP-REP 751 amyloid precursor                            |
| N_Geneseq_36:Q69003  | +    | 92.00 | 263.11 | 4.7e-07 | 2085 | ! Mouse amyloid precursor protein                          |
| N_Geneseq_36:Q27801  | +    | 92.00 | 263.10 | 4.7e-07 | 2088 | ! APP95. Polynucleotide probe Q                            |
| N_Geneseq_36:R80604  | +    | 92.00 | 262.39 | 5.2e-07 | 2256 | ! Lambda APCP16814 amino acids                             |
| N_Geneseq_36:Q10014  | +    | 92.00 | 262.39 | 5.2e-07 | 2256 | ! Clone lambda APCP16814 of beta                           |
| N_Geneseq_36:Q0532   | +    | 92.00 | 262.39 | 5.2e-07 | 2256 | ! Sequence of clone LambdaAPCP16                           |
| N_Geneseq_36:Q42661  | +    | 92.00 | 262.39 | 5.2e-07 | 2256 | ! Lambda clone APCP16814 encodes                           |
| N_Geneseq_36:Q27802  | +    | 92.00 | 262.35 | 5.2e-07 | 2255 | ! APP751. Polynucleotide probe Q                           |
| N_Geneseq_36:Q8983   | +    | 92.00 | 262.35 | 5.e-07  | 2265 | ! Amyloid precursor protein (APP                           |
| N_Geneseq_36:Y10322  | +    | 92.00 | 262.15 | 5.3e-07 | 2310 | ! Unfolded-protein-response element; UPR; BiP.             |
| N_Geneseq_36:Q48860  | +    | 92.00 | 262.15 | 5.3e-07 | 2313 | ! expression cassette; P53;                                |
| N_Geneseq_36:Q74708  | +    | 92.00 | 262.16 | 5.3e-07 | 2313 | ! beta-amyloid peptide; Plant;                             |

N\_Geneseq\_36:N91050 + 92.00 259.93 7.1e-07 2949 ! Sequence encoding novel any  
 N\_Geneseq\_36:Q05086 + 92.00 259.93 7.1e-07 2949 ! Sequence encodes NAP-2 gene  
 N\_Geneseq\_36:N91049 + 92.00 259.76 7.2e-07 3006 ! Sequence encoding novel any  
 N\_Geneseq\_36:Q05085 + 92.00 259.76 7.2e-07 3006 ! Sequence encodes NAP gene a

seq\_name: N\_Geneseq\_36:T38687

seq\_documentation\_block:

ID T38687; standard; DNA; 58 BP.  
 AC T38687; DT 21-JUL-1997 (first entry)  
 DE Mouse amyloid precursor protein exon 16 primer ST61.  
 KW Exon 16; murine; mouse; amyloid; Precursor; protein; APP;  
 KW humanisation; homozygous; heterozygous; human; Abeta; Swedish;  
 KW familial; Alzheimer's disease; FAD; mutation; tool; model;  
 KW elucidation; pathology; symptomatology; screen; inhibition;  
 KW transgenic; polymerase chain reaction; primer; PCR;  
 KW amplification; ss.  
 OS Synthetic.

PN W09334097-A1.

PD 31-OCT-1996.

PF 05824.

PR 26-APR-1995; US-129207.

PA (CEPH-) CEPHALON INC.

PI Hoffman EK, Reaume AG, Scott RW, Siman R, Truskov SP;

DR WPI: 96-497639/49.

PT Transgenic mice with humanised amyloid precursor protein gene - having at least 1 Swedish FAD mutation, useful as tools or models to elucidate role of human A-beta in Alzheimer's disease

PS Example 1; Page 75; 123pp; English.

CC The present sequence is a primer for the PCR amplification of exon 16 of the mouse amyloid precursor protein (APP) gene, into which 6 humanising base pair changes was introduced. The exon was then used in the preparation of mice homozygous or heterozygous for a targeted APP encoding gene, comprising a human Abeta peptide encoding sequence in place of the endogenous murine sequence, and at least 1 Swedish Familial Alzheimer's Disease (FAD) mutation. The mice can be used as tools, or models to elucidate the role of human Abeta in AD pathology and symptomatology. They can also be used to screen chemical compounds for the ability to inhibit in vivo processing of APP, to yield the human Abeta peptide by administering the chemical compounds to mouse and measuring the relative amounts of amyloidogenic and nonamyloidogenic processing of APP in a sample from the mouse at an appropriate interval after administration of the chemical compounds.

CC alignment\_scores:

SQ Sequence 58 BP; SQ Sequence 58 BP;

CC Percent Identity: 100.000

CC alignment\_block:

US-09-155-076-2 x T38687 ..

Align seg 1/1 to: T38687 from: 1 to: 58

Length: 16 Gaps: 0

Percent Similarity: 100.000

Identity: 100.000

seq\_name: N\_Geneseq\_36:T38687

seq\_documentation\_block:

ID T14516 standard; DNA; 85 BP.

AC T14516.

DT 30-OCT-1996 (first entry)

1 ASPAlagliupheargHisaPSerGlyTyrcLyuValHisGlnLys 16

1 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

8 GATGCCAAATTCAAGATCATGATATGAGTCACCATCAAAAA 55

seq\_name: N\_Geneseq\_36:T38687

KW protein aggregation inhibitor; Alzheimer's disease; cancer; therapy; ds.  
 OS Synthetic.  
 FH Location/Qualifiers  
 FT misc\_feature 1..60  
 FT /\*tag- a /note- "5, overhang"  
 FT misc\_feature complement (85)  
 FT /\*tag- b /note- "site of 60 bp 5' overhang"  
 FT  
 PN WO9608561-A1.  
 PD 21-MAR-1996.  
 PF 04-SEP-1995; E03475.  
 PS 16-SEP-1994; EP-8-0536.  
 PA (CIBA ) CIBA GEIGY AG.  
 PI Chaudhuri B, Stephan C;  
 DR WPI; 96-179938/18.  
 PT Host used to determine influence of cpds. on appearance of malformed  
 PT protein - also to identify cpds. that inhibit the aggregation of  
 PT protein, pref. beta-amyloid, useful in treatment of Alzheimer's  
 PT disease  
 PS Example 10: Page 18: 59PP: English.  
 CC This sequence represents the beta-amyloid peptide. This sequence is  
 CC amplified using the primers shown in T14517 and T14518, and is used in  
 CC one of the expression cassettes of the invention. The first expression  
 CC cassette contains one or more copies of the unfolded-protein-response  
 CC element (see T14511) operably linked to a reporter element. The  
 CC second expression cassette comprises a promoter operably linked to a  
 CC signal sequence, a DNA encoding a protein whose malfoilding is to be  
 CC studied, and a terminator sequence. The protein encoding sequence in the  
 CC second expression cassette is preferably a prion, p3, beta-amyloid  
 CC peptide, or functional derivatives of these. The two cassettes are used  
 CC to transform a host cell that is capable of excreting proteins. The host  
 CC cell can be a plant, animal or insect cell, but is preferably a fungal  
 CC cell (especially saccharomyces cerevisiae). The transformed host can be  
 CC used to determine the influence of a compound on the appearance of a  
 CC malformed protein. This is done by culturing the host cell under  
 CC suitable conditions, applying the compound to be tested and measuring the  
 CC amount of reporter gene activation. Compounds identified by this method  
 CC can be used to inhibit protein aggregation, especially for the treatment  
 CC of Alzheimer's disease or cancer. Sequence 85 BP; 22 A; 18 C; 21 G; 24 T;  
 SQ

alignment\_scores:  
 PT Diagnosing Alzheimer's disease - by determining an alternation in the  
 PT normal base sequence at the end of APC coding sequence of the pre-APC  
 PT gene.  
 PS Disclosure: Fig.1; 11PP: English.  
 CC Region of the pre-APC protein corresponds to the APC protein. New probes  
 CC may be used to detect an alteration in this base sequence, which indicates  
 CC Alzheimer's disease or a predisposition to develop it  
 SQ Sequence 177 BP; 54 A; 27 C; 46 U;

alignment\_scores:  
 PT Quality: 92.00 Length: 16  
 PS Ratio: 5.750 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
 US-09-155-076-2 x N92266 ..

Align seg 1/1 to: N92266 from: 1 to: 177

seq\_name: N\_Geneseq\_36:077992

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16  
 ||||| ..  
 13 GAUCCAGAAAUCCGACAUAGACUCAGGAAUGAGGUCAUACA AAAA 60

seq\_documentation\_block:

ID Q77992 standard; cDNA: 189 BP.  
 ID Q77992; ..

AC 13-JUL-1995 (first entry)  
 DT 13-JUL-1995 (first entry)  
 CC DNA encoding the APP leader sequence fused to beta amyloid peptide.  
 DE APP precursor protein; beta/A4 peptide; Alzheimer's disease;  
 KW model; transgenic animal; leader sequence; transgene; ss.  
 KW synthetic.  
 OS WO944266 A.

CC PD 27-OCT-1994; U04026.  
 CC PR 12-APR-1994; U04026.  
 CC PR 19-APR-1993; US-050574.  
 CC PA (UNIV. ) UNIV ILLINOIS FOUND.  
 CC PI Beech RD, Ross SR, Young C;  
 CC DR WPI; 94-3418/84/2.  
 CC PT Transgenic animal models overexpressing alpha-1-antichymotrypsin  
 PT or beta/A4 peptide in the brain - useful as models of  
 PT Alzheimer's disease  
 PS Example 1; Page 19; 64PP; English.  
 CC The plasmid pADbetaA+L11 config. the APP (amyloid precursor protein)  
 CC leader sequence and the beta amyloid peptide (beta/A4) was constructed  
 CC using primers Q77985-91 in such a way that the 3' end of the leader  
 CC sequence overlapped with the 5' end of the gene fragment encoding the  
 CC beta/A4 peptide. The 2 fragments were then annealed and extended using  
 CC the splicing by overlap extension method (Horton et al.) to create a  
 CC new artificial gene encoding a single polypeptide comprising the leader  
 CC sequence fused to the beta/A4 peptide with all of the intervening  
 CC sequences deleted. This transgene  
 CC can be used in transgenic animals as a model to test potential therapies  
 CC for the treatment of Alzheimer's disease (AD). (Also see Q77993-96 for  
 CC the construction of PADABACT-1, which is also used in a animal models  
 CC for AD.)

CC Sequence 189 BP; 43 A; 41 C; 58 G; 47 T;

alignment\_scores:  
 PT Quality: 92.00 Length: 16  
 PS Ratio: 5.750 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
 US-09-155-076-2 x Q77992 ..

Align seg 1/1 to: Q77992 from: 1 to: 189

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16  
 ||||| ..  
 11 GRCGCTGAATTAGACRGACTCTGGTTACCAAGTCAACCAAAG 58

seq\_name: N\_Geneseq\_36:N92266

seq\_documentation\_block:  
 ID N92266 standard; RNA; 177 BP.  
 AC N92266; ..

DT 23-APR-1990 (first entry)  
 DE Region of pre-APC coding sequence.  
 KW Alzheimer's disease; pre-APC coding sequence; APC protein.  
 PN EP-341491-A.  
 PD 15-NOV-1989.  
 PF 26-APR-1989; 101531.  
 PS 13-MAY-1988; US-194053.  
 PA (MOLE-) Molecular Therapeutics Inc.  
 PI Scangos G, Rae P, Unterbeck A, Kamarck ME;  
 DR WPI; 89-333369/46.  
 DR P-PSDB: P93373.

seq\_name: N\_Geneseq\_36:V23754  
 seq\_documentation\_block:  
     ID V23754 standard; DNA; 262 BP.  
     AC V23754;  
     DT 18-Aug-1998 (first entry)  
     DE Alzras coding sequence.  
     DS alzras; DSAsp; alzas; Down's syndrome; diagnosis; therapy; human;  
     KW Alzheimer's disease; ss.  
     OS Homo sapiens.  
     PH Key Location/Qualifiers  
     CD50 .205  
     FT /\*tsg= a /product= ALZASp1 /note= "specifically claimed fragment"  
     FT WO9807850-A2.  
     PN PD 26-FEB-1998.  
     PF 22-AG-1997; E04599.  
     PR 22-AUG-1996; CA-18301.  
     PA (BERG/ ) BERGMANN J E.  
     PA (PREB/ ) PREDDIE E R.  
     PI Bergmann JE; Preddie ER;  
     DR WPI: 98-169155-15.  
     DR P-PSDB; W53984.  
     PT Nucleic acid molecules dsas, and alzas - used for detecting and  
     PT treating Down's syndrome and Alzheimer's disease  
     PS Claim 13; Fig 11; 96pp; English.  
     CC This sequence represents the human alzras nucleic acid. The dsas  
     CC and alzas DNA sequences are the nucleic acids of the invention. Reagents  
     CC specifically for DSAsP can be used for the diagnosis of Down's syndrome  
     CC in humans and especially in pregnant women. Molecules that inhibit the  
     CC activity of the promoters (PDS1, PDS2, PDS3, and PDS4) for dsas can be  
     CC used for treating Down's syndrome. The reagent capable of detecting  
     CC alzas can be used for detecting Alzheimer's disease, especially in the  
     CC pre-symptomatic stage. Substances that inhibit the promoters for alzas  
     CC can be used in treating Alzheimer's disease.  
     Sequence 262 BP; 96 A; 43 C; 52 G; 71 T;  
  
     alignment\_scores:  
         US-09-15-076-2 x V23754 .  
         Align seg 1/1 to: V23754 from: 1 to: 262  
             1 ASPAlaGlupheArchiAspSerGlyTyrIluValHisIleGlnLys 16  
             1 GATGAGAATTCCGGATGACTCAGGATATGAAGTTCACTCAAAA 48  
  
     seq\_name: N\_Geneseq\_36:Q88697  
     seq\_documentation\_block:  
         ID Q88697 standard; cDNA to mRNA; 297 BP.  
         AC Q88697;  
         DT 11-NOV-1995 (first entry)  
         DE Beta amyloid precursor protein C-terminal peptide mutant gene.  
         DS Human; beta-amyloid precursor protein mutant; C-terminal peptide;  
         KW gene transfer; transgenic animal; Alzheimer disease model;  
         KW gene therapy; ss.  
         OS Homo sapiens.  
         PN EP-653154-A.  
         PD 17-MAY-1995.  
         PF 07-NOV-1994; 117512.  
         PR 12-NOV-1993; JP-306026.  
         PA (FARH ) HOECHST JAPAN LTD.  
         PA (FARH ) HOECHST JAPAN KK.  
         PI Kawarabayashi T; Kobayashi T; Sato M; Shoji M; Tada N;  
         DR WPI: 95-180492/24.  
         DR P-PSDB; R74694.  
         PT Transgenic animal model for Alzheimer's disease - contains DNA encoding  
         PT part of beta=amyloid precursor protein in a gene construct designed for  
         PT Claim 2; Page 12-13; 32pp; English.  
         CC The sequence encodes a human brain beta-amyloid precursor protein  
         CC (APP) mutant C-terminal peptide, and differs from Q88696 by a Glu  
         CC to Gln conversion at codon-22. The DNA may be transferred along  
         CC with an APP signal peptide gene (e.g. Q88695) into somatic and germ  
         CC cells of a non-human mammal, and the resulting transgenic animal may  
         CC be used as a model for Alzheimer disease (AD). The animal model  
         CC exhibits symptoms similar to AD, producing large quantities of APP  
         CC C-terminal peptide, death of neuron cells in pyramidal cells at  
         CC cerebral amyloid regions, increases in glial cells and deposition  
         CC of abnormally phosphorylated tau protein. The animal model may  
         CC be used to develop new therapies for AD, including gene therapy  
         Sequence 297 BP; 86 A; 65 C; 77 G; 69 T;  
  
     seq\_name: N\_Geneseq\_36:Q88696  
     seq\_documentation\_block:  
         ID Q88696 standard; cDNA to mRNA; 297 BP.  
         AC Q88696;  
         DT 11-NOV-1995 (first entry)  
         DE Beta-amyloid precursor protein C-terminal peptide gene.  
         DS Human; beta-amyloid precursor protein; C-terminal peptide;  
         KW gene transfer; transgenic animal; Alzheimer disease model;  
         KW gene therapy; ss.  
         OS Homo sapiens.  
         PN EP-653154-A.  
         PD 17-MAY-1995.  
         PF 07-NOV-1994; 117512.  
         PR 12-NOV-1993; JP-306026.  
         PA (FARH ) HOECHST JAPAN LTD.  
         PA (FARH ) HOECHST JAPAN KK.  
         PI Kawarabayashi T; Kobayashi T; Sato M; Shoji M; Tada N;  
  
     seq\_name: N\_Geneseq\_36:Q88695  
     seq\_documentation\_block:  
         ID Q88695 standard; cDNA to mRNA; 297 BP.  
         AC Q88695;  
         DT 11-NOV-1995 (first entry)  
         DE Beta-amyloid precursor protein C-terminal peptide gene.  
         DS Human; beta-amyloid precursor protein; C-terminal peptide;  
         KW gene transfer; transgenic animal; Alzheimer disease model;  
         KW gene therapy; ss.  
         OS Homo sapiens.  
         PN EP-653154-A.  
         PD 17-MAY-1995.  
         PF 07-NOV-1994; 117512.  
         PR 12-NOV-1993; JP-306026.  
         PA (FARH ) HOECHST JAPAN LTD.  
         PA (FARH ) HOECHST JAPAN KK.  
         PI Kawarabayashi T; Kobayashi T; Sato M; Shoji M; Tada N;





KW Alzheimer's disease; mutation; diagnosis; transgenic model; study;  
 KW cognitive; beta A4 domain; exon 17; senility; ss .

OS Homo sapiens.

FH Location/Qualifiers  
 Key 1. .336  
 FT /tag= a  
 FT /number= 17  
 FT /transl\_except= pos: 175-177, aa: Ile  
 FT /note= "encodes amino acids 640-751 of full APP isoform 751, the translation exception at posn. 175-177 is the site of a Val to Ile mutation in isoform 751, bases 175-177 probably should be ARC and not TTC"  
 FT misc\_feature 43. .168  
 FT /tag= b  
 FT /note= "encodes the beta-A4 domain"

PN WO960927-A1.

PD 07-MAR-1995; U10920.  
 PR 28-AUG-1995; US-299872.

PS 01-SEP-1994; US-299872.

PA (MERCK & CO INC.

PI Chen HY, Heavens RB, Singh G, Srinathsinghji DJS;  
 PI Smith DW, Trumboer ME, Van Der Ploeg LHT,  
 PI Zheng H;

DR WPI; 96-160358/16.  
 DR P-PSDB; R95556.

PT transgenic animal expressing familial form of human amyloid precursor protein - used to evaluate compounds affecting Alzheimer's disease and other cognitive disorders

PS Example 1; Fig 7; 31PP; English.

CC r18082 represents exon 17 of the amyloid precursor protein (APP) isoform 751 gene from a patient diagnosed with familial Alzheimer's disease (FAD). The sequence given corresponds to the coding sequence for amino acids 640-751 of FAD APP 751. A feature of FAD is a Val to Ile substitution at posn. 698 of the full APP (encoded by bases 175 to 177 of this sequence). DNA encoding this sequence was used to construct expression vectors for the prodn. of transgenic animals (esp. mice) carrying the FAD APP 751 mutation. The transgenic animals are useful for the evaluation of test cdfs, affecting Alzheimer's disease and other cognitive disorders and for identification of new targets in Alzheimer's disease since the progression of the disease can be followed gradually.

CC N.B. the V-I mutation encoded at base 175-177, is given in the sequence specification as a trnc codon (most probably this should be ATC).

CC Sequence 336 BP; 102 A; 69 C; 88 G; 77 T;

alignment\_scores:  
 Quality: 92.00 Length: 16  
 Ratio: 5.750 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
 US-09-155-076-2 x T18082 ..

Align seg 1/1 to: T18082 from: 1 to: 336

seq\_name: N\_Geneseq\_36:v20380

seq\_documentation\_block:  
 ID V20380 standard; DNA; 354 BP.  
 AC V20380;  
 DT 26-JUN-1998 (first entry)  
 DE DNA for APP C-terminal fragment mutant SPA4CT Thr43Ala/Val46Phe;  
 KW Human; amyloid precursor protein; APP; carboxy-terminal fragment;  
 KW mutant SPA4CT Thr43Ala/Val46Phe; disease model; treatment;  
 KW Homo sapiens.

OS Synthetic.

Location/Qualifiers  
 1. .336  
 FT /tag= a  
 FT /note= "stop codon not given"

PN WO9803643-A2.

PD 29-JAN-1998.  
 PR 08-MAY-1997; GB-009239.  
 PR 08-MAY-1997; GB-015351.  
 PR 22-JUL-1996; GB-018904.  
 PR 09-SEP-1996; GB-018804.  
 PA (SMIK ) SMITHKLINE BECHAM AUSTRALIA PTY LTD.  
 PA (SMIK ) SMITHKLINE BECHAM PHARMA GMBH.  
 PA Beyreuther K, Lichtenthaler S, Masters CL, Prior P;  
 DR WPI: 98-120768/11.

PR P-PSDB; W50027.

PT Construct containing sequence for mutant form of amyloid precursor protein - or its C-terminal fragment, and related transgenic animals or transformed cells, used for identifying potential drugs for Alzheimer's disease

PS Claim 10; Page 10; 15PP; English.  
 PS The present sequence encodes the human amyloid precursor protein (APP) C-terminal fragment (ACT) mutant SPA4CT Thr43Ser.

CC The mutation results in a higher ratio of beta A4 1-42 to beta A4 1-40, useful in disease models to identify potential drugs for the treatment of Alzheimer's disease

CC Sequence 354 BP; 89 A; 83 C; 99 G; 83 T;

alignment\_scores:  
 Quality: 92.00 Length: 16  
 Ratio: 5.750 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
 US-09-155-076-2 x V20377 ..

Align seg 1/1 to: V20377 from: 1 to: 354

1 AspAlaGlupheargHisAspSerGlyTyrGluValIleHisGlnLys 16  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 40 GATGCCAGATTCCGACATGACTGGATATGAAGTTCATCAAAAAA 105

58 GATGCCAGATTCCGACATGACTGGATATGAAGTTCATCAAAAAA 105

seq\_name: N\_Geneseq\_36:v20380

seq\_documentation\_block:  
 ID V20380 standard; DNA; 354 BP.  
 AC V20380;  
 DT 26-JUN-1998 (first entry)  
 DE DNA for APP C-terminal fragment mutant SPA4CT Thr43Ala/Val46Phe;  
 KW Human; amyloid precursor protein; APP; carboxy-terminal fragment;  
 KW mutant SPA4CT Thr43Ala/Val46Phe; disease model; treatment;  
 KW Homo sapiens.

OS Synthetic.

Location/Qualifiers  
 1. .336  
 FT /tag= a  
 FT /note= "stop codon not given"

PN WO9803643-A2.

PD 29-JAN-1998.  
 PR 08-MAY-1997; GB-009239.  
 PR 08-MAY-1997; GB-015351.  
 PR 22-JUL-1996; GB-018904.  
 PR 09-SEP-1996; GB-018804.  
 PA (SMIK ) SMITHKLINE BECHAM AUSTRALIA PTY LTD.  
 PA (SMIK ) SMITHKLINE BECHAM PHARMA GMBH.  
 PA Beyreuther K, Lichtenthaler S, Masters CL, Prior P;  
 DR W50027.

PR P-PSDB; W50030.

PT Construct containing sequence for mutant form of amyloid precursor protein - or its C-terminal fragment, and related transgenic animals or transformed cells, used for identifying potential drugs for Alzheimer's disease

OS Synthetic.

**Claim 10:** Page 11; 15pp; English.  
**PS** The present sequence encodes the human amyloid precursor protein (APP) C-terminal fragment (ACT) mutant SPA4CT Thr43Ala/Tyr46Phe. The mutation results in a higher ratio of beta A4 1-42 to beta A4 1-40, useful in disease models to identify potential drugs for the treatment of Alzheimer's disease. Sequence 354 BP; 91 A; 82 C; 98 G; 83 T;

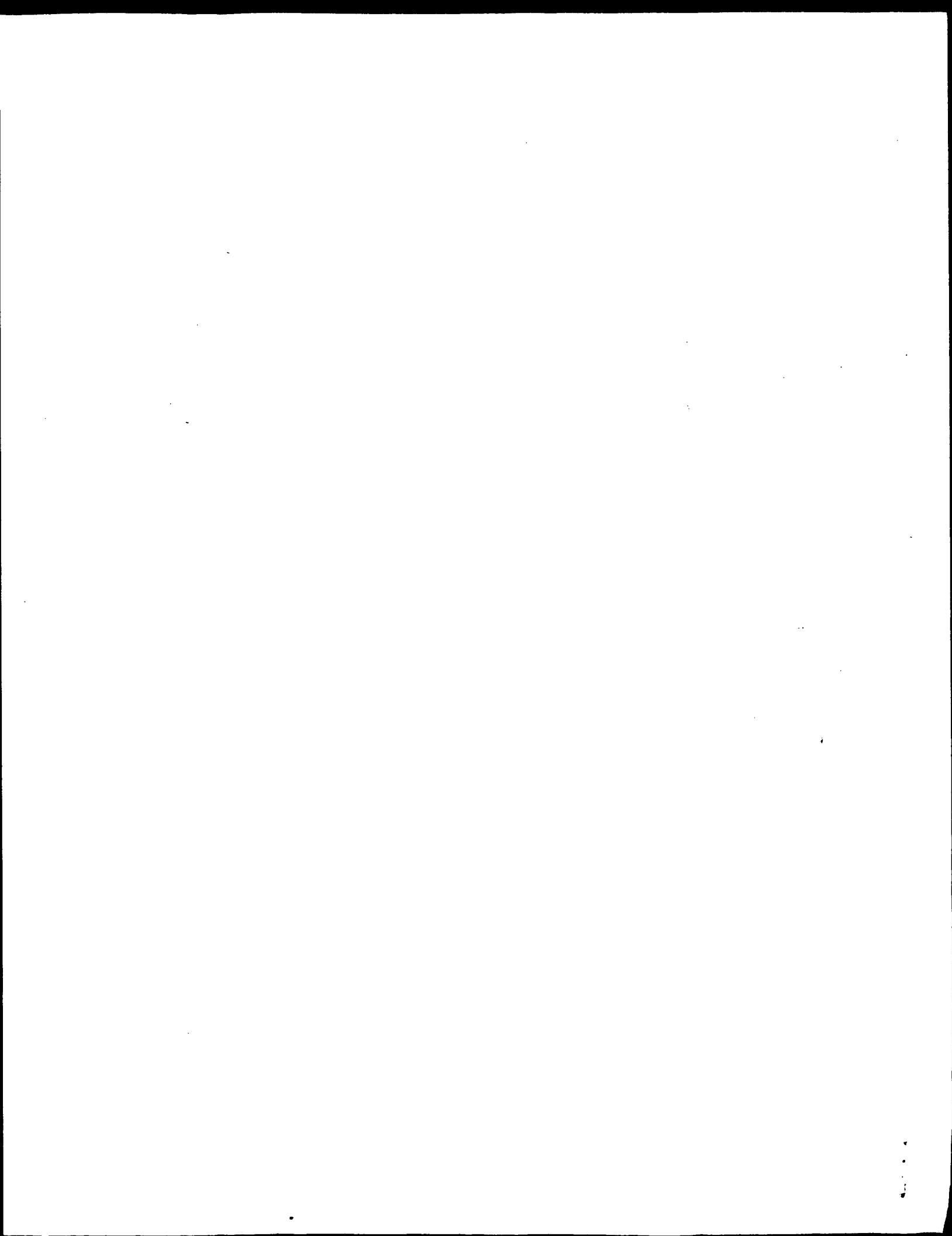
alignment\_scores: Quality: 92.00 Ratio: 5.750 Percent Similarity: 100.000 Percent Identif.: 100.000 Length: 16 Gaps: 0

allowing the government to block:

US-09-155-076-2 x V20380 ..

ארתיג'ן דסרגי 1/1 סס: V20380 תינוק: I סס: 3334

|    |  |     |
|----|--|-----|
| 1  | ASPLAGIUPHEAR THIS ASPER GLY TYR GLUA HI SGIN LY S | 16  |
| 58 | GATGCAGAATTCCGACATGACTCAGGATAGAAGTTCAATCATCAAAAA   | 105 |



OM of: US-09-155-076-2 to: Issued\_Patents\_NA: \* out\_format : pfs  
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 About: Results were produced by the Gencore software, version 4.5,  
 Copyright (c) 1993-2000 Compugen Ltd.

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 Database length: 68777915  
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| /cgn2_6/pctodata/2/ina/6_COMB.seq;US-08-339-708A-3     | +   | 92.00 | 290.37 | 1.1e-08 | 297  | 1             | S     |
| /cgn2_6/pctodata/2/ina/6_COMB.seq;US-08-339-708A-5     | +   | 92.00 | 290.37 | 1.1e-08 | 297  | 1             | S     |
| /cgn2_6/pctodata/2/ina/6_COMB.seq;US-08-339-708A-7     | +   | 92.00 | 290.37 | 1.1e-08 | 297  | 1             | S     |
| /cgn2_6/pctodata/2/ina/backfile1.seq;5220013-9         | +   | 92.00 | 290.27 | 1.1e-08 | 300  | 1             | Paten |
| /cgn2_6/pctodata/2/ina/backfile1.seq;5234382-9         | +   | 92.00 | 290.27 | 1.1e-08 | 300  | 1             | Paten |
| /cgn2_6/pctodata/2/ina/6_COMB.seq;US-08-339-708A-9     | +   | 92.00 | 289.99 | 1.2e-08 | 309  | 1             | S     |
| /cgn2_6/pctodata/2/ina/6_COMB.seq;US-08-339-708A-11    | +   | 92.00 | 289.99 | 1.2e-08 | 309  | 1             | S     |
| /cgn2_6/pctodata/2/ina/5C_COMB.seq;US-08-729-245-2     | +   | 92.00 | 288.70 | 1.4e-08 | 354  | 1             | S     |
| /cgn2_6/pctodata/2/ina/backfile1.seq;5187153-3         | +   | 92.00 | 282.72 | 2.0e-08 | 485  | 1             | Paten |
| /cgn2_6/pctodata/2/ina/backfile1.seq;5220013-3         | +   | 92.00 | 285.70 | 2.0e-08 | 486  | 1             | Paten |
| /cgn2_6/pctodata/2/ina/backfile1.seq;5223482-3         | +   | 92.00 | 285.70 | 2.0e-08 | 486  | 1             | Paten |
| /cgn2_6/pctodata/2/ina/5B_COMB.seq;US-08-428-4         | +   | 92.00 | 285.06 | 2.1e-08 | 520  | 1             | S     |
| /cgn2_6/pctodata/2/ina/5B_COMB.seq;US-08-480-498-3     | +   | 92.00 | 274.88 | 8.1e-08 | 1521 | 1             | S     |
| /cgn2_6/pctodata/2/ina/5D_COMB.seq;US-08-659-984A-3    | +   | 92.00 | 274.88 | 8.1e-08 | 1521 | 1             | S     |
| /cgn2_6/pctodata/2/ina/5A_COMB.seq;US-08-919-193-4     | +   | 92.00 | 274.61 | 8.1e-08 | 1521 | 1             | S     |
| /cgn2_6/pctodata/2/ina/5A_COMB.seq;US-08-371-930-9     | +   | 92.00 | 271.89 | 1.2e-07 | 1521 | 1             | S     |
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| /cgn2_6/pctodata/2/ina/backfile1.seq;5187153-1         | +   | 92.00 | 267.38 | 2.1e-07 | 3533 | 1             | Paten |
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| /cgn2_6/pctodata/2/ina/5A_COMB.seq;US-08-123-702-3     | +   | 92.00 | 267.98 | 2.0e-07 | 3148 | 1             | Paten |
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| /cgn2_6/pctodata/2/ina/backfile1.seq;5218100-1         | +   | 92.00 | 267.38 | 2.1e-07 | 3353 | 1             | Paten |
| /cgn2_6/pctodata/2/ina/5D_COMB.seq;US-08-422-333-20    | +   | 92.00 | 266.92 | 2e-07   | 3520 | 1             | Paten |
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| /cgn2_6/pctodata/2/ina/5C_COMB.seq;US-08-453-552-5     | +   | 92.00 | 260.26 | 5.3e-07 | 7106 | 1             | Paten |
| /cgn2_6/pctodata/2/ina/5B_COMB.seq;US-08-710-637-3     | +   | 92.00 | 260.26 | 5.3e-07 | 7298 | 1             | Paten |
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| /cgn2_6/pctodata/2/ina/5A_COMB.seq;US-08-123-659A-6    | +   | 92.00 | 258.46 | 6.6e-07 | 8591 | 1             | Paten |
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| seq_documentation_block:  |                           |
|---|---------------------------|
| Patent No. 5,777,194  | Application US/08636876   |
| Attorney/Agent Information:   |                           |
| Applicant: Scott, Richard W.  |                           |
| Applicant: Beaume, Andrew G.  |                           |
| Applicant: Trusko, Stephen P.   |                           |
| Applicant: Siman, Robert  |                           |
| Title of Invention: GENE-TARGETED NON-HUMAN MAMMAL WITH NUMBER OF SEQUENCES: 16 |                           |
| Correspondence Address:   |                           |
| Addressee: Fish & Richardson P.C.   |                           |
| Street: 225 Franklin Street Suite 3100  |                           |
| City: Boston  |                           |
| State: MA   |                           |
| Country: USA  |                           |
| ZIP: 02110-2804   |                           |
| Computer Readable Form:   |                           |
| Medium Type: Floppy disk  |                           |
| Computer: IBM PC compatible   |                           |
| Operating System: PC-DOS/MS-DOS   |                           |
| Software: PatentIn Release #1.0, Version #1.30                                  |                           |
| Current Application Data:   |                           |
| Application Number: US/08/636,876   |                           |
| Filing Date:  |                           |
| Attorney/Agent Information:   |                           |
| Name: Clark, Paul T.  |                           |
| Registration Number: 30,162   |                           |
| Reference/DoCKET NUMBER: 02655/055001   |                           |
| Telecommunication Information:  |                           |
| Telephone: (617) 542-5070   |                           |
| Telex: (617) 542-8906   |                           |
| Telex: 200154   |                           |
| Information for SEQ ID NO: 15:  |                           |
| Sequence Characteristics:   |                           |
| Length: 59 base pairs   |                           |
| Type: nucleic acid  |                           |
| Strandedness: single  |                           |
| Topology: linear  |                           |
| Molecule Type: DNA (genomic)  |                           |
| US-08-636-876-15 alignment_scores:  |                           |
| Quality: 92.00  | Length: 16                |
| Ratio: 5.750  | Gaps: 0                   |
| Percent Similarity: 100.000   | Percent Identity: 100.000 |
| Align seg 1/1 to: US-08-636-876-15 from: 1 to: 58                               |                           |
| 1 AspAlaGluIleArgHisAspSerGlyTruValHisHisGlnLys 16                              |                           |
| 8 GATGCCAGTTACAGACATGATTCAAGATTAAGTCACCATCARRAA 55                              |                           |
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| Sequence 8, Application PC/TUS9404026   |                           |
| General Information:  |                           |
| Applicant:  |                           |
| Title of Invention: Transgenic Animal Models for Alzheimer's Disease            |                           |
| Number of Sequences: 12   |                           |

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
 STREET: 6300 Sears Tower - 233 South Wacker Drive  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60606-6402

COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT-US94/04026  
 FILING DATE:  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Clough, Ph.D., David W.  
 REGISTRATION NUMBER: 36.107  
 REFERENCE/DOCKET NUMBER: 31188  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312/474-6300  
 TELEFAX: 312/474-0448  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 189 base pairs  
 TYPE: nucleic acid  
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 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 ORIGINAL SOURCE:  
 ORGANISM: Human  
 PCT-US94/04026-8

alignment\_scores:  
 Quality: 92.00 Length: 16  
 Ratio: 5.750 Gaps: 0  
 Percent Similarity: 100.000 Identity: 100.000

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1 AspalaGlupheArgHisAspSerGlyTyrGluValHisGlnLys 16  
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seq\_documentation\_block:  
 Sequence 3, Application US/08339708A  
 Patent No. 6037521

GENERAL INFORMATION:  
 APPLICANT: Sato, Masahiro  
 APPLICANT: Takashi, Kobayashi  
 APPLICANT: Tada, No. 6037521hiro  
 APPLICANT: Shoji, Mikio  
 APPLICANT: Kawarabayashi, Takeshi  
 TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR ALZHEIMER'S  
 TITLE OF INVENTION: DISEASE  
 NUMBER OF SEQUENCES: 23  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Foley & Lardner  
 STREET: 3000 K Street, N.W., Suite 500  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20007-5109

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible  
; COMPUTER SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE: 14-NOV-1994  
; PRIORITY NUMBER: US/08/339,708A  
; PRIORITY NUMBER: JP 306026/93  
; FILING DATE: 12-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SANDERCOCK, COLIN G.  
; REGISTRATION NUMBER: 31,298  
; REFERENCE/DOCKET NUMBER: 026083/0159  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 297 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: homo sapiense  
; STRAIN: human brain  
; FEATURE:  
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; LOCATION: 1..297  
; OTHER INFORMATION: /note= "1. human beta-amyloid  
; 2. C-terminal peptide"  
; OTHER INFORMATION: precursor;  
; OTHER INFORMATION: /note= "1. human beta-amyloid  
; 2. C-terminal peptide"  
; OTHER INFORMATION: precursor;  
; OTHER INFORMATION: /note= "1. human beta-amyloid  
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; OTHER INFORMATION: precursor;  
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; 2. C-terminal peptide"  
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1 GATGCCGAAATTCCGACATGACTCAGGATATGGAGTTCATCATCAAAA 48

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seq\_documentation\_block:  
; Sequence 7, Application US/08339708A  
; GENERAL INFORMATION:  
; APPLICANT: Sato, Masahiro  
; APPLICANT: Takeshi Kobayashi  
; APPLICANT: Tada, No. 6037521hiro  
; APPLICANT: Shoji, Mikio  
; APPLICANT: Kawarabayashi, Takeshi  
; TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR ALZHEIMER'S  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/339,708A  
; FILING DATE: 14-NOV-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 306026/93  
; FILING DATE: 12-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SANDERCOCK, COLIN G.  
; REGISTRATION NUMBER: 31,298  
; REFERENCE/DOCKET NUMBER: 026083/0159  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 297 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
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; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: homo sapiense  
; STRAIN: human brain  
; FEATURE:  
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; LOCATION: 1..297  
; OTHER INFORMATION: /note= "1. human beta-amyloid  
; 2. C-terminal peptide"  
; OTHER INFORMATION: precursor;  
; OTHER INFORMATION: /note= "1. human beta-amyloid  
; 2. C-terminal peptide"  
; OTHER INFORMATION: precursor;

alignment\_scores:  
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; Ratio: 5.750 Gaps: 0  
; Percent Similarity: 100.000 Percent Identity: 100.000

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; US-09-155-076-2 x US-08-339-708A-7 ..

Align seg 1/1 to: US-08-339-708A-7 from: 1 to: 297

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seq\_documentation\_block:  
; Patent No. 5220013  
; APPLICANT: PONTE, PHYLLIS A.; CORDELL, BARBARA  
; TITLE OF INVENTION: DNA SEQUENCE USEFUL FOR THE DETECTION  
; OF ALZHEIMER'S DISEASE  
; NUMBER OF SEQUENCES: 30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/444,118  
; FILING DATE: 30-NOV-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 87,002  
; FILING DATE: 16-AUG-1987  
; APPLICATION NUMBER: 8,810  
; FILING DATE: 30-JAN-1987  
; APPLICATION NUMBER: 946,376  
; FILING DATE: 31-DEC-1986  
; APPLICATION NUMBER: 932,193  
; FILING DATE: 17-NOV-1986  
; SEQ ID NO: 9;

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; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339-708A
; FILING DATE: 14-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 306026/93
; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SANDERCOCK, COLIN G.
; REGISTRATION NUMBER: 31-298
; REFERENCE/DOCKET NUMBER: 026083/0159
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: homo sapiense
; STRAIN: human brain
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..309
; OTHER INFORMATION: /note= "1. human beta-amyloid
; precursor; 2. C-terminal peptide"
; US-08-339-708A-9

; alignment_scores:
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; Percent Similarity: 100.000 Identity: 100.000
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; 1 ASPAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
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; seq_documentation_block:
; Sequence 9, Application US/08339708A
; Patent No. 6037521
; GENERAL INFORMATION:
; APPLICANT: Sato, Masahiro
; APPLICANT: Takashi, Kobayashi
; APPLICANT: Tada, No. 6037521hiro
; APPLICANT: Shoji, Mikio
; APPLICANT: Kawarabayashi, Takeshi
; TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR ALZHEIMER'S
; TITLE OF INVENTION: DISEASE

; alignment_scores:
; Quality: 92.00 Length: 16
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; US-09-155-076-2 x US-08-339-708A-9 ...
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; 13 GATGCCGAAATTCCGACATGACTAGGGATATAAGTCATCATCAAAA 60
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; seq_documentation_block:
; Sequence 11, Application US/08339708A
; Patent No. 6037521
; GENERAL INFORMATION:
; APPLICANT: Sato, Masahiro
; APPLICANT: Takashi, Kobayashi
; APPLICANT: Tada, No. 6037521hiro
; APPLICANT: Shoji, Mikio
; APPLICANT: Kawarabayashi, Takeshi
; TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR ALZHEIMER'S
; 
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; TITLE OF INVENTION: DISEASE  
 ; NUMBER OF SEQUENCES: 23  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Foley & Lardner  
 ; STREET: 3000 K Street, N.W., Suite 500  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTY: USA  
 ; ZIP: 20007-5108  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentnet Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/339,708A  
 ; FILING DATE: 14-NOV-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: JP 306026/93  
 ; FILING DATE: 12-NOV-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: SANDEROCK COLIN G.  
 ; REGISTRATION NUMBER: 31,298  
 ; REFERENCE/DOCKET NUMBER: 026083/0159  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202)672-5300  
 ; TELEFAX: (202)672-5399  
 ; TELEX: 904136  
 ; INFORMATION FOR SEQ ID NO: 11:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 309 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA to mRNA  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: homo sapiense  
 ; STRAIN: human brain  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 1..309  
 ; OTHER INFORMATION: /note= "1. human beta-amyloid  
 ; OTHER INFORMATION: precursor; 2. C-terminal peptide"  
 ; US-08-339-708A-11  
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 Ratio: 5.750 Gaps: 0  
 Percent Similarity: 100.000 Identity: 100.000  
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 ; Patent No. 5187153  
 ; APPLICANT: CORDELL, BARBARA; SCHILLING, JAMES W.; KATUNMA, NOBUHIKO  
 ; TITLE OF INVENTION: METHODS OF TREATMENT USING ALZHEIMER'S  
 ; AMYLOID POLYPEPTIDE DERIVATIVES  
 ; NUMBER OF SEQUENCES: 33  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/502,273  
 ; FILING DATE: 29-MAR-1990  
 ; PRIORITY APPLICATION DATA:  
 ; Application No. 5849999  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Neve, Rachael L.  
 ; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMAL  
 ; TITLE OF INVENTION: EXPRESSING FLAG-APP-C100 FUSION PROTEIN  
 ; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Fish & Richardson P.C.  
 ; STREET: 225 Franklin Street  
 ; CITY: Boston  
 ; STATE: MA  
 ; COUNTRY: US  
 ; ZIP: 02110-2804  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FASTSEQ Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/729,345  
 ; FILING DATE: 16-OCT-1996  
 ; CLASSIFICATION: 800  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Clark, Paul T.  
 ; REGISTRATION NUMBER: 30,162  
 ; REFERENCE/DOCKET NUMBER: 04843/027001  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 617-542-5070  
 ; TELEFAX: 617-542-8906  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 354 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
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 ; Sequence 2, Application US/08729345  
 ; Patent No. 5849999  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Berger-Sweeney, Joanne  
 ; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMAL  
 ; TITLE OF INVENTION: EXPRESSING FLAG-APP-C100 FUSION PROTEIN  
 ; NUMBER OF SEQUENCES: 9

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; APPLICATION NUMBER: US/07/361,912
; FILING DATE: 30-JAN-1987
; APPLICATION NUMBER: 948,376
; FILING DATE: 31-DEC-1986
; APPLICATION NUMBER: 932,133
; FILING DATE: 17-NOV-1986
; SEQ ID NO:3
; LENGTH: 485
5187153-3

alignment_scores:
Quality: 92.00 Length: 16
Ratio: 5.750 Gaps: 0
Percent Similarity: 100.000 Identity: 100.000

alignment_block:
US-09-155-076-2 x 5187153-3 ..

Align seg 1/1 to: 5187153-3 from: 1 to: 485
1 ASPALAGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |
240 GATGAGAATTCCGACATRACTGGATGAGTTCATCATCAAAA 287

seq_name: /cgn2_6/ptodata/2/ina/backfiles1.seq:5220013-3

seq_documentation_block:
;PATENT NO. 5220013
;APPLICANT: PONTE, PHYLLIS A.;CORDELL, BARBARA
;TITLE OF INVENTION: DNA SEQUENCE USEFUL FOR THE DETECTION
;OF ALZHEIMER'S DISEASE
;NUMBER OF SEQUENCES: 30
;CURRENT APPLICATION DATA:
;APPLICATION NUMBER: US/07/444,118
;FILING DATE: 30-NOV-1989
;PRIOR APPLICATION DATA:
;APPLICATION NUMBER: 87,002
;FILING DATE: 18-AUG-1987
;APPLICATION NUMBER: 8,810
;FILING DATE: 30-JAN-1987
;APPLICATION NUMBER: 948,376
;FILING DATE: 31-DEC-1986
;APPLICATION NUMBER: 932,193
;FILING DATE: 17-NOV-1986
;SEQ ID NO:3:
;LENGTH: 486
5220013-3

alignment_scores:
Quality: 92.00 Length: 16
Ratio: 5.750 Gaps: 0
Percent Similarity: 100.000 Identity: 100.000

alignment_block:
US-09-155-076-2 x 5220013-3 ..

Align seg 1/1 to: 5220013-3 from: 1 to: 486
1 ASPALAGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
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241 GATGAGAATTCCGACATRACTGGATGAGTTCATCATCAAAA 288

seq_name: /cgn2_6/ptodata/2/ina/backfiles1.seq:5223482-3

seq_documentation_block:
;Sequence 9, Application US/08268348A
;Patent No. 5750374
;GENERAL INFORMATION:
;APPLICANT: Dobell, Heinz
;APPLICANT: Draeger, Nicholas
;APPLICANT: Drottman, Gerda H
;APPLICANT: Jakob, Peter
;APPLICANT: Stuber, Dietrich
;TITLE OF INVENTION: Process for Producing Hydrophobic Polypeptides and Proteins, and Fusion Proteins for Use in
;TITLE OF INVENTION: Producing Same
;NUMBER OF SEQUENCES: 12
;CORRESPONDENCE ADDRESS:
;ADDRESSEE: Hoffmann-La Roche Inc.
;STREET: 340 Kingsland Street
;CITY: Nutley
;STATE: New Jersey
;COUNTRY: U.S.A.
;ZIP: 07110
;COMPUTER READABLE FORM:
;COMPUTER: IBM PC Compatible
;OPERATING SYSTEM: PC DOS/MS-DOS
;SOFTWARE: Patentn Release #1.0, Version #1.25
;CURRENT APPLICATION DATA:
;APPLICATION NUMBER: US/08/268,348A
;FILING DATE: 29-JUN-1994
;CLASSIFICATION: 435
;PRIOR APPLICATION DATA:
;APPLICATION NUMBER: EP 93110755 1
;FILING DATE: 06-JUL-1993
;ATTORNEY/AGENT INFORMATION:
;NAME: Parisi, John P.
;REGISTRATION NUMBER: 34,403
;REFERENCE/DOCID: 4105/157
;TELECOMMUNICATION INFORMATION:
;TELEPHONE: (201) 235-3500
;TELEFAX: (201) 235-3500
;
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; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 520 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE KEY: CDS
; LOCATION: 115..516
; OTHER INFORMATION: /product= "Amyloid Protein AA"
US-08-268-348A-9

alignment_scores:
; Sequence 3, Application US-08-268-348A-9
; Patent No. 574446
; GENERAL INFORMATION:
; APPLICANT: Chrysler, Susanna M.S.
; APPLICANT: Sinha, Suktano
; APPLICANT: Keim, Pamela S.
; APPLICANT: Anderson, John P.
; TITLE OF INVENTION: Beta-Secretase
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US-08/480,498
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 015270-002200
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1521 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-480-498-3

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alignment_scores:
; Sequence 3, Application US-08-268-348A-9
; Patent No. 574446
; GENERAL INFORMATION:
; APPLICANT: Chrysler, Susanna M.S.
; APPLICANT: Sinha, Suktano
; APPLICANT: Keim, Pamela S.
; APPLICANT: Anderson, John P.
; TITLE OF INVENTION: Beta-Secretase
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US-08/480,498
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 015270-002200
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1521 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-480-498-3

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## OM protein - protein search, using sw model

Run on: September 13, 2000, 02:22:33 ; Search time 18.63 Seconds  
(without alignment summaries)  
53.148 Million cell updates/sec

Title: US-09-155-076-2

Perfect score: 92  
Sequence: 1 DAEFRHDSGYEVHHQK 16

Scoring table: BLOSUM62

Gapext 0.5

Searched: 178050 seqs, 61884766 residues

Total number of hits satisfying chosen parameters: 178050

Minimum DB seq length: 0  
Maximum DB seq length: 10000000Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR-64:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query | Match | Length | DB ID  | Description         |
|------------|-------|-------|-------|--------|--------|---------------------|
| 1          | 92    | 100.0 | 42    | 2      | PN0512 | beta-amyloid prote  |
| 2          | 92    | 100.0 | 57    | 2      | E60045 | Alzheimer's disease |
| 3          | 92    | 100.0 | 57    | 2      | F60045 | Alzheimer's disease |
| 4          | 92    | 100.0 | 57    | 2      | G60045 | Alzheimer's disease |
| 5          | 92    | 100.0 | 57    | 2      | D60045 | Alzheimer's disease |
| 6          | 92    | 100.0 | 57    | 2      | A60045 | Alzheimer's disease |
| 7          | 92    | 100.0 | 57    | 2      | B60045 | Alzheimer's disease |
| 8          | 92    | 100.0 | 82    | 2      | P0438  | Alzheimer's disease |
| 9          | 92    | 100.0 | 695   | 1      | A49795 | Alzheimer's disease |
| 10         | 92    | 100.0 | 770   | 1      | ORHUA4 | Alzheimer's disease |
| 11         | 77    | 83.7  | 747   | 2      | JH0773 | Alzheimer's disease |
| 12         | 73    | 79.3  | 33    | 2      | S23094 | beta-amyloid prote  |
| 13         | 73    | 79.3  | 695   | 2      | A27485 | Alzheimer's disease |
| 14         | 73    | 79.3  | 695   | 2      | S00550 | Alzheimer's disease |
| 15         | 50.5  | 54.9  | 284   | 2      | S04723 | genome polyprotein  |
| 16         | 50.5  | 54.9  | 327   | 2      | S11435 | genome polyprotein  |
| 17         | 50.5  | 54.9  | 519   | 2      | PC1072 | nuclear inclusion   |
| 18         | 50.5  | 54.9  | 1555  | 2      | JT0959 | polyprotein - pota  |
| 19         | 49.5  | 53.8  | 971   | 2      | D70128 | conserved hypothet  |
| 20         | 48.5  | 52.7  | 330   | 2      | A26205 | coat protein precu  |
| 21         | 48.5  | 52.7  | 3063  | 2      | JS0166 | genome polyprotein  |
| 22         | 45.5  | 49.5  | 313   | 2      | JT0960 | polyprotein - pota  |
| 23         | 45.5  | 49.5  | 427   | 2      | JA0073 | genome polyprotein  |
| 24         | 44    | 47.8  | 274   | 2      | A64978 | hypothetical prote  |
| 25         | 43    | 46.7  | 629   | 2      | S60385 | probable membrane   |
| 26         | 42.5  | 46.2  | 539   | 2      | T39150 | probable heat shoc  |
| 27         | 42    | 45.7  | 113   | 2      | A64064 | ferredoxin [2Fe-2S] |
| 28         | 42    | 45.7  | 373   | 2      | D64971 | GDP-d-mannose dehy  |
| 29         | 42    | 45.7  | 373   | 2      | S28470 | vibfd protein - Vib |

## ALIGNMENTS

| RESULT | Query   | Match  | Length | 2: | Score | 92; | DB | 2: | Length |
|--------|---|--|--------|----|-------|-----|----|----|--------|
| 1      | PN0512  | beta-amyloid protein - guinea pig (fragment) |        |    |       |     |    |    |        |
|        | C;Species: Cavia Porcellus (guinea pig)   |  |        |    |       |     |    |    |        |
|        | C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999           |  |        |    |       |     |    |    |        |
|        | C;Accession: PN0512   |  |        |    |       |     |    |    |        |
|        | R;Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno |  |        |    |       |     |    |    |        |
|        | Biochem Biophys Res Commun 193, 624-630, 1993   |  |        |    |       |     |    |    |        |
|        | A;Title: Receptor-mediated specific biological activity of a beta-amyloid protein fra |  |        |    |       |     |    |    |        |
|        | A;Reference number: PN0512; MUID:93290653   |  |        |    |       |     |    |    |        |
|        | A;Molecule type: Protein  |  |        |    |       |     |    |    |        |
|        | A;Residues: 1-42 (SH1>  |  |        |    |       |     |    |    |        |
|        | C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteins  |  |        |    |       |     |    |    |        |
|        | C;Keywords: alternative splicing; amyloid   |  |        |    |       |     |    |    |        |

| RESULT | Query   | Match                 | Length | 2: | Score | 92; | DB | 2: | Length |
|--------|---|-----------------------|--------|----|-------|-----|----|----|--------|
| 1      | DAEFRHDSGYEVHHQK 16   |                       |        |    |       |     |    |    |        |
|        | Best Local Similarity 100.0%; Pred. No. 1.5e-08;            |                       |        |    |       |     |    |    |        |
|        | Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |                       |        |    |       |     |    |    |        |
|        | Db  | 1 DAEFRHDSGYEVHHQK 16 |        |    |       |     |    |    |        |
|        | RESULTS   |                       |        |    |       |     |    |    |        |
| 2      | QY  | 1 DAEFRHDSGYEVHQK 16  |        |    |       |     |    |    |        |
|        | Best Local Similarity 100.0%; Pred. No. 1.5e-08;            |                       |        |    |       |     |    |    |        |
|        | Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |                       |        |    |       |     |    |    |        |
|        | Db  | 1 DAEFRHDSGYEVHQK 16  |        |    |       |     |    |    |        |
|        | RESULTS   |                       |        |    |       |     |    |    |        |
| 3      | QY  | 1 DAEFRHDSGYEVHQK 16  |        |    |       |     |    |    |        |
|        | Best Local Similarity 100.0%; Pred. No. 1.5e-08;            |                       |        |    |       |     |    |    |        |
|        | Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |                       |        |    |       |     |    |    |        |
|        | Db  | 1 DAEFRHDSGYEVHQK 16  |        |    |       |     |    |    |        |
|        | RESULTS   |                       |        |    |       |     |    |    |        |
| 4      | QY  | 1 DAEFRHDSGYEVHQK 16  |        |    |       |     |    |    |        |
|        | Best Local Similarity 100.0%; Pred. No. 1.5e-08;            |                       |        |    |       |     |    |    |        |
|        | Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |                       |        |    |       |     |    |    |        |
|        | Db  | 1 DAEFRHDSGYEVHQK 16  |        |    |       |     |    |    |        |
|        | RESULTS   |                       |        |    |       |     |    |    |        |
| 5      | QY  | 1 DAEFRHDSGYEVHQK 16  |        |    |       |     |    |    |        |
|        | Best Local Similarity 100.0%; Pred. No. 1.5e-08;            |                       |        |    |       |     |    |    |        |
|        | Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |                       |        |    |       |     |    |    |        |
|        | Db  | 1 DAEFRHDSGYEVHQK 16  |        |    |       |     |    |    |        |
|        | RESULTS   |                       |        |    |       |     |    |    |        |
| 6      | QY  | 1 DAEFRHDSGYEVHQK 16  |        |    |       |     |    |    |        |
|        | Best Local Similarity 100.0%; Pred. No. 1.5e-08;            |                       |        |    |       |     |    |    |        |
|        | Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |                       |        |    |       |     |    |    |        |
|        | Db  | 1 DAEFRHDSGYEVHQK 16  |        |    |       |     |    |    |        |
|        | RESULTS   |                       |        |    |       |     |    |    |        |
| 7      | QY  | 1 DAEFRHDSGYEVHQK 16  |        |    |       |     |    |    |        |
|        | Best Local Similarity 100.0%; Pred. No. 1.5e-08;            |                       |        |    |       |     |    |    |        |
|        | Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |                       |        |    |       |     |    |    |        |
|        | Db  | 1 DAEFRHDSGYEVHQK 16  |        |    |       |     |    |    |        |
|        | RESULTS   |                       |        |    |       |     |    |    |        |
| 8      | QY  | 1 DAEFRHDSGYEVHQK 16  |        |    |       |     |    |    |        |
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|        | Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |                       |        |    |       |     |    |    |        |
|        | Db  | 1 DAEFRHDSGYEVHQK 16  |        |    |       |     |    |    |        |
|        | RESULTS   |                       |        |    |       |     |    |    |        |
| 9      | QY  | 1 DAEFRHDSGYEVHQK 16  |        |    |       |     |    |    |        |
|        | Best Local Similarity 100.0%; Pred. No. 1.5e-08;            |                       |        |    |       |     |    |    |        |
|        | Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |                       |        |    |       |     |    |    |        |
|        | Db  | 1 DAEFRHDSGYEVHQK 16  |        |    |       |     |    |    |        |
|        | RESULTS   |                       |        |    |       |     |    |    |        |
| 10     | QY  | 1 DAEFRHDSGYEVHQK 16  |        |    |       |     |    |    |        |
|        | Best Local Similarity 100.0%; Pred. No. 1.5e-08;            |                       |        |    |       |     |    |    |        |
|        | Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |                       |        |    |       |     |    |    |        |
|        | Db  | 1 DAEFRHDSGYEVHQK 16  |        |    |       |     |    |    |        |
|        | RESULTS   |                       |        |    |       |     |    |    |        |
| 11     | QY  | 1 DAEFRHDSGYEVHQK 16  |        |    |       |     |    |    |        |
|        | Best Local Similarity 100.0%; Pred. No. 1.5e-08;            |                       |        |    |       |     |    |    |        |
|        | Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |                       |        |    |       |     |    |    |        |
|        | Db  | 1 DAEFRHDSGYEVHQK 16  |        |    |       |     |    |    |        |
|        | RESULTS   |                       |        |    |       |     |    |    |        |
| 12     | QY  | 1 DAEFRHDSGYEVHQK 16  |        |    |       |     |    |    |        |
|        | Best Local Similarity 100.0%; Pred. No. 1.5e-08;            |                       |        |    |       |     |    |    |        |
|        | Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |                       |        |    |       |     |    |    |        |
|        | Db  | 1 DAEFRHDSGYEVHQK 16  |        |    |       |     |    |    |        |
|        | RESULTS   |                       |        |    |       |     |    |    |        |
| 13     | QY  | 1 DAEFRHDSGYEVHQK 16  |        |    |       |     |    |    |        |
|        | Best Local Similarity 100.0%; Pred. No. 1.5e-08;            |                       |        |    |       |     |    |    |        |
|        | Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |                       |        |    |       |     |    |    |        |
|        | Db  | 1 DAEFRHDSGYEVHQK 16  |        |    |       |     |    |    |        |
|        | RESULTS   |                       |        |    |       |     |    |    |        |
| 14     | QY  | 1 DAEFRHDSGYEVHQK 16  |        |    |       |     |    |    |        |
|        | Best Local Similarity 100.0%; Pred. No. 1.5e-08;            |                       |        |    |       |     |    |    |        |
|        | Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |                       |        |    |       |     |    |    |        |
|        | Db  | 1 DAEFRHDSGYEVHQK 16  |        |    |       |     |    |    |        |
|        | RESULTS   |                       |        |    |       |     |    |    |        |
| 15     | QY  | 1 DAEFRHDSGYEVHQK 16  |        |    |       |     |    |    |        |
|        | Best Local Similarity 100.0%; Pred. No. 1.5e-08;            |                       |        |    |       |     |    |    |        |
|        | Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |                       |        |    |       |     |    |    |        |
|        | Db  | 1 DAEFRHDSGYEVHQK 16  |        |    |       |     |    |    |        |
|        | RESULTS   |                       |        |    |       |     |    |    |        |
| 16     | QY  | 1 DAEFRHDSGYEVHQK 16  |        |    |       |     |    |    |        |
|        | Best Local Similarity 100.0%; Pred. No. 1.5e-08;            |                       |        |    |       |     |    |    |        |
|        | Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |                       |        |    |       |     |    |    |        |
|        | Db  | 1 DAEFRHDSGYEVHQK 16  |        |    |       |     |    |    |        |
|        | RESULTS   |                       |        |    |       |     |    |    |        |
| 17     | QY  | 1 DAEFRHDSGYEVHQK 16  |        |    |       |     |    |    |        |
|        | Best Local Similarity 100.0%; Pred. No. 1.5e-08;            |                       |        |    |       |     |    |    |        |
|        | Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |                       |        |    |       |     |    |    |        |
|        | Db  | 1 DAEFRHDSGYEVHQK 16  |        |    |       |     |    |    |        |
|        | RESULTS   |                       |        |    |       |     |    |    |        |
| 18     | QY  | 1 DAEFRHDSGYEVHQK 16  |        |    |       |     |    |    |        |
|        | Best Local Similarity 100.0%; Pred. No. 1.5e-08;            |                       |        |    |       |     |    |    |        |
|        | Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |                       |        |    |       |     |    |    |        |
|        | Db  | 1 DAEFRHDSGYEVHQK 16  |        |    |       |     |    |    |        |
|        | RESULTS   |                       |        |    |       |     |    |    |        |
| 19     | QY  | 1 DAEFRHDSGYEVHQK 16  |        |    |       |     |    |    |        |
|        | Best Local Similarity 100.0%; Pred. No. 1.5e-08;            |                       |        |    |       |     |    |    |        |
|        | Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |                       |        |    |       |     |    |    |        |
|        | Db  | 1 DAEFRHDSGYEVHQK 16  |        |    |       |     |    |    |        |
|        | RESULTS   |                       |        |    |       |     |    |    |        |
| 20     | QY  | 1 DAEFRHDSGYEVHQK 16  |        |    |       |     |    |    |        |
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|        | Db  | 1 DAEFRHDSGYEVHQK 16  |        |    |       |     |    |    |        |
|        | RESULTS   |                       |        |    |       |     |    |    |        |
| 21     | QY  | 1 DAEFRHDSGYEVHQK 16  |        |    |       |     |    |    |        |
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|        | Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |                       |        |    |       |     |    |    |        |
|        | Db  | 1 DAEFRHDSGYEVHQK 16  |        |    |       |     |    |    |        |
|        | RESULTS   |                       |        |    |       |     |    |    |        |
| 22     | QY  | 1 DAEFRHDSGYEVHQK 16  |        |    |       |     |    |    |        |
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|        | RESULTS   |                       |        |    |       |     |    |    |        |
| 23     | QY  | 1 DAEFRHDSGYEVHQK 16  |        |    |       |     |    |    |        |
| </td   |   |                       |        |    |       |     |    |    |        |

RESULT 3

P60045 Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)

C;Species: Sus scrofa domestica (domestic Pig)

C;Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 13-Aug-1999

C;Accession: F60045

R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog

A;Reference number: A60045; MUID:92017079

A;Accession: F60045

A;Molecule type: mRNA

A;Residues: 1-57 <JOH>

A;Cross-references: EMBL:X6127; NID:91895; PIDN:CAA39592.1; PMID:91896

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1

C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 92; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 2.1e-08;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGEYVHQK 16

Db 6 DAEFRHDSGEYVHQK 21

RESULT 4

G60045 Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)

C;Species: Cavia porcellus (guinea pig)

C;Accession: G60045

R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog

A;Reference number: A60045; MUID:92017079

A;Accession: G60045

A;Molecule type: mRNA

A;Residues: 1-57 <JOH>

A;Cross-references: EMBL:X56126

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1

C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 92; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 2.1e-08;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGEYVHQK 16

Db 6 DAEFRHDSGEYVHQK 21

RESULT 5

D60045 Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995

C;Accession: D60045

R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog

A;Reference number: A60045; MUID:92017079

A;Accession: D60045

A;Molecule type: mRNA

A;Residues: 1-57 <JOH>

A;Cross-references: EMBL:X56124

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1

C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 92; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 2.1e-08;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDGSEYVHQK 16

Db 6 DAEFRHDGSEYVHQK 21

RESULT 6

A60045 Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)

C;Species: Canis lupus familiaris (dog)

C;Accession: A60045

R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d

A;Reference number: A60045; MUID:92017079

A;Accession: A60045

A;Molecule type: mRNA

A;Residues: 1-57 <JOH>

A;Cross-references: EMBL:X56125

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas 1

C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 92; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 2.1e-08;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDGSEYVHQK 16

Db 6 DAEFRHDGSEYVHQK 21

RESULT 7

B60045 Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)

C;Species: Ursus maritimus (polar bear)

C;Accession: B60045

R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d

A;Reference number: A60045; MUID:92017079

A;Accession: B60045

A;Molecule type: mRNA

A;Residues: 1-57 <JOH>

A;Cross-references: EMBL:X56128; NID:92165; PIDN:CAA39593.1; PID:92166

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas 1

C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 92; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 2.1e-08;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDGSEYVHQK 16

Db 6 DAEFRHDGSEYVHQK 21

RESULT 8

PQ0438 Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 30-Sep-1993 #sequence\_revision 19-Oct-1995 #text\_change 19-Oct-1995

C;Accession: PQ0438; C60045

R;Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, I.E.

Biochem. Biophys. Res. Commun. 188, 905-911, 1992

A;Title: Sequence and methylation of the beta/A4 region of the rabbit amyloid precurs

A;Reference number: PQ0438; MUID:93073180



A; Reference number: A44017; MUID:93035397  
A; Accession: A44017  
A; Molecule type: DNA  
A; Cross-references: GB:S45136; NID:9257379; PIDN:CAA30050.1; PID:g28721  
A; Residues: 687-692, 'G', 694-718 <KAM1>  
A; Experimental source: familial Alzheimer disease family SB  
A; Note: sequence extracted from NCBI backbone (NCBIP:113374)  
A; Accession: B44017  
A; Molecule type: DNA  
A; Residues: 687-718 <KAM2>  
A; Cross-references: GB:S45136; NID:9257379; PIDN:AAB23646.1; PID:9257380  
A; Experimental source: familial Alzheimer disease family LIT  
A; Note: sequence extracted from NCBI backbone (NCBIP:113376)  
A; Note: this sequence has a silent mutation  
R; Kang, J.; Lemire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;  
R; Kang, J.; Lemire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;  
R; Kang, J.; Lemire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;  
R; Kang, J.; Lemire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;  
A; Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface  
A; Reference number: A03134; MUID:87144572  
A; Accession: A03134  
A; Molecule type: mRNA  
A; Residues: 1-288, 'V', 305-770 <KAN>  
A; Cross-references: GB:100264; PIDN:928525; PIDN:CAA68374.1; PID:g28526  
A; Note: alternative splice form APP(695)  
R; Robakisi, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.  
Proc. Natl. Acad. Sci. U.S.A. 84: 4190-4194, 1987  
A; Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular a  
A; Reference number: A29030; MUID:87231971  
A; Accession: A29030  
A; Molecule type: mRNA  
A; Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>  
A; Cross-references: GB:116765; NID:9178539; PIDN:AAA51722.1; PID:g178540  
A; Note: the authors translated the codon GAG for residue 647 as ASP  
A; Accession: A47584  
A; Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid  
A; Reference number: A47584; MUID:87120328  
A; Molecule type: mRNA  
A; Residues: 4756, 'S', 758-770 <GOI>  
A; Cross-references: GB:MI5533; NID:9178706; PIDN:AAA55540.1; PID:g1778707  
A; Experimental source: brain  
R; Tanzi, R.E.; Gusell, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke  
Science 235: 880-884, 1987  
A; Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th  
A; Reference number: A47585; MUID:87120329  
A; Accession: A47585  
A; Molecule type: mRNA  
A; Residues: 674-703 <TAN1>  
A; Cross-references: GB:MI5532; NID:9177957; PIDN:AAA51564.1; PID:g177958  
R; Dykens, T.; Weidemann, A.; Miltztaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Mueller  
EMBO J. 7: 949-957, 1988  
A; Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 pre  
A; Reference number: S02638; MUID:88296437  
A; Accession: S02638  
A; Molecule type: mRNA  
A; Residues: 672-678 <DYR>  
R; Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve  
Nature 331: 528-530, 1988  
A; Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat  
A; Reference number: S00707; MUID:88122640  
A; Accession: S00707  
A; Molecule type: mRNA  
A; Residues: 286-344, 'I', 365-366 <TAN2>  
A; Cross-references: EMBL:X06982; NID:928817; PIDN:CAA30042.1; PID:g29612  
A; Experimental source: promyelocytic leukemia cell line HL60  
A; Note: alternative splice form APP(51)  
R; Ponte, P.; Gonzalez-Dewitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Da  
R; Ponte, P.; 55-527, 1988  
A; Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibit  
A; Reference number: S00925; MUID:88122639  
A; Accession: S00925  
A; Molecule type: mRNA  
A; Residues: 1-344, 'I', 365-770 <PO2>

RESULT 11  
Alzheimer's disease amyloid beta protein precursor - African clawed frog  
C; Species: Xenopus laevis (African clawed frog)  
C; Accession: JH0773  
R; Okado, H.; Okamoto, H.  
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992  
A; Title: A Xenopus homologue of the human beta-amyloid precursor protein: development  
A; Reference number: JH0773; MUID:93129227  
A; Accession: JH0773  
A; Molecule type: mRNA  
A; Residues: 1-747 <OKA>  
A; Cross References: GB:S52417; NID:9263150; PIDN:AAB24853.1; PID:g26151  
A; Experimental source: larva  
C; Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas  
C; Keywords: alternative splicing; amyloid  
F; 287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BF1>

Query Match 83.7%  
Best Local Similarity 75.0%  
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Query Match 83.7%  
Best Local Similarity 75.0%  
Pred. No. 9.4e-05;  
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Query 1 DAEFRHDSGYEVHK 16  
 Db 597 DSEYRHDAYEVHK 612

RESULT 12  
 S23094 beta-amyloid protein precursor - rat  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 03-May-1996  
 C;Accession: S23094  
 R;Kojima, S.; Omori, M.  
 PDB Lett. 304, 57-60, 1992  
 A;Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic proteinase  
 A;Reference number: S23094; MUID:92316198  
 A;Accession: S23094  
 A;Molecule type: protein  
 A;Residues: 1-33 <KOT>  
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase I  
 Query Match Score 73; DB 2; Length 33;  
 Best Local Similarity 81.2%; Prd. No. 1.e-05;  
 Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHK 16  
 Db 6 DAEFRHDSGYEVHK 21

RESULT 13  
 A27485 Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse  
 N;Alternate names: proteinase nexin II  
 C;Species: Mus musculus (house mouse)  
 C;Date: 31-Mar-1989 #sequence\_revision 31-Mar-1989 #text\_change 13-Aug-1999  
 C;Accession: A27485; S19777; T49485  
 R;Yanada, T.; Sakai, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.  
 Biochem. Biophys. Res. Commun. 149, 665-671, 1987  
 A;Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precursor  
 A;Reference number: A27485; MUID:88106489  
 A;Accession: A27485  
 A;Molecule type: mRNA  
 A;Residues: 1-65 <PAM>  
 A;Cross-references: GB:MI18373; NID:9191568; PID:AAA37139.1; PID:93090985  
 A;Experimental source: brain  
 A;de Strooper, B.; van Leuven, F.; van den Berghe, H.  
 Biochim. Biophys. Acta 1129, 141-143, 1991  
 A;Title: The amyloid beta protein precursor or proteinase nixin II from mouse is closer  
 A;Accession number: S19727; MUID:92096458  
 A;Accession: S19727  
 A;Molecule type: mRNA  
 A;Residues: 1-210, 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>  
 A;Cross-references: EMBL:X59379  
 R;Izumi, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.  
 Gene 112, 189-195, 1992  
 A;Title: Positive and negative regulatory elements for the expression of the Alzheimer's  
 A;Reference number: I49485; MUID:92209998  
 A;Accession: I49485  
 A;Status: translated from GB/ENBLL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-19 <RES>  
 A;Cross-references: GB:DI0603; NID:9220328; PID:BA01456.1; PID:9220329  
 C;Genetics:  
 A;Map Position: 16C3  
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase I  
 C;Keywords: alternative splicing; amyloid; transmembrane protein

Query Match Score 73; DB 2; Length 695;  
 Best Local Similarity 81.2%; Prd. No. 0.00039;  
 Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHK 16  
 Db 597 DAEFRHDSGYEVHK 612

RESULT 14  
 S00550 Alzheimer's disease amyloid beta protein precursor - rat  
 N;Alternate names: beta A4 amyloid protein  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 13-Aug-1999  
 C;Accession: S00550; A1245; A39820; S46251  
 R;Shivers, B.D.; Hilbich, C.; Multaup, G.; Multaup, M.; Salbaum, M.; Seeburg, P.H.  
 EMBO J. 7, 1365-1370, 1988  
 A;Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain  
 A;Reference number: S00550; MUID:88312583  
 A;Accession: S00550  
 A;Molecule type: RNA  
 A;Residues: 1-695 <SH1>  
 A;Cross-references: EMBL:X07648; NID:955616; PID:CAA30488.1; PID:g55617  
 R;Schubert, D.; Schroeder, R.; LaCorbiere, M.; Saitoh, T.; Cole, G.  
 Science 241, 223-226, 1988  
 A;Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core  
 A;Reference number: A41245; MUID:88264430  
 A;Accession: A41245  
 A;Molecule type: protein  
 A;Residues: 18-37 'X' 39-40, 'X' 42-44 <SCH>  
 A;Note: evidence for heparan sulfate attachment  
 R;Reiss, L.; Behar, D.; Masters, C.L.; Multaup, G.  
 FEBS Lett. 349, 109-116, 1994  
 A;Title: The beta A4 amyloid precursor protein binding to copper.  
 A;Reference number: S42251; MUID:94320627  
 A;Contents: annotation: copper binding sites  
 A;Note: rt peptides were isolated but not sequenced  
 R;Potempka, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.  
 J. Biol. Chem. 266, 864-869, 1991  
 A;Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain  
 A;Reference number: A39820; MUID:91217087  
 A;Accession: A39820  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 18-32 <POT>  
 A;Experimental source: brain  
 C;Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is  
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase I  
 C;Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein  
 F;625-648/Domain: transmembrane #status predicted <TM>

Query Match Score 73; DB 2; Length 695;  
 Best Local Similarity 81.2%; Prd. No. 0.00039;  
 Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHK 16  
 Db 597 DAEFRHDSGYEVHK 612

RESULT 15  
 S04723 genome polyprotein - potato virus Y (strain O) (fragment)  
 N;Contains: coat protein; replicase  
 C;Species: potato virus Y, PVY  
 C;Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 20-Sep-1999  
 C;Accession: S04723  
 R;Bravo-Almonacid, F.; Mentaberry, A.N.  
 Nucleic Acids Res. 17, 4401, 1989  
 A;Title: Nucleotide cDNA sequence coding for the PVY coat protein.  
 A;Reference number: S04723  
 A;Accession: S04723  
 A;Status: translation not shown  
 A;Molecule type: genomic RNA

A; Residues: 1-284 <BRA>  
A; Cross-references: ENBL:X14136; NID:961445; PID:CAA32356.1; PID:g61446  
C; Superfamily: tobacco etch virus genome polyprotein; DEAD/H box helicase homology  
C; Keywords: Polyprotein

Query Match 54.9%; Score 50.5%; DB 2; Length 284;  
Best Local Similarity 73.3%; Pred. No. 0.68;  
Matches 11; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
Qy 1 DAEFRHDSGYEVHQ 15  
| | | | |||||  
Db 4 DDEFEFDs-YEVHQ 17

Search completed: September 13, 2000, 02:22:34  
Job time: 132 sec

| SUMMARIES  |       |             |        |               |                                 |  |  |
|------------|-------|-------------|--------|---------------|---------------------------------|--|--|
| Result No. | Score | Query Match | Length | DB ID         | Description                     |  |  |
| 1          | 92    | 100.0       | 57     | 1 A4_PIG      | Q29023 sus scrofa               |  |  |
| 2          | 92    | 100.0       | 57     | 1 A4_PIG      | Q29149 urus marit               |  |  |
| 3          | 92    | 100.0       | 58     | 1 A4_CANFA    | Q28280 canis familiaris         |  |  |
| 4          | 92    | 100.0       | 58     | 1 A4_RABBT    | Q28748 oryctolagus cuniculus    |  |  |
| 5          | 92    | 100.0       | 58     | 1 A4_SHEEP    | Q28757 ovis aries               |  |  |
| 6          | 92    | 100.0       | 59     | 1 A4_BOVIN    | Q28533 bos taurus               |  |  |
| 7          | 92    | 100.0       | 751    | 1 A4_SAISC    | Q95241 saimiri sciureus         |  |  |
| 8          | 92    | 100.0       | 770    | 1 A4_HUMAN    | P05067 homo sapiens             |  |  |
| 9          | 73    | 79.3        | 770    | 1 A4_MOUSE    | P12033 mus musculus             |  |  |
| 10         | 73    | 79.3        | 770    | 1 A4_RAT      | P08592 rattus norvegicus        |  |  |
| 11         | 50.5  | 54.9        | 284    | 1 P01G_PYYO   | P11897 potato virus             |  |  |
| 12         | 50.5  | 54.9        | 327    | 1 P01G_PYYCH  | P051246 potato virus            |  |  |
| 13         | 49.5  | 53.8        | 971    | 1 Y228_BORBU  | P07933 pepper mott              |  |  |
| 14         | 48.5  | 52.7        | 330    | 1 COAT_PENY   | P018247 p genome po             |  |  |
| 15         | 48.5  | 52.7        | 3063   | 1 P0LG_PYYN   | P76454 escherichia coli         |  |  |
| 16         | 44    | 47.8        | 274    | 1 YOHM_ECOLI  | Q12333 haemophilus              |  |  |
| 17         | 43    | 46.7        | 629    | 1 FRE7_YEAST  | P44428 cyprinus carpio          |  |  |
| 18         | 41    | 44.6        | 848    | 1 FPR_HAECIN  | P32054 escherichia coli         |  |  |
| 19         | 41    | 44.6        | 112    | 1 HXB1_CYPRA  | P32054 saccharomyces cerevisiae |  |  |
| 20         | 42    | 45.7        | 315    | 1 GM4D_ECOLI  | P04920 homo sapiens             |  |  |
| 21         | 42    | 45.7        | 373    | 1 CATR_ASPPNG | P03673 mycobacterium smegmatis  |  |  |
| 22         | 42    | 45.7        | 667    | 1 EM70_YEAST  | P03673 yersinia enterocolitica  |  |  |
| 23         | 41    | 44.6        | 494    | 1 COBQ_MYCTU  | P06730 yersinia enterocolitica  |  |  |
| 24         | 41    | 44.6        | 848    | 1 233A_HUMAN  | P09849 yersinia enterocolitica  |  |  |
| 25         | 41    | 44.6        | 1926   | 1 LPH_RABBIT  | P15297 yersinia enterocolitica  |  |  |
| 26         | 40    | 43.5        | 403    | 1 NOF2_DROME  | P15297 yersinia enterocolitica  |  |  |
| 27         | 40    | 43.5        | 418    | 1 MTM1_MORSP  | P15297 yersinia enterocolitica  |  |  |
| 28         | 40    | 43.5        | 730    | 1 NOF_DROME   | P15297 yersinia enterocolitica  |  |  |
| 29         | 40    | 43.5        | 984    | 1 NOF_DROME   | P15297 yersinia enterocolitica  |  |  |
| 30         | 39.5  | 42.9        | 3061   | 1 P0LG_PYYHU  | P55727 yersinia enterocolitica  |  |  |
| 31         | 39    | 42.4        | 182    | 1 Y4YS_RHISN  | P55727 yersinia enterocolitica  |  |  |
| 32         | 39    | 42.4        | 372    | 1 GM4D_YEREN  | P55872 yersinia enterocolitica  |  |  |
| 33         | 38    | 41.3        | 489    | 1 RS4_YEAST   | P39970 yersinia enterocolitica  |  |  |

| ALIGNMENTS            |   |                                   |               |                           |            |        |  |
|-----------------------|---|-----------------------------------|---------------|---------------------------|------------|--------|--|
| RESULT                | 1   | A4_PIG                            | A4_PIG        | STANDARD;                 | PRT;       | 57 AA. |  |
| ID                    | Q29023;   |                                   |               |                           |            |        |  |
| AC                    |   |                                   |               |                           |            |        |  |
| DT                    | 01-NOV-1997   | (Rel. 35, Created)                |               |                           |            |        |  |
| DT                    | 01-NOV-1997   | (Rel. 35, Last sequence update)   |               |                           |            |        |  |
| DT                    | 15-JUL-1999   | (Rel. 38, Last annotation update) |               |                           |            |        |  |
| DE                    | ALZHEIMER'S DISEASE AMYLOID PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID PROTEIN (BETA-APP) (FRAGMENT)].   |                                   |               |                           |            |        |  |
| GN                    | APP.  |                                   |               |                           |            |        |  |
| OS                    | Sus scrofa (Pig).   |                                   |               |                           |            |        |  |
| OC                    | Bukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.   |                                   |               |                           |            |        |  |
| RN                    | [1]   |                                   |               |                           |            |        |  |
| RP                    | SEQUENCE FROM N.A.  |                                   |               |                           |            |        |  |
| RC                    | TISSUE=BRAIN;   |                                   |               |                           |            |        |  |
| RA                    | Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;  |                                   |               |                           |            |        |  |
| RT                    | "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis."  |                                   |               |                           |            |        |  |
| RL                    | Brain Res. Mol. Brain Res. 10:299-305(1991).  |                                   |               |                           |            |        |  |
| CC                    | -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALLING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O) (BY SIMILARITY).  |                                   |               |                           |            |        |  |
| CC                    | -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  |                                   |               |                           |            |        |  |
| CC                    | -1- SIMILARITY: BELONGS TO THE APP FAMILY.  |                                   |               |                           |            |        |  |
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| CC                    | CC  |                                   |               |                           |            |        |  |
| CC                    | CC  |                                   |               |                           |            |        |  |
| CC                    | CC  |                                   |               |                           |            |        |  |
| DR                    | X56127; CAA39592; 1-.   |                                   |               |                           |            |        |  |
| DR                    | HSSP; P05067; 1AML.   |                                   |               |                           |            |        |  |
| DR                    | PROSITE; PS03120; A4_EXTRA; PARTIAL.  |                                   |               |                           |            |        |  |
| DR                    | PROSITE; PS03119; A4_INTRAA; PARTIAL.   |                                   |               |                           |            |        |  |
| FT                    | NON_TER   | 1                                 | 1             |                           |            |        |  |
| FT                    | CHAIN   | 6                                 | 48            |                           |            |        |  |
| FT                    | DONAIN  | <1                                | 33            |                           |            |        |  |
| FT                    | TRANSMEM  | 34                                | 57            |                           |            |        |  |
| FT                    | NON_TER   | 57                                | 57            |                           |            |        |  |
| SQ                    | SEQUENCE  | 57 AA:                            | 6172 MW;      | 84209388EBAS82DDFA CRC64; |            |        |  |
| Query                 | Match   | 100.0%                            | Score 92;     | DB 1;                     | Length 57; |        |  |
| Best Local Similarity | 100.0%  | Pred. No. 1.8e-08;                |               |                           |            |        |  |
| Matches               | 16;   | Conservative 0;                   | Mismatches 0; | Indels 0;                 | Gaps 0;    |        |  |
| QY                    | 1   | DAEFRHDGYEVHHQK 16                |               |                           |            |        |  |
| Db                    | 6   | DAEFRHDGYEVHHQK 21                |               |                           |            |        |  |

**RESULT 2**

A4\_URSMA STANDARD; PRT; 57 AA.

AC Q29449; 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID PROTEIN (BETA-APP) (FRAGMENT).]

GN APP.

OS Ursus maritimus (Polar bear) (Thalarctos maritimus).

OC Ursidae; Carnivora; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Thalactos.

RN [1] SEQUENCE FROM N.A.

RP TISSUE=KIDNEY;

RC MEDLINE: 92017079.

RX Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.; "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis."

RT Brain Res. Mol. Brain Res. 10:299-305(1991).

RT -I- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN APP.

CC G(O) (BY SIMILARITY).

CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -I- SIMILARITY: BELONGS TO THE APP FAMILY.

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CC -I- EMBL: X56125; CAA39590; 1.

CC -I- DR HSSP: PS00319; A4\_EXTRA; PARTIAL.

CC -I- DR PROSITE: PS00320; A4\_INTRAA; PARTIAL.

CC -I- DR GLYCOPROTEIN; Amyloid<sup>-</sup>; Neurone; Transmembrane.

CC -I- KW NON-TER 1 1 BETA-AMYLOID PROTEIN (POTENTIAL).

CC -I- FT CHAIN 7 49 EXTRACELLULAR (POTENTIAL).

CC -I- FT DOMAIN <1 34 POTENTIAL.

CC -I- FT TRANSMEM 35 58

CC -I- FT NON-TER 58 58

CC -I- SQ SEQUENCE 58 AA; 6285 MW; 8469D48BA2E12DFA CRC64;

Query Match Score 92; DB 1; Length 58;

Best Local Similarity 100.0%; Pred. No. 1.8e-08;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DR HSSP: P05667; 1AML.

DR PROSITE: PS00319; A4\_EXTRA; PARTIAL.

DR GLYCOPROTEIN; Amyloid<sup>-</sup>; Neurone; Transmembrane.

KW NON-TER 1 1 BETA-AMYLOID PROTEIN (POTENTIAL).

FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).

FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 34 57 POTENTIAL.

FT NON-TER 57 57

SQ SEQUENCE 57 AA; 6172 MW; 84209D88EBA82DFA CRC64;

RESULT 4

A4\_RABBIT STANDARD; PRT; 58 AA.

AC Q28748; 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID PROTEIN (BETA-APP) (FRAGMENT).]

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

RN [1] SEQUENCE FROM N.A.

RP TISSUE=BRAIN;

RC MEDLINE: 92017079.

RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.; "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis."

RT Brain Res. Mol. Brain Res. 10:299-305(1991).

RT -I- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN APP.

CC G(O) (BY SIMILARITY).

CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -I- SIMILARITY: BELONGS TO THE APP FAMILY.

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|    |  |                                      |                       |                      |                             |        |                          |                                   |
|----|--|--------------------------------------|-----------------------|----------------------|-----------------------------|--------|--------------------------|-----------------------------------|
| CC | DR   | HSSP; P05067; 1AML.                  | FT                    | NON_TER              | 1                           | 1      | 48                       | BETA-AMYLOID PROTEIN (POTENTIAL). |
| CC | DR   | PROSITE; PS00319; A4_EXTRA; PARTIAL. | FT                    | CHAIN                | 6                           | 6      | 33                       | EXTRACELLULAR (POTENTIAL).        |
| CC | DR   | PROSITE; PS00320; A4_INTR; PARTIAL.  | FT                    | DOMAIN               | <1                          | 34     | 57                       | POTENTIAL.                        |
| KW | Glycoprotein; Amyloid; Neurone; Transmembrane. | FT                                   | TRANSEM               | 34                   | 58                          | >58    | CYTOPLASMIC (POTENTIAL). |                                   |
| FT | NON_TER  | 1                                    | FT                    | DOMAIN               | 58                          | 58     | 58                       |                                   |
| FT | CHAIN  | 6                                    | FT                    | NON_TER              | 58                          | 6300   | MW;                      | F434209D88EBAB2D CRC64;           |
| FT | DOMAIN   | <1                                   | SQ                    | SEQUENCE             | 58 AA;                      |        |                          |                                   |
| FT | TRANSEM  | 34                                   |                       |                      |                             |        |                          |                                   |
| FT | DOMAIN   | 58                                   |                       |                      |                             |        |                          |                                   |
| FT | NON_TER  | 58                                   |                       |                      |                             |        |                          |                                   |
| SQ | SEQUENCE                                       | 58 AA;                               |                       |                      |                             |        |                          |                                   |
| DR | X56129; CAA39594.1; -.                         |                                      |                       |                      |                             |        |                          |                                   |
| DR | HSSP; P05067; 1AML.                            | Query Match                          | Score 92;             | DB 1;                | Length 58;                  |        |                          |                                   |
| DR | PROSITE; PS00319; A4_EXTRA; PARTIAL.           | Best Local Similarity                | 100.0%                | Pred. No. 1.8e-08;   |                             |        |                          |                                   |
| DR | PROSITE; PS00320; A4_INTR; PARTIAL.            | Matches                              | 16;                   | Mismatches           | 0;                          | Indels | 0;                       | Gaps 0;                           |
| KW | Glycoprotein; Amyloid; Neurone; Transmembrane. | QY                                   | 1                     | DAEFRHDSGEVHHQK 16   |                             |        |                          |                                   |
| FT | NON_TER  | 1                                    | Db                    | 6 DAEFRHDSGEVHHQK 21 |                             |        |                          |                                   |
| FT | CHAIN  | 6                                    |                       |                      |                             |        |                          |                                   |
| FT | DOMAIN   | <1                                   |                       |                      |                             |        |                          |                                   |
| FT | TRANSEM  | 34                                   |                       |                      |                             |        |                          |                                   |
| FT | DOMAIN   | 58                                   |                       |                      |                             |        |                          |                                   |
| FT | NON_TER  | 58                                   |                       |                      |                             |        |                          |                                   |
| SQ | SEQUENCE                                       | 58 AA;                               |                       |                      |                             |        |                          |                                   |
| DR | X56129; CAA39594.1; -.                         | RESULT                               | 6                     |                      |                             |        |                          |                                   |
| DR | HSSP; P05067; 1AML.                            | ID                                   | A4_BOVIN              | STANDARD;            |                             |        |                          |                                   |
| DR | PROSITE; PS00319; A4_EXTRA; PARTIAL.           | ID                                   | A4_BOVIN              | PRT;                 | 59 AA.                      |        |                          |                                   |
| DR | PROSITE; PS00320; A4_INTR; PARTIAL.            | AC                                   | Q28053;               |                      |                             |        |                          |                                   |
| DR | Glycoprotein; Amyloid; Neurone; Transmembrane. | AC                                   | Q28053;               | Created)             |                             |        |                          |                                   |
| FT | NON_TER  | 1                                    | AC                    | Q28053;              | (Rel. 35.                   |        |                          |                                   |
| FT | CHAIN  | 6                                    | AC                    | Q28053;              | 35. Last sequence update)   |        |                          |                                   |
| FT | DOMAIN   | <1                                   | AC                    | Q28053;              | 35. Last annotation update) |        |                          |                                   |
| FT | TRANSEM  | 34                                   | AC                    | Q28053;              | 38. Last annotation update) |        |                          |                                   |
| FT | DOMAIN   | 58                                   | AC                    | Q28053;              | 38. Last annotation update) |        |                          |                                   |
| FT | NON_TER  | 58                                   | AC                    | Q28053;              | 38. Last annotation update) |        |                          |                                   |
| SQ | SEQUENCE                                       | 58 AA;                               | AC                    | Q28053;              | 38. Last annotation update) |        |                          |                                   |
| DR | X56129; CAA39594.1; -.                         | QY                                   | 1                     | DAEFRHDSCSYEVHQK 16  |                             |        |                          |                                   |
| DR | HSSP; P05067; 1AML.                            | Db                                   | 6 DAEFRHDSCSYEVHQK 21 |                      |                             |        |                          |                                   |
| DR | PROSITE; PS00319; A4_EXTRA; PARTIAL.           |                                      |                       |                      |                             |        |                          |                                   |
| DR | PROSITE; PS00320; A4_INTR; PARTIAL.            |                                      |                       |                      |                             |        |                          |                                   |
| KW | Glycoprotein; Amyloid; Neurone; Transmembrane. |                                      |                       |                      |                             |        |                          |                                   |
| FT | NON_TER  | 1                                    |                       |                      |                             |        |                          |                                   |
| FT | CHAIN  | 6                                    |                       |                      |                             |        |                          |                                   |
| FT | DOMAIN   | <1                                   |                       |                      |                             |        |                          |                                   |
| FT | TRANSEM  | 34                                   |                       |                      |                             |        |                          |                                   |
| FT | DOMAIN   | 58                                   |                       |                      |                             |        |                          |                                   |
| FT | NON_TER  | 58                                   |                       |                      |                             |        |                          |                                   |
| SQ | SEQUENCE                                       | 58 AA;                               |                       |                      |                             |        |                          |                                   |
| DR | X56129; CAA39594.1; -.                         | RESULT                               | 5                     |                      |                             |        |                          |                                   |
| DR | HSSP; P05067; 1AML.                            | ID                                   | A4_SHEEP              | STANDARD;            |                             |        |                          |                                   |
| DR | PROSITE; PS00319; A4_EXTRA; PARTIAL.           | ID                                   | A4_SHEEP              | PRT;                 | 58 AA.                      |        |                          |                                   |
| DR | PROSITE; PS00320; A4_INTR; PARTIAL.            | AC                                   | Q28757;               |                      |                             |        |                          |                                   |
| DR | Glycoprotein; Amyloid; Neurone; Transmembrane. | AC                                   | Q28757;               | Created)             |                             |        |                          |                                   |
| FT | NON_TER  | 1                                    | AC                    | Q28757;              | (Rel. 35.                   |        |                          |                                   |
| FT | CHAIN  | 6                                    | AC                    | Q28757;              | 35. Last sequence update)   |        |                          |                                   |
| FT | DOMAIN   | <1                                   | AC                    | Q28757;              | 35. Last sequence update)   |        |                          |                                   |
| FT | TRANSEM  | 34                                   | AC                    | Q28757;              | 35. Last sequence update)   |        |                          |                                   |
| FT | DOMAIN   | 58                                   | AC                    | Q28757;              | 35. Last sequence update)   |        |                          |                                   |
| FT | NON_TER  | 58                                   | AC                    | Q28757;              | 35. Last sequence update)   |        |                          |                                   |
| SQ | SEQUENCE                                       | 58 AA;                               | AC                    | Q28757;              | 35. Last sequence update)   |        |                          |                                   |
| DR | X56129; CAA39594.1; -.                         | QY                                   | 1                     | DAEPRHDSCSYEVHQK 16  |                             |        |                          |                                   |
| DR | HSSP; P05067; 1AML.                            | Db                                   | 6 DAEPRHDSCSYEVHQK 21 |                      |                             |        |                          |                                   |
| DR | PROSITE; PS00319; A4_EXTRA; PARTIAL.           |                                      |                       |                      |                             |        |                          |                                   |
| DR | PROSITE; PS00320; A4_INTR; PARTIAL.            |                                      |                       |                      |                             |        |                          |                                   |
| KW | Glycoprotein; Amyloid; Neurone; Transmembrane. |                                      |                       |                      |                             |        |                          |                                   |
| FT | NON_TER  | 1                                    |                       |                      |                             |        |                          |                                   |
| FT | CHAIN  | 6                                    |                       |                      |                             |        |                          |                                   |
| FT | DOMAIN   | <1                                   |                       |                      |                             |        |                          |                                   |
| FT | TRANSEM  | 34                                   |                       |                      |                             |        |                          |                                   |
| FT | DOMAIN   | 58                                   |                       |                      |                             |        |                          |                                   |
| FT | NON_TER  | 58                                   |                       |                      |                             |        |                          |                                   |
| SQ | SEQUENCE                                       | 58 AA;                               |                       |                      |                             |        |                          |                                   |
| DR | X56129; CAA39594.1; -.                         | RESULT                               | 4                     |                      |                             |        |                          |                                   |
| DR | HSSP; P05067; 1AML.                            | ID                                   | A4_OVIS               | STANDARD;            |                             |        |                          |                                   |
| DR | PROSITE; PS00319; A4_EXTRA; PARTIAL.           | ID                                   | A4_OVIS               | PRT;                 | 58 AA.                      |        |                          |                                   |
| DR | PROSITE; PS00320; A4_INTR; PARTIAL.            | AC                                   | Q28757;               |                      |                             |        |                          |                                   |
| DR | Glycoprotein; Amyloid; Neurone; Transmembrane. | AC                                   | Q28757;               | Created)             |                             |        |                          |                                   |
| FT | NON_TER  | 1                                    | AC                    | Q28757;              | (Rel. 35.                   |        |                          |                                   |
| FT | CHAIN  | 6                                    | AC                    | Q28757;              | 35. Last sequence update)   |        |                          |                                   |
| FT | DOMAIN   | <1                                   | AC                    | Q28757;              | 35. Last sequence update)   |        |                          |                                   |
| FT | TRANSEM  | 34                                   | AC                    | Q28757;              | 35. Last sequence update)   |        |                          |                                   |
| FT | DOMAIN   | 58                                   | AC                    | Q28757;              | 35. Last sequence update)   |        |                          |                                   |
| FT | NON_TER  | 58                                   | AC                    | Q28757;              | 35. Last sequence update)   |        |                          |                                   |
| SQ | SEQUENCE                                       | 58 AA;                               | AC                    | Q28757;              | 35. Last sequence update)   |        |                          |                                   |
| DR | X56129; CAA39594.1; -.                         | QY                                   | 1                     | DAEPRHDSCSYEVHQK 16  |                             |        |                          |                                   |
| DR | HSSP; P05067; 1AML.                            | Db                                   | 6 DAEPRHDSCSYEVHQK 21 |                      |                             |        |                          |                                   |
| DR | PROSITE; PS00319; A4_EXTRA; PARTIAL.           |                                      |                       |                      |                             |        |                          |                                   |
| DR | PROSITE; PS00320; A4_INTR; PARTIAL.            |                                      |                       |                      |                             |        |                          |                                   |
| KW | Glycoprotein; Amyloid; Neurone; Transmembrane. |                                      |                       |                      |                             |        |                          |                                   |
| FT | NON_TER  | 1                                    |                       |                      |                             |        |                          |                                   |
| FT | CHAIN  | 6                                    |                       |                      |                             |        |                          |                                   |
| FT | DOMAIN   | <1                                   |                       |                      |                             |        |                          |                                   |
| FT | TRANSEM  | 34                                   |                       |                      |                             |        |                          |                                   |
| FT | DOMAIN   | 58                                   |                       |                      |                             |        |                          |                                   |
| FT | NON_TER  | 58                                   |                       |                      |                             |        |                          |                                   |
| SQ | SEQUENCE                                       | 58 AA;                               |                       |                      |                             |        |                          |                                   |
| DR | X56129; CAA39594.1; -.                         | RESULT                               | 3                     |                      |                             |        |                          |                                   |
| DR | HSSP; P05067; 1AML.                            | ID                                   | A4_BOVINE             | STANDARD;            |                             |        |                          |                                   |
| DR | PROSITE; PS00319; A4_EXTRA; PARTIAL.           | ID                                   | A4_BOVINE             | PRT;                 | 59 AA.                      |        |                          |                                   |
| DR | PROSITE; PS00320; A4_INTR; PARTIAL.            | AC                                   | Q28053;               |                      |                             |        |                          |                                   |
| DR | Glycoprotein; Amyloid; Neurone; Transmembrane. | AC                                   | Q28053;               | Created)             |                             |        |                          |                                   |
| FT | NON_TER  | 1                                    | AC                    | Q28053;              | (Rel. 35.                   |        |                          |                                   |
| FT | CHAIN  | 6                                    | AC                    | Q28053;              | 35. Last sequence update)   |        |                          |                                   |
| FT | DOMAIN   | <1                                   | AC                    | Q28053;              | 35. Last sequence update)   |        |                          |                                   |
| FT | TRANSEM  | 34                                   | AC                    | Q28053;              | 35. Last sequence update)   |        |                          |                                   |
| FT | DOMAIN   | 58                                   | AC                    | Q28053;              | 35. Last sequence update)   |        |                          |                                   |
| FT | NON_TER  | 58                                   | AC                    | Q28053;              | 35. Last sequence update)   |        |                          |                                   |
| SQ | SEQUENCE                                       | 58 AA;                               | AC                    | Q28053;              | 35. Last sequence update)   |        |                          |                                   |
| DR | X56129; CAA39594.1; -.                         | QY                                   | 1                     | DAEPRHDSCSYEVHQK 16  |                             |        |                          |                                   |
| DR | HSSP; P05067; 1AML.                            | Db                                   | 6 DAEPRHDSCSYEVHQK 21 |                      |                             |        |                          |                                   |
| DR | PROSITE; PS00319; A4_EXTRA; PARTIAL.           |                                      |                       |                      |                             |        |                          |                                   |
| DR | PROSITE; PS00320; A4_INTR; PARTIAL.            |                                      |                       |                      |                             |        |                          |                                   |
| KW | Glycoprotein; Amyloid; Neurone; Transmembrane. |                                      |                       |                      |                             |        |                          |                                   |
| FT | NON_TER  | 1                                    |                       |                      |                             |        |                          |                                   |
| FT | CHAIN  | 6                                    |                       |                      |                             |        |                          |                                   |
| FT | DOMAIN   | <1                                   |                       |                      |                             |        |                          |                                   |
| FT | TRANSEM  | 34                                   |                       |                      |                             |        |                          |                                   |
| FT | DOMAIN   | 58                                   |                       |                      |                             |        |                          |                                   |
| FT | NON_TER  | 58                                   |                       |                      |                             |        |                          |                                   |
| SQ | SEQUENCE                                       | 58 AA;                               |                       |                      |                             |        |                          |                                   |
| DR | X56129; CAA39594.1; -.                         | RESULT                               | 2                     |                      |                             |        |                          |                                   |
| DR | HSSP; P05067; 1AML.                            | ID                                   | A4_CAA39595           | STANDARD;            |                             |        |                          |                                   |
| DR | PROSITE; PS00319; A4_EXTRA; PARTIAL.           | ID                                   | A4_CAA39595           | PRT;                 | 59 AA.                      |        |                          |                                   |
| DR | PROSITE; PS00320; A4_INTR; PARTIAL.            | AC                                   | Q28053;               |                      |                             |        |                          |                                   |
| DR | Glycoprotein; Amyloid; Neurone; Transmembrane. | AC                                   | Q28053;               | Created)             |                             |        |                          |                                   |
| FT | NON_TER  | 1                                    | AC                    | Q28053;              | (Rel. 35.                   |        |                          |                                   |
| FT | CHAIN  | 6                                    | AC                    | Q28053;              | 35. Last sequence update)   |        |                          |                                   |
| FT | DOMAIN   | <1                                   | AC                    | Q28053;              | 35. Last sequence update)   |        |                          |                                   |
| FT | TRANSEM  | 34                                   | AC                    | Q28053;              | 35. Last sequence update)   |        |                          |                                   |
| FT | DOMAIN   | 58                                   | AC                    | Q28053;              | 35. Last sequence update)   |        |                          |                                   |
| FT | NON_TER  | 58                                   | AC                    | Q28053;              | 35. Last sequence update)   |        |                          |                                   |
| SQ | SEQUENCE                                       | 59 AA;                               | AC                    | Q28053;              | 35. Last sequence update)   |        |                          |                                   |
| DR | X56129; CAA39594.1; -.                         | QY                                   | 1                     | DAEPRHDSCSYEVHQK 16  |                             |        |                          |                                   |
| DR | HSSP; P05067; 1AML.                            | Db                                   | 6 DAEPRHDSCSYEVHQK 21 |                      |                             |        |                          |                                   |
| DR | PROSITE; PS00319; A4_EXTRA; PARTIAL.           |                                      |                       |                      |                             |        |                          |                                   |
| DR | PROSITE; PS00320; A4_INTR; PARTIAL.            |                                      |                       |                      |                             |        |                          |                                   |
| KW | Glycoprotein; Amyloid; Neurone; Transmembrane. |                                      |                       |                      |                             |        |                          |                                   |
| FT | NON_TER  | 1                                    |                       |                      |                             |        |                          |                                   |
| FT | CHAIN  | 6                                    |                       |                      |                             |        |                          |                                   |
| FT | DOMAIN   | <1                                   |                       |                      |                             |        |                          |                                   |
| FT | TRANSEM  | 34                                   |                       |                      |                             |        |                          |                                   |
| FT | DOMAIN   | 58                                   |                       |                      |                             |        |                          |                                   |
| FT | NON_TER  | 59                                   |                       |                      |                             |        |                          |                                   |
| SQ | SEQUENCE                                       | 59 AA;                               |                       |                      |                             |        |                          |                                   |
| DR | X56129; CAA39594.1; -.                         | RESULT                               | 1                     |                      |                             |        |                          |                                   |
| DR | HSSP; P05067; 1AML.                            | ID                                   | A434209D88EBAB2D      | STANDARD;            |                             |        |                          |                                   |
| DR | PROSITE; PS00319; A4_EXTRA; PARTIAL.           | ID                                   | A434209D88EBAB2D      | PRT;                 | 59 AA.                      |        |                          |                                   |
| DR | PROSITE; PS00320; A4_INTR; PARTIAL.            | AC                                   | Q28053;               |                      |                             |        |                          |                                   |
| DR | Glycoprotein; Amyloid; Neurone; Transmembrane. | AC                                   | Q28053;               | Created)             |                             |        |                          |                                   |
| FT | NON_TER  | 1                                    | AC                    | Q28053;              | (Rel. 35.                   |        |                          |                                   |
| FT | CHAIN  | 6                                    | AC                    | Q28053;              | 35. Last sequence update)   |        |                          |                                   |
| FT | DOMAIN   | <1                                   | AC                    | Q28053;              | 35. Last sequence update)   |        |                          |                                   |
| FT | TRANSEM  | 34                                   | AC                    | Q28053;              | 35. Last sequence update)   |        |                          |                                   |
| FT | DOMAIN   | 58                                   | AC                    | Q28053;              | 35. Last sequence update)   |        |                          |                                   |
| FT | NON_TER  | 59                                   | AC                    | Q28053;              | 35. Last sequence update)   |        |                          |                                   |
| SQ | SEQUENCE                                       | 59 AA;                               | AC                    | Q28053;              | 35. Last sequence update)   |        |                          |                                   |
| DR | X56129; CAA39594.1; -.                         | QY                                   | 1                     | DAEPRHDSCSYEVHQK 16  |                             |        |                          |                                   |
| DR | HSSP; P05067; 1AML.                            | Db                                   | 6 DAEPRHDSCSYEVHQK 21 |                      |                             |        |                          |                                   |
| DR | PROSITE; PS00319; A4_EXTRA; PARTIAL.           |                                      |                       |                      |                             |        |                          |                                   |
| DR | PROSITE; PS00320; A4_INTR; PARTIAL.            |                                      |                       |                      |                             |        |                          |                                   |
| KW | Glycoprotein; Amyloid; Neurone; Transmembrane. |                                      |                       |                      |                             |        |                          |                                   |
| FT | NON_TER  | 1                                    |                       |                      |                             |        |                          |                                   |
| FT | CHAIN  | 6                                    |                       |                      |                             |        |                          |                                   |
| FT | DOMAIN   | <1                                   |                       |                      |                             |        |                          |                                   |
| FT | TRANSEM  | 34                                   |                       |                      |                             |        |                          |                                   |
| FT | DOMAIN   | 58                                   |                       |                      |                             |        |                          |                                   |
| FT | NON_TER  | 59                                   |                       |                      |                             |        |                          |                                   |
| SQ | SEQUENCE                                       | 59 AA;                               |                       |                      |                             |        |                          |                                   |
| DR | X56129; CAA39594.1; -.                         | RESULT                               | 0                     |                      |                             |        |                          |                                   |
| DR | HSSP; P05067; 1AML.                            | ID                                   | A434209D88EBAB2D      | STANDARD;            |                             |        |                          |                                   |
| DR | PROSITE; PS00319; A4_EXTRA; PARTIAL.           | ID                                   | A434209D88EBAB2D      | PRT;                 | 59 AA.                      |        |                          |                                   |
| DR | PROSITE; PS00320; A4_INTR; PARTIAL.            | AC                                   | Q28053;               |                      |                             |        |                          |                                   |
| DR | Glycoprotein; Amyloid; Neurone; Transmembrane. | AC                                   | Q28053;               | Created)             |                             |        |                          |                                   |
| FT | NON_TER  | 1                                    | AC                    | Q28053;              | (Rel. 35.                   |        |                          |                                   |
| FT | CHAIN  | 6                                    | AC                    | Q28053;              | 35. Last sequence update)   |        |                          |                                   |
| FT | DOMAIN   | <1                                   | AC                    | Q28053;              | 35. Last sequence update)   |        |                          |                                   |
| FT | TRANSEM  | 34                                   | AC                    | Q28053;              | 35. Last sequence update)   |        |                          |                                   |
| FT | DOMAIN   | 58                                   | AC                    | Q28053;              | 35. Last sequence update)   |        |                          |                                   |
| FT | NON_TER  | 59                                   | AC                    | Q28053;              | 35. Last sequence update)   |        |                          |                                   |





P12023; AC X59379; CC NOT\_ANNOTATED\_CDS.

DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 15-FEB-2000 (Rel. 39, Last annotation update)

DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG PRECURSOR  
 DE (AMYLOIDGENIC GLYCOPROTEIN) (AG).

GN APP.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

RN [1] SEQUENCE OF 1-289 AND 365-770 FROM N.A.

RP STRAIN=BALB/C; TISSUE=BRAIN; PRECURSOR

RC MEDLINE: 9209458.

RX de Strooper B., van Leuven F., van den Berghe H.; "The amyloid beta protein precursor or protease nexin II from mouse is closer related to its human homolog than previously reported.", Biochem. Biophys. Acta 1129:141-143 (1991).

RN [2] SEQUENCE OF 1-289 AND 365-770 FROM N.A.

RP TISSUE=BRAIN;

RC MEDLINE: 88106489.

RA Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sakaki Y.; "Complementary DNA for the mouse homolog of the human amyloid beta protein precursor"; Biochem. Biophys. Res. Commun. 149: 665-671(1987).

RN [3] REVISIONS.

RA Yamada T.; Submittetd (MAR-1988) to the EMBL/GenBank/DBJ databases.

RN [4] SEQUENCE OF 289-364 FROM N.A.

RP STRAIN=CD-1; TISSUE=PLACENTA;

RC MEDLINE: 8934511.

RA Fukuchi K., Martin G.M., Deeb S.S.; "Sequence of the protease inhibitor domain of the A4 amyloid protein precursor of *Mus domesticus*"; Nucleic Acids Res. 17:5396-5396 (1989).

RN [5] SEQUENCE OF 1-19 FROM N.A.

RP TISSUE=BRAIN, AND KIDNEY;

RC MEDLINE: 92209998.

RA Izumi R., Yamada T., Yoshihiko S.I., Sasaki H., Hattori M., Sakai Y.; "Structure and expression of the alternatively-spliced forms of mRNA for the mouse homolog of Alzheimer's disease amyloid beta protein precursor"; Biochem. Biophys. Res. Commun. 112:189-193 (1982).

RN [6] SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPlicing.

RP DOMAIN=BRAIN; APP(751) AND APP(770) (SHOWN HERE); WHICH ARE PRODUCED BY ALTERNATIVE SPlicing.

CC -I- TISSUE SPECIFICITY: AAA(770) IS EXPRESSED IN KIDNEY. AAA(751) IS WIDELY EXPRESSED. AAA(695) IS EXPRESSED IN BRAIN, KIDNEY AND LIVER.

CC -I- SIMILARITY: BELONGS TO THE APP FAMILY.

CC -I- SIMILARITY: APP(751) AND APP(770) CONTAIN A PROTEASE INHIBITOR DOMAIN BELONGING TO THE BPT1/KUNITZ FAMILY OF INHIBITORS.

CC -I- DOMAIN BELONGING TO THE BPT1/KUNITZ FAMILY OF INHIBITORS.

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CC DR EMBL; X59379; AC X59379; DR EMBL; M19373; AC X59379; DR EMBL; X15210; CAA3280; DR EMBL; D10603; BAA01456; DR EMBL; M24397; AAA19929; DR PIR; A27485; A27485; DR PIR; S04855; S04855; DR PIR; S19727; S19727; DR MGDB; MGDB; APP.

CC DR PFAM; PF00014; Kunitz\_BPT1; DR PRINTS; PR00303; AMYLOID4.

CC DR PRINTS; PR00204; BETAMYLOID.

CC DR PRINTS; PR00759; BASICPT1.

CC DR PROSITE; PS00280; BPT1\_KUNITZ; 1.

CC DR PROSITE; PS00319; A4\_EXTRA; 1.

CC DR PROSITE; PS00320; A4\_INTRA; 1.

CC KW Glycoprotein; Amyloid; Neuron; Transmembrane; Signal;

CC KW Alternative splicing; Serine protease inhibitor.

CC FT SIGNAL; 1 17 BY SIMILARITY.

CC FT CHAIN 18 770 ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG.

CC FT DOMAIN 18 699 EXTRACELLULAR (POTENTIAL).

CC FT TRANSEM 700 723 POTENTIAL.

CC FT DOMAIN 724 770 CYTOPASIC (POTENTIAL).

CC FT DOMAIN 673 715 EQUIVALENT OF BETA-AMYLOID PROTEIN.

CC FT DOMAIN 287 345 BPT1/KUNITZ INHIBITOR.

CC FT SITE 759 762 CLATHRIN BINDING (BY SIMILARITY).

CC FT DISUFID 291 341 BY SIMILARITY.

CC FT DISUFID 300 324 BY SIMILARITY.

CC FT DISUFID 316 337 BY SIMILARITY.

CC FT CARBOHYD 542 542 POTENTIAL.

CC FT CARBOHYD 571 571 POTENTIAL.

CC FT VARSPIC 289 289 E->V (IN ISOFORM APP(695)).

CC FT VARSPIC 290 364 MISSING (IN ISOFORM APP(695)).

CC FT VARSPIC 346 380 MISSING (IN ISOFORM APP(751)).

CC SQ SEQUENCE 770 AA; 86752 MW; 2650DE090CAF7A CRC64;

Query Match 79.3%; Score 73; DB 1; Length 770;  
 Best Local Similarity 81.2%; Pred. No. 0.0003;  
 Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DAEFRHDGSGEVHRK 16  
 Db 672 DAEFGHDGSGEVHRK 687

RESULT 10

A4\_RAT ID A4\_RAT STANDARD; PRT; 770 AA.

AC P08592; DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)

RT 15-FEB-2000 (Rel. 39, Last annotation update)

DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG PRECURSOR (AMYLOIDGENIC GLYCOPROTEIN) (AG).

DE (AG).

GN Rattus norvegicus (Rat).

OS Rattus norvegicus (Rat).

RC MEDLINE: 88112583.

RA Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K., Seubert P.H.; "Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain suggests a role in cell contact"; EMBO J. 7:1365-1370(1988).

RA Seeber P.H.; "Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain suggests a role in cell contact"; [2]

RN 2650DE090CAF7A CRC64;

RP SEQUENCE OF 289 AND 365-770 FROM N.A.

CC TISSUE-BRAIN;

CC MEDLINE: 88112583.

CC Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K., Seubert P.H.; "Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain suggests a role in cell contact"; [2]

CC TISSUE-LIVER;

RX MEDLINE; 89183625.  
 RA "The sequence of the two extra exons in rat preA4.";  
 RL Nucleic Acids Res 17:2130-2130(1989).  
 CC -!- ALTERNATIVE LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -!- ALTERNATIVE PRODUCTS: SIX FORMS OF APP ARE FOUND: APP(395),  
 CC APP(563), APP(695), APP(751) AND APP(770) (SHOWN HERE); WHICH ARE  
 CC PRODUCED BY ALTERNATIVE SPLICING.  
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.  
 CC -!- SIMILARITY: APP(751) AND APP(770) CONTAIN A PROTEASE INHIBITOR  
 CC DOMAIN BELONGING TO THE BPT1/KUNITZ FAMILY OF INHIBITORS.  
 CC  
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 DR EMBL; X07648; CAA30488.1; .  
 DR PIR; X14066; CA3A32229.1; .  
 DR PIR; S00550; S00550.  
 DR PIR; S03607; S03607.  
 DR PFAM; PF00014; Kunitz\_BPT1; 1.  
 DR PRINTS; PRO0203; AMYLOIDAA.  
 DR PRINTS; PRO0204; BETAAMYLOID.  
 DR PRINTS; PRO0759; BASICPTASE.  
 DR PROSITE; PS00280; BPT1\_KUNITZ; 1.  
 DR PROSITE; PS00319; A4\_EXTRA; 1.  
 DR PROSITE; PS00320; A4\_INTRA; 1.  
 KW Glycoprotein; Amyloid; Neuron; Transmembrane; Signal;  
 KW Alternative splicing; Serine protease inhibitor.  
 FT SIGNAL 1 17 BY SIMILARITY.  
 FT CHAIN 18 770 ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN  
 FT DOMAIN 18 699 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 700 723 HOMOLOG.  
 FT DOMAIN 724 770 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 673 715 EQUIVALENT OF BETA-AMYLOID PROTEIN.  
 FT DOMAIN 287 345 BPT1/KUNITZ INHIBITOR.  
 FT SITE 759 762 CLATHRIN-BINDING (BY SIMILARITY).  
 FT DISULFID 291 341 BY SIMILARITY.  
 FT DISULFID 300 324 BY SIMILARITY.  
 FT DISULFID 316 337 BY SIMILARITY.  
 FT CARBOYD 542 542 BY SIMILARITY.  
 FT CARBOYD 571 571 POTENTIAL.  
 FT VARSPLIC 289 289 E->V (IN ISOFORM APP(695)).  
 FT VARSPLIC 290 364 MISSING (IN ISOFORM APP(95)).  
 SQ SEQUENCE 770 AA; 86704 MW; C26CD6BB2D923A7 CRC64; .

Query Match Score 73; DB 1; Length 770;  
 Best Local Similarity 81.28; Pred No. 0.0003; 2; Indels 0; Gaps 0;  
 Matches 13; Conservative 1; Mismatches 1; Gaps 0;

RESULT 11  
 ID POLG\_PVYYO STANDARD; PRT; 284 AA.  
 AC P11897; .  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last annotation update)  
 DT 15-DEC-1998 (Rel. 31, Last annotation update)  
 DE GENOME POLYPROTEIN (CONTAINS: NUCLEAR INCLUSION PROTEIN B (NI-B) (NIB)  
 DE (FRAGMENT).  
 DE (RNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.48); COAT PROTEIN (CP)  
 DE (FRAGMENT).  
 SQ 672 DAEFGHDGSFVVRHQK 687

Query Match Score 73; DB 1; Length 770;  
 Best Local Similarity 81.28; Pred No. 0.0003; 2; Indels 0; Gaps 0;  
 Matches 13; Conservative 1; Mismatches 1; Gaps 0;

RESULT 11  
 ID POLG\_PVYYO STANDARD; PRT; 284 AA.  
 AC P11897; .  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last annotation update)  
 DT 15-DEC-1998 (Rel. 31, Last annotation update)  
 DE GENOME POLYPROTEIN (CONTAINS: NUCLEAR INCLUSION PROTEIN B (NI-B) (NIB)  
 DE (FRAGMENT).  
 DE (RNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.48); COAT PROTEIN (CP)  
 DE (FRAGMENT).  
 SQ 672 DAEFGHDGSFVVRHQK 687

OC Potato virus Y (strain Chinese isolate) (PVY).  
 OC ssRNA positive-strand viruses, no DNA stage; Potyviridae;  
 OC Potyvirus.  
 [1]  
 RN SEQUENCE FROM N.A.  
 RN  
 RX  
 RT Zhou X.R., Fang R.X., Wang C.Q., Wang K.Q.;  
 RT Nucleic Acids Res. 18:5554-5554(1990).  
 CC -!- SIMILARITY: BELONGS TO THE PVY genome (the Chinese  
 CC sequence of the 3'-coding region of PVY).  
 CC  
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|   |                            |                          |
|---|----------------------------|--------------------------|
| EMBL; X54058;   | CAA33793.1;                | -                        |
| PIR; S11549;  | S11549.                    |                          |
| HSSP; P05067;   | 1AMB.                      |                          |
| PFAM; PF00767;  | Poly-coat;                 | 1.                       |
| TRANSFERASE; RNA-directed RNA polymerase; Coat protein; Polyprotein.  |                            |                          |
| NON-TPR   | 1                          | 1                        |
| CHAIN   | <1                         | 60                       |
| CHAIN   | 61                         | 327                      |
| SEQUENCE  | 327 AA;                    | 36868 MW;                |
|   |                            | 8FB355E2DBE6F2F18 CRC64; |
| Query Match   | Score 50.5;                | DB 1;                    |
| Best Local Similarity   | 73.3%                      | Length 327;              |
| Matches 11;   | Conservative               | Pred. No. 0.47;          |
| 0;  | Mismatches 3;              | Indels 1;                |
| Gaps 1;   |                            |                          |
| 1 DAEFRHDSGYEVHHQ 15  |                            |                          |
| 47 DDEFFEDS-YEVHQ 60  |                            |                          |
| RESULT 13   |                            |                          |
| BB0228_BORBU  | STANDARD;                  | PRT;                     |
| Y228_BORBU  |                            | 971 AA.                  |
| 051246;   |                            |                          |
| 15-DEC-1998 (Rel. 37, Created)  |                            |                          |
| 15-DEC-1998 (Rel. 37, Last sequence update)   |                            |                          |
| 15-DEC-1998 (Rel. 37, Last annotation update)   |                            |                          |
| HYPOTHETICAL PROTEIN BB0228.  |                            |                          |
| Borrelia burgdorferi (Lyme disease spirochete).   |                            |                          |
| Bacteria; Spirochaetales; Spirochaetaceae; Borreliae.   |                            |                          |
| SEQUENCE FROM N.A.  |                            |                          |
| STRAIN=ATCC 35210 / B31;  |                            |                          |
| MEDLINE; 98065943.  |                            |                          |
| Fraser C.M., Caspiens S., Huang W.M., Sutton G.G., Clayton R.A.,  |                            |                          |
| Lathigra R., White P., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,  |                            |                          |
| Lathigra B., Tomb J.-F., Fleischmann R.D., Richardson D.,   |                            |                          |
| Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,  |                            |                          |
| Van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,   |                            |                          |
| Uterbeck T., Wathey L., McDonald L., Artiach P., Bowman C.,   |                            |                          |
| Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,  |                            |                          |
| Smith H.O., Venter J.C.;  |                            |                          |
| "Genomic sequence of a Lyme disease spirochaete, <i>Borrelia</i> burgdorferi".  |                            |                          |
| Nature 390:580-586(1997).   |                            |                          |
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| TIGR; BB0228;   | -                          |                          |
| HYPOTHETICAL PROTEIN  |                            |                          |
| SEQUENCE 971 AA;  | 112959 MW;                 | 088A688D7BBC591A CRC64;  |
| Y   | 1 DAEFRHDSGYEVHHQ 16       |                          |
| b   | 19 DAEGYYFRHESSGLEVFHLK 37 |                          |
| Query Match   | Score 53.8%;               | DB 1;                    |
| Best Local Similarity   | 57.9%;                     | Length 971;              |
| Matches 11;   | Conservative               | Pred. No. 2.1;           |
| 2;  | Mismatches 3;              | Indels 3;                |
| Gaps 1;   |                            |                          |
| SEQUENCE FROM N.A.  |                            |                          |
| RN  | RP                         | SEQUENCE FROM N.A.       |
| MEDLINE; 89273275.  |                            |                          |
| Durand-Tardif M., Tronchet M., Boudazin G.,   |                            |                          |
| Robaglia C., Durand-Tardif M., Tronchet M., Boudazin G.,  |                            |                          |
| Astier-Manificier S., Casse-Delbart F.;   |                            |                          |
| "Nucleotide sequence of potato virus Y (N Strain) genomic RNA.";  |                            |                          |
| J. Gen. Virol. 70:935-947(1989).  |                            |                          |
| [2]   | REVISIONS.                 |                          |
| Durand-Tardif M.,   | RP                         |                          |
| Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.  |                            |                          |
| -!- FUNCTION: HELPER COMPONENT-PROTEINASE IS REQUIRED FOR APHID TRANSMISSION AND ALSO HAS PROTEOLYTIC ACTIVITY.   |                            |                          |
| CC  |                            |                          |
| RESULTS 14  |                            |                          |

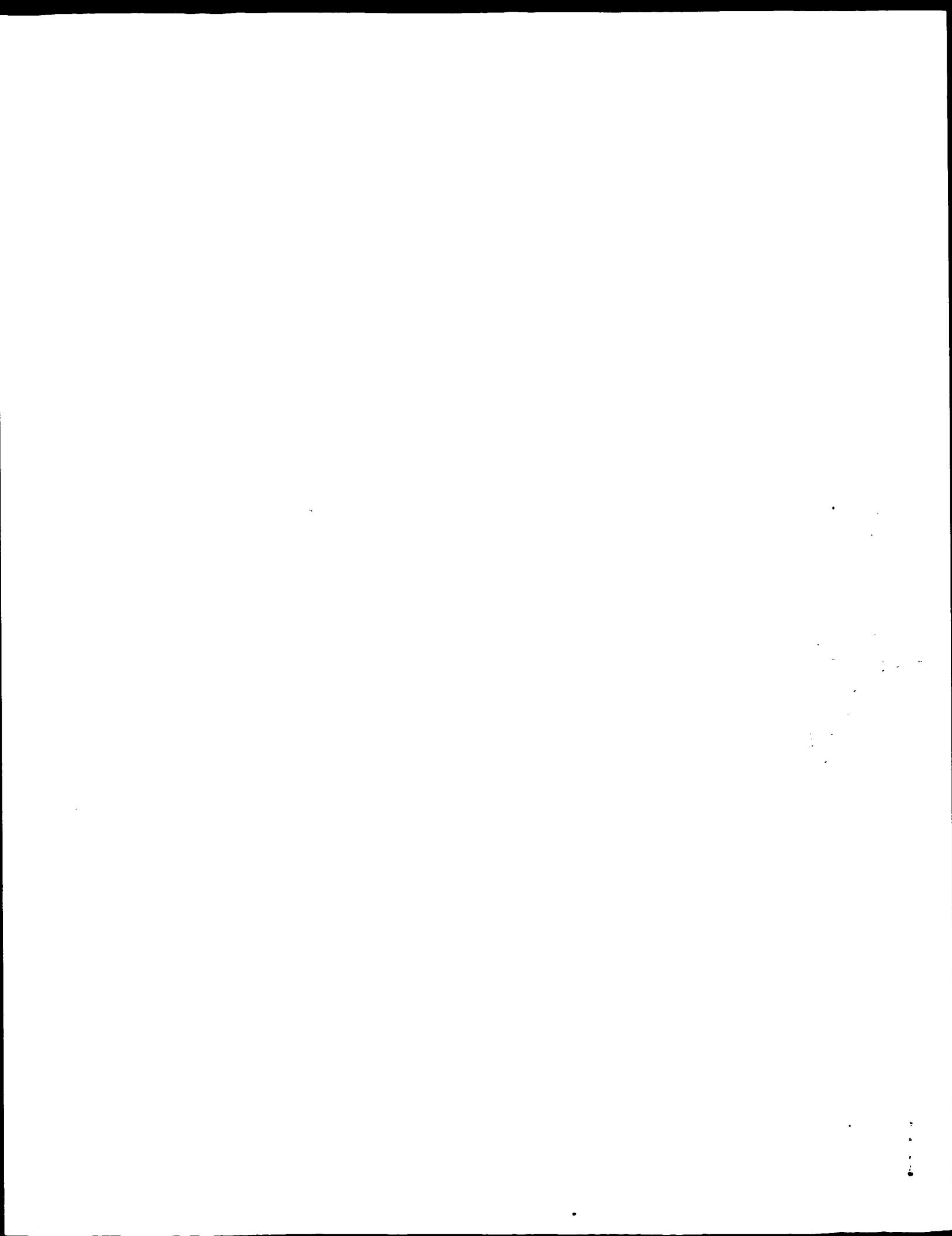
CC -!- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY. IT  
 CC MAY BE INVOLVED IN REPLICATION.  
 CC -!- FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.  
 CC -!- PTM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.  
 CC -!- PTM: THE VIRAL RNA OF POIVIRUSES IS EXPRESSED AS A SINGLE  
 CC POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC  
 CC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT  
 CC INDIVIDUAL PROTEINS.  
 CC -!- SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.  
 CC -!- SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4.  
 CC -!- SIMILARITY: BELONGS TO THE POIVIRUSES POLYPROTEIN FAMILY.

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DR EMBL; D00441; BAA00342.1; -.  
 DR PIR; JS0166; JS0166.  
 DR PF00270; DEAD; 1.  
 DR PFAM; PF00863; Peptidase\_C4; 1.  
 DR PFAM; PF00851; Peptidase\_C6; 1.  
 DR PFAM; PF01577; Poty\_P1; 1.  
 DR PF00767; Poty\_coat; 1.  
 DR PF00680; RNA\_dep\_RNA\_poli; 1.  
 DR PF00271; helicase\_C; 1.  
 PRNTS; PR0096; NIAPOLYTPASE.  
 KW Hydrolase; Transferase; Thiol protease; RNA-directed RNA Polymerase;  
 KW Coat protein; Polyprotein; Covalent protein-RNA linkage; Helicase;  
 KW ATP-binding.  
 FT CHAIN 1 275 N-TERMINAL PROTEIN.  
 FT CHAIN 276 824 HELPER COMPONENT PROTEINASE.  
 FT CHAIN 825 ? PROTEIN P3.  
 FT CHAIN ? 1157 6 kDa PROTEIN 1.  
 FT CHAIN 1158 1791 CYTOPLASMIC INCLUSION PROTEIN.  
 FT CHAIN 1792 1843 6 kDa PROTEIN 2.  
 FT CHAIN 1844 ? GENOME-LINKED PROTEIN.  
 FT CHAIN ? 2275 NUCLEAR INCLUSION PROTEIN A.  
 FT CHAIN 2276 2796 NUCLEAR INCLUSION PROTEIN B.  
 FT BINDING 2197 3063 COAT PROTEIN.  
 FT BINDING 1907 1907 COVALENT LINKAGE OF VIRAL RNA (BY  
 SIMILARITY).  
 FT NP\_BIND 1242 1249 ATP (POTENTIAL).  
 SQ SEQUENCE 3063 AA: 347535 MW: 3EC79125DE33F1BB CRC64;

Query Match 52.7%; Score 48.5%; Length 3063;  
 Best Local Similarity 73.3%; Pred. No. 10;  
 Matches 11; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
 Qy 1 DAEPFRHDGSGYEVHHQ 15  
 Db 2783 DDEFELDS-YEVHHQ 2796

Search completed: September 13, 2000, 02:24:32  
 Job time: 170 sec



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## OM protein - protein search, using sw model

Run on: September 13, 2000, 02:24:09 ; Search time 22.49 seconds  
(without alignments)  
49.326 Million cell updates/sec

Title: US-09-155-076-2  
Perfect score: 92  
Sequence: 1 DAEFRHDSGYEVHK 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 10000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL\_12;\*

1: sp\_archaea;\*  
2: sp\_bacteria;\*  
3: sp\_fungi;\*  
4: sp\_human;\*  
5: sp\_invertebrate;\*  
6: sp\_mammal;\*  
7: sp\_mhc;\*  
8: sp\_organelle;\*  
9: sp\_phage;\*  
10: sp\_plant;\*  
11: sp\_rhodent;\*  
12: sp\_virus;\*  
13: sp\_vertebrate;\*  
14: sp\_unclassified;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Match Length | DB ID | Description                         |
|------------|-------|--------------|-------|-------------------------------------|
| 1          | 92    | 100.0        | 82    | 4 Q16020 homo sapien                |
| 2          | 92    | 100.0        | 82    | 4 Q16019 homo sapien                |
| 3          | 92    | 100.0        | 82    | 4 Q16014 homo sapien                |
| 4          | 92    | 100.0        | 82    | 4 P78438 homo sapien                |
| 5          | 92    | 100.0        | 534   | 13 Q93296 gallus gallus             |
| 6          | 92    | 100.0        | 695   | 11 Q60496 cavia porcellus           |
| 7          | 82    | 89.1         | 97    | 4 Q13778 homo sapien                |
| 8          | 77    | 83.7         | 747   | 13 Q91963 xenopus laevis            |
| 9          | 73    | 79.3         | 79    | 11 Q35463 cricetus cricetus         |
| 10         | 73    | 79.3         | 695   | 11 P97487 mus musculus              |
| 11         | 72    | 78.3         | 699   | 13 P07394 narke japonica            |
| 12         | 50.5  | 54.9         | 292   | 12 Q85276 potato virus              |
| 13         | 50.5  | 54.9         | 365   | 12 Q9WGO5 tetrododon flavimaculatus |
| 14         | 50.5  | 54.9         | 1555  | 12 Q85274 potato virus              |
| 15         | 50    | 54.3         | 780   | 13 Q73683 fugu rubripinnis          |
| 16         | 49    | 53.3         | 737   | 13 Q93279 escherichia coli          |
| 17         | 47    | 51.1         | 206   | 2 Q49454 borrelia burgdorferi       |
| 18         | 46    | 50.0         | 372   | 2 Q85339 escherichia coli           |
| 19         | 45.5  | 49.5         | 313   | 12 Q85259 potato virus              |

|    |      |      |      |  |
|----|------|------|------|--|
| 20 | 45.5 | 49.5 | 976  | 12 Q85104 potato virus                   |
| 21 | 45.5 | 49.5 | 3061 | 12 Q85265 potato virus                   |
| 22 | 44.5 | 48.4 | 519  | 12 Q72606 potato virus                   |
| 23 | 44.5 | 48.4 | 3081 | 12 Q85105 potato virus                   |
| 24 | 44   | 47.8 | 297  | 2 Q9NC1 nitrosoomona schizosaccharomyces |
| 25 | 42.5 | 46.2 | 539  | 3 Q14283 schizosaccharomyces pombe       |
| 26 | 42   | 45.7 | 339  | 4 Q75357 homo sapiens                    |
| 27 | 42   | 45.7 | 372  | 4 Q60547 homo sapiens                    |
| 28 | 42   | 45.7 | 373  | 2 Q69312 hevea brasiliensis              |
| 29 | 42   | 45.7 | 667  | 3 Q12101 saccharomyces cerevisiae        |
| 30 | 41   | 44.6 | 213  | 6 Q29520 oryctolagus cuniculus           |
| 31 | 41   | 44.6 | 213  | 6 Q29521 oryctolagus cuniculus           |
| 32 | 41   | 44.6 | 213  | 6 Q29521 hevea brasiliensis              |
| 33 | 41   | 44.6 | 356  | 10 Q22331 hevea brasiliensis             |
| 34 | 41   | 44.6 | 367  | 3 Q43120 schizosaccharomyces pombe       |
| 35 | 41   | 44.6 | 494  | 2 Q53677 mycobacterium tuberculosis      |
| 36 | 41   | 44.6 | 551  | 2 Q52519 pseudomonas aeruginosa          |
| 37 | 41   | 44.6 | 672  | 2 Q04562 saccharomyces cerevisiae        |
| 38 | 41   | 44.6 | 944  | 4 Q14697 homo sapiens                    |
| 39 | 41   | 44.6 | 966  | 11 Q08794 mus musculus                   |
| 40 | 41   | 44.6 | 1919 | 6 Q29518 oryctolagus cuniculus           |
| 41 | 41   | 44.6 | 1920 | 6 Q29519 oryctolagus cuniculus           |
| 42 | 40.5 | 44.0 | 559  | 10 Q23409 arabidopsis thaliana           |
| 43 | 40   | 43.5 | 104  | 2 Q9ZP5 enterococcus faecalis            |
| 44 | 40   | 43.5 | 155  | 5 Q19475 caenorhabditis elegans          |
| 45 | 40   | 43.5 | 311  | 10 Q39500 cylindrothele aggregata        |

## ALIGNMENTS

| RESULT | 1 | PRELIMINARY; |         |    |         | PRT;            | 82 AA.  |
|--------|---|--------------|---------|----|---------|-----------------|---|
| Q16020 | 1 | ID           | Q16020; | AC | Q16020; | DT              | 01-NOV-1996 (TREMBLrel. 01, Created)  |
|        |   |              |         |    |         | DT              | 01-NOV-1996 (TREMBLrel. 01, Last sequence update)   |
|        |   |              |         |    |         | DE              | BETA-AMYLOID PEPTIDE (FRAGMENT).  |
|        |   |              |         |    |         | OS              | Homo sapiens (Human).   |
|        |   |              |         |    |         | OC              | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;   |
|        |   |              |         |    |         | RN              | Eutheria; Primates; Catarrhini; Hominidae; Homo. [1]  |
|        |   |              |         |    |         | RP              | SEQUENCE FROM N.A. MEDLINE: 93136601.   |
|        |   |              |         |    |         | RX              |   |
|        |   |              |         |    |         | RA              | DENMAN R.B., ROSENZWAIG R., MILLER D.J.: "A system for studying the effects of familial Alzheimer disease mutations on the processing of the beta-amyloid peptide precursor." |
|        |   |              |         |    |         | RT              | mutations on the processing of the beta-amyloid peptide precursor.  |
|        |   |              |         |    |         | RL              | Biochem. Biophys. Res. Commun. 192:96-103(1993).  |
|        |   |              |         |    |         | DR              | EMBL; S61383; CAB32006.1; -.  |
|        |   |              |         |    |         | DR              | HSSP; P05067; 1AML.   |
|        |   |              |         |    |         | FT              | NON_TER 1   |
|        |   |              |         |    |         | FT              | NON_TER 1   |
|        |   |              |         |    |         | SEQUENCE 82 AA; | 8882 MW; 55734509 CRC32;  |
|        |   |              |         |    |         |                 |   |

| Query  | Match | Best Local Similarity 100.0%; Pred. No. 4.9e-08; Mismatches 0; Indels 0; Gaps 0; |         |                    |         |      |   |
|--------|-------|--|---------|--------------------|---------|------|---|
| QY     | 1     | DAEFRHDSGYEVHKQ 16   |         |                    |         |      |   |
|        |       |  |         |                    |         |      |   |
|        |       | Db   | 18      | DAEFRHDSGYEVHKQ 33 | 33      |      |   |
|        |       |  |         |                    |         |      |   |
| RESULT | 2     | PRELIMINARY;   |         |                    |         | PRT; | 82 AA.  |
| Q16019 | 1     | ID   | Q16019; | AC                 | Q16019; | DT   | 01-NOV-1996 (TREMBLrel. 01, Created)              |
|        |       |  |         |                    |         | DT   | 01-NOV-1996 (TREMBLrel. 01, Last sequence update) |
|        |       |  |         |                    |         | DE   | BETA-AMYLOID PEPTIDE (FRAGMENT).                  |

OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 [1]

SEQUENCE FROM N.A.  
 MEDLINE: 93236601  
 RXN  
 RP  
 RX  
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).  
 DR S61380; CAB2007.1; -.  
 HSSP: P05067; IAML.  
 FT NON\_TER 1 1  
 FT NON\_TER 82 82  
 SQ SEQUENCE 82 AA; 8938 MW; 4C8B0E6E CRC32;

Query Match 3  
 ID Q16014 PRELIMINARY; PRT; 82 AA.  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
 DE BETA AMYLOID PEPTIDE (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA DENMAN R.B.; ROSENZWAIG R.; MILLER D.L.;  
 RT "A system for studying the effect(s) of familial Alzheimer disease  
 mutations on the processing of the beta-amyloid peptide precursor.";  
 RT mutations on the processing of the beta-amyloid peptide precursor.  
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).  
 DR S6021; CAB31088.1; -.  
 HSSP: P05067; IAML.  
 FT NON\_TER 1 1  
 FT NON\_TER 82 82  
 SQ SEQUENCE 82 AA; 8932 MW; 30147E4F CRC32;

Query Match 4  
 ID Q16014 PRELIMINARY; PRT; 82 AA.  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DE AMYLOID PROTEIN (BETA-AMYLOID PROTEIN) (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE: 89392030.  
 RA JOHNSTONE E.M.; CHANEY M.O.; MOORE R.E.; WARD K.E.; NORRIS F.H.;  
 RA LITTLE S.P.;  
 RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows  
 similarity to soybean trypsin inhibitor.";  
 RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).  
 [2]  
 RN  
 RP SEQUENCE OF 19-48 FROM N.A.  
 RX MEDLINE: 87120329.  
 RA TANZI R.E.; GUSELLA J.F.; WATKINS P.C.; BRUNS G.A.; ALONSO M.E.; PULST S.M.,  
 RA VAN KEUREN M.L.; PATTERSON D.; PAGAN S.; KURNIT D.M.; NEVE R.L.;  
 RT "Amyloid beta protein gene: cDNA, mRNA distribution, and genetic  
 linkage near the Alzheimer locus.";  
 RL Science 235:880-884(1987).  
 RN [3]  
 RP SEQUENCE OF 32-63 FROM N.A.  
 RX MEDLINE: 93035397.  
 RA KAMINO K.; ORR H.T.; PAYAMI H.; WIJSMAN E.M.; ALONSO M.E., PULST S.M.,  
 RA ANDERSON L.; O'DAHL S.; NEMENS E.; WHATE J.A.;  
 RT "Linkage and mutational analysis of familial Alzheimer disease  
 kindreds for the APP gene region.";  
 RT kindreds for the APP gene region.  
 RL Am. J. Hum. Genet. 51:988-1014(1992).  
 DR EMBL: M29170; AAA51768.1;  
 DR EMBL: M29169; AAA51768.1; JOINED.  
 DR EMBL: M15332; AAA51564.1;  
 DR EMBL: S45136; AAB23646.1; -.  
 DR HSSP; P05067; IAML.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 82 AA; 8994 MW; 5399FFA4 CRC32;

Query Match 5  
 ID Q16014 PRELIMINARY; PRT; 82 AA.  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
 DE BETA AMYLOID PEPTIDE (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MILLIGAN C.E.; BARNESE N.Y.; LANG L.; YOSHIKAWA K.; SCHWARTZ L.M.; OPPENHEIM R.W.,  
 RA BARNES N.Y.; LANG L.; YOSHIKAWA K.; SCHWARTZ L.M.; OPPENHEIM R.W.,  
 RA MILLIGAN C.E.; BARNESE N.Y.; LANG L.; YOSHIKAWA K.; SCHWARTZ L.M.; OPPENHEIM R.W.,  
 RT Increased production of amyloid precursor protein provides a  
 RT substrate (JAN-1998) to the caspase 3 in dying motoneurons.";  
 RT Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL: AF042098; AAC25052.1; -.  
 DR HSSP; P05067; IAML.  
 DR PROSITE; PS00319; A4\_EXTRA; 1.  
 DR PROSITE; PS00320; A4\_INTRAA; 1.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 534 AA; 60597 MW; 6F117D2F CRC32;

Query Match 6  
 ID Q16014 PRELIMINARY; PRT; 82 AA.  
 DT 01-MAY-1997 (TREMBLrel. 03, Created)  
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
 DE AMYLOID PROTEIN (BETA-AMYLOID PROTEIN) (FRAGMENT).  
 GN APP.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 RN [1]

Query Match 7  
 ID P78438 PRELIMINARY; PRT; 82 AA.  
 AC P78438  
 DT 01-MAY-1997 (TREMBLrel. 03, Created)  
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
 DE AMYLOID PROTEIN (BETA-AMYLOID PROTEIN) (FRAGMENT).  
 GN APP.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 RN [1]

Query Match 8  
 ID P78438 PRELIMINARY; PRT; 82 AA.  
 AC P78438  
 DT 01-MAY-1997 (TREMBLrel. 03, Created)  
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
 DE AMYLOID PROTEIN (BETA-AMYLOID PROTEIN) (FRAGMENT).  
 GN APP.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 RN [1]

Db 436 DAEFRHDSGYEVHHQK 451

RESULT 6  
 Q60496 PRELIMINARY; PRT; 695 AA.  
 ID Q60496; PRELIMINARY;  
 AC Q60496;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last annotation update)  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Xenopodinae;  
 OC Xenopus.  
 OC  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 93190227.  
 RA OKADA H.; OKAMOTO H.;  
 RT "A Xenopus homologue of the human beta-amyloid precursor protein: developmental regulation of its gene expression."  
 RL Biochem. Biophys. Res. Commun. 189:1561-1568(1992).  
 DR EMBL: S22417; AAB24853; 1; -.  
 DR PROSITE; PS00320; M\_IMTRNA; 1.  
 DR PROSITE; PS0280; BPT1\_KUNTZ; 1.  
 DR PROSITE; PS00319; A4\_EXTRA; 1.  
 DR PFAM; PF00014; Kunitz\_BPTI; 1.  
 DR PRINTS; PR0003; AMYLOIDA4.  
 DR PRINTS; PR0004; BETAAMYLOID.  
 DR PRINTS; PR0059; BASICPTIDE.  
 DR SERINE protease inhibitor.  
 KW MW; A7580143 CRC32;  
 SQ SEQUENCE 747 AA; 84892 MW; A7580143 CRC32;

Query Match 100.0%; Score 92; DB 11; Length 695;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16  
 DR 597 DAEFRHDSGYEVHHQK 612

RESULT 7  
 Q13778 PRELIMINARY; PRT; 97 AA.  
 ID Q13778; PRELIMINARY;  
 AC Q13778;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1999 (TREMBLrel. 01, Last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
 DE AMYLOID PROTEIN (AD-AP) (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 CC Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE; 871203228.

RA GOLDGABER D.; LERNER M.I.; MCBRIDE O.W.; SAFFIOTTI U.; GAJDUSEK D.C.;  
 RT "Characterization and chromosomal localization of a cDNA encoding brain amyloid of Alzheimer's disease." ;  
 RT EMBL: M15533; AAA35540.1; -.  
 DR HSSP; P05067; 1AML.  
 DR NON\_TER 1 1  
 FT SQ SEQUENCE 97 AA; 10884 MW; C4D32AA2 CRC32;

Query Match 89.1%; Score 82; DB 4; Length 97;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EFRHDSGYEVHHQK 16  
 DR 1 EFRHDSGYEVHHQK 14

RESULT 8  
 Q91963 PRELIMINARY; PRT; 747 AA.  
 ID Q91963; PRELIMINARY;  
 AC Q91963; PRELIMINARY;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Xenopodinae;  
 OC Xenopus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 93190227.  
 RA OKADA H.; OKAMOTO H.;  
 RT "A Xenopus homologue of the human beta-amyloid precursor protein: developmental regulation of its gene expression."  
 RL Biochem. Biophys. Res. Commun. 189:1561-1568(1992).  
 DR EMBL: S22417; AAB24853; 1; -.  
 DR PROSITE; PS00320; M\_IMTRNA; 1.  
 DR PROSITE; PS0280; BPT1\_KUNTZ; 1.  
 DR PROSITE; PS00319; A4\_EXTRA; 1.  
 DR PFAM; PF00014; Kunitz\_BPTI; 1.  
 DR PRINTS; PR0003; AMYLOIDA4.  
 DR PRINTS; PR0004; BETAAMYLOID.  
 DR PRINTS; PR0059; BASICPTIDE.  
 DR SERINE protease inhibitor.  
 KW MW; A7580143 CRC32;

Query Match 83.7%; Score 77; DB 13; Length 747;  
 Best Local Similarity 85.0%; Pred. No. 0.00013; Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 SQ

RESULT 9  
 Q35463 PRELIMINARY; PRT; 79 AA.  
 ID Q35463; PRELIMINARY;  
 AC Q35463;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
 DE ALZHEIMER'S AMYLOID BETA PROTEIN PRECURSOR (FRAGMENT).  
 GN BETA APP.  
 OS Cricetulus griseus (Chinese hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 CC Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Cricetus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA SAMBAMURTI K.; PINNIX J.; GANDHI S.;  
 RT Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
 RL EMBL: AF030413; AAB86608.1; -.  
 DR HSSP; P05067; 1QCM.  
 FT NON\_TER 1 1  
 FT SQ SEQUENCE 79 AA; 8538 MW; EB3BB61F CRC32;

Query Match 79.3%; Score 73; DB 11; Length 79;  
 Best Local Similarity 81.2%; Pred. No. 5.5e-05; Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 SQ

1 DAEFRHDSGYEVHHQK 16  
 21 DAEFRHDSGYEVHHQK 36

RESULT 10

P97487 PRELIMINARY; PRT; 695 AA.  
 AC P97487; P97942;  
 DT 01-MAY-1997 (TREMBLrel. 03, Created)  
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
 DE HIPPOCAMPAL AMYLOID PROTEIN  
 GN APP.  
 OS Mus musculus (Mouse).  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.  
 OC [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SAMP8; TISSUE=HIPPOCAMPUS;  
 RA FLOOD J.F., KUDMAR V.B., SASSER T., WORD J.E., MORLEY J.E.;  
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF N.A.  
 RC STRAIN=129SV;  
 RA WRAGG M.A., BUSFIELD F., DUFF K., KORENBLAT K., CAPECCHI M.,  
 RA LORING J.F., GOATE A.M.; WORD J.E., MORLEY J.E.;  
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
 DR U84012; U83624; AAB40919.1; -.  
 DR PROSITE; PS00319; A4\_EXTRAA; 1.  
 DR PROSITE; PS00320; A4\_INTRAA; 1.  
 DR PROSITE; PR00204; BETAAMYLOID.  
 DR PRINTS; PR00203; ANFOLOIDA.  
 SQ SEQUENCE 695 AA; 78414 MW; B709D560 CRC32;

Query Match 79.3%; Score 73; DB 11; Length 695;  
 Best Local Similarity 81.2%; Pred. No. 0.0054; Indels 0; Gaps 0;  
 Matches 13; Conservative 1; Mismatches 2;

Qy 1 DAEFRHDSGYEVHHQK 16  
 Db 597 DAEFRHDSGYEVHHQK 612

RESULT 11  
 ID 057394 PRELIMINARY; PRT; 699 AA.  
 AC 057394;  
 DT 01-JUN-1998 (TREMBLrel. 06, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DE EL ANHYDRO PRECURSOR PROTEIN 699.  
 GN APP699.  
 OS Narke japonica (Electric ray).  
 OC Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
 OC Blasmodbranchii; Rajiformes; Narke.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=ELECTRIC LOBE;  
 RC SUZUKI T.; LEE D.; OKUTSU J.; TOMITA S.; HIRASHIMA N.; KIRINO Y.;  
 RA SUZUKI T.; Biochem. J. 0:0-0 (1998).  
 RL EMBL; AB00544; BAA24230.1; -.  
 DR PROSITE; PS00319; A4\_EXTRAA; 1.  
 DR PROSITE; PS00320; A4\_INTRAA; 1.  
 DR PRINTS; PR00203; BETAAMYLOID.  
 DR PRINTS; PR00204; BETAAMYLOID.  
 SQ SEQUENCE 699 AA; 78879 MW; 11604C05 CRC32;

Query Match 78.3%; Score 72; DB 13; Length 699;  
 Best Local Similarity 75.0%; Pred. No. 0.00079; Indels 0; Gaps ~0;  
 Matches 12; Conservative 2; Mismatches 2;

Qy 1 DAEFRHDSGYEVHHQK 16  
 Db 601 DAEFRHDSGYEVHHQK 616

RESULT 12  
 ID Q85276 PRELIMINARY; PRT; 292 AA.  
 AC Q85276;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 08, Last sequence update)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
 DE POLYPROTEIN (FRAGMENT).  
 OS Potato virus Y.  
 OC ssRNA positive-strand viruses, no DNA stage; Potyviridae;  
 OC Potyvirus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA GRIFFIN J.D., SHIEL P.S., BERGER P.H., THORNBURY D.W.;  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; MB1435; AAA7185.1; -.  
 DR PFAM; PF00767; Poty\_coat; 1.  
 KW Polyprotein.  
 FT NON\_TER 1 1 NIB.  
 FT CHAIN 1 25 COAT PROTEIN.  
 FT CHAIN 26 292 AA; 32945 MW; 8CB34E72 CRC32;  
 SQ SEQUENCE 292 AA; 32945 MW;

Query Match 54.9%; Score 50.5%; DB 12; Length 292;  
 Best Local Similarity 73.3%; Pred. No. 0.94%; 3; Indels 1; Gaps 1;

Qy 1 DAEFRHDSGYEVHHQ 15  
 Db 12 DDEFEDDS-YEVHHQ 25

RESULT 13  
 ID Q9WG05 PRELIMINARY; PRT; 365 AA.  
 AC Q9WG05;  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
 DE POLYPROTEIN (FRAGMENT).  
 OS Potato virus Y.  
 OC ssRNA positive-strand viruses, no DNA stage; Potyviridae;  
 OC Potyvirus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ORDINARY, O.  
 RA BHAT A.I., VARMA A., PAPPU H.R., RAJAMANNAR M., JAIN R.K., PRAVEEN S.;  
 RT "N-terminal serology and sequence relationships indicate that a  
 RT potyvirus from eggplant, Solanum melongena L., is a strain of potato  
 RT virus Y.";  
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
 DR AF118153; AAD24563.1; -.  
 KW Polyprotein.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 365 AA; 41418 MW; F3CE9EBD CRC32;

Query Match 54.9%; Score 50.5%; DB 12; Length 365;  
 Best Local Similarity 73.3%; Pred. No. 1.2%; Mismatches 0; Indels 1; Gaps 1;

Qy 1 DAEFRHDSGYEVHHQ 15  
 Db 85 DDEFEDDS-YEVHHQ 98

RESULT 14  
 ID Q85274 PRELIMINARY; PRT; 1555 AA.  
 AC Q85274;

DT 01-NOV-1996 (TREMBLrel. 01; Created)  
 DT 01-NOV-1996 (TREMBLrel. 01; Last sequence update)  
 DT 01-MAY-1999 (TREMBLrel. 10; Last annotation update)  
 DE POLYPROTEIN (FRAGMENT).  
 OS Potato virus Y.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;  
 OC Potyvirus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=O;  
 RX MEDLINE; 92335011.  
 RA HIDAKA M.; YOSHIDA Y.; MASAKI H.; NAMBA S.; YAMASHITA S.;  
 RA TSUCHIZAKI T.; UOZUMI T.;  
 RT "Cloning and sequencing of the 3' half of a potato virus Y (O strain) genome encoding the 5k protein, protease, polymerase and coat protein";  
 RT Nucleic Acids Res. 20:3515-3515(1992).  
 DR EMBL; D12539; BA02107.1;  
 DR PFAM; PF00863; Peptidase\_C4; 1.  
 DR PFAM; PF00767; Poty\_coat; 1.  
 DR PFAM; PF00680; RNA\_dep\_RNA\_Pol; 1.  
 KW POLYPROTEIN; Coat protein; Protease.  
 FT NON\_TER 1 1  
 FT CHAIN 1 285 CYTOPLASMIC INCLUSION BODY.  
 FT CHAIN 286 337 5-KD PROTEIN.  
 FT CHAIN 338 769 PROTEASE.  
 FT CHAIN 770 1288 RNA POLYMERASE.  
 FT CHAIN 1289 1555 COAT PROTEIN.  
 SQ SEQUENCE 1555 AA; 176933 MW; 4403DDF0 CRC32;

Query Match 54.9%; Score 50.5%; Length 1555;  
 Best Local Similarity 73.3%; Pred. No. 5.4;  
 Matches 11; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 DAEFRHDSGYVRHQ 15  
 Db 1275 DDEFFEDS-YEVHQ 1288

RESULT 15  
 073683 PRELIMINARY; PRT; 780 AA.  
 ID 073683;  
 AC 073683;  
 DT 01-AUG-1998 (TREMBLrel. 07; Created)  
 DT 01-AUG-1998 (TREMBLrel. 07; Last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12; Last annotation update)  
 DE AMYLOID PRECURSOR PROTEIN.  
 OS Tetradon fluviatilis (Puffer fish).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;  
 OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percormorpha;  
 OC Tetraodontiformes; Tetraodontoidae; Tetraodontidae; Tetraodon.  
 RN [1] FROM N.A.  
 RP MEDLINE; 98252138.  
 RA VILLARD L.; TASSONE F.; CRNOGORAC-JURCEVIC T.; CLANCY K.; GARDINER K.;  
 RT "Analysis of pufferfish homologues of the AT-rich human APP gene.";  
 RL Gene 210:17-24(1998).  
 DR EMBL; AF018165; AAC1275.1;  
 DR PROST1; PS00339; A4\_EXTRA; 1.  
 DR PROST2; PS00320; A4\_INTRA; 1.  
 DR PFAM; PF0001; Kunitz\_BPTI; 1.  
 DR PRINTS; PRO202; AMYLOID4;  
 DR PRINTS; PRO0204; BETAAMYLOID.  
 DR PRINTS; PRO0755; BASICPASE.  
 SQ SEQUENCE 780 AA; 88238 MW; 99DD89A8 CRC32;

Query Match 54.3%; Score 50; DB 13; Length 780;  
 Best Local Similarity 56.2%; Pred. No. 3.2;  
 Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYVRHQ 16



```

OM of: US-09-155-076-2 to: EST:*      out_format : pfs
Date: Sep 13, 2000 2:42 AM

About: Results were produced by the GenCore software
Copyright (C) 1993-2000 Compugen Ltd.

Command line parameters:
-MODEL="frameret_p2n.mdl" -DEV=x1p
-Q="/cgn2_1/OSPI_spool/_US0315506/runat_29082000_09
-DB=EST -QMT=fastap -SUFFIX=_rst -GAPOP=12,000 -GAP
-MINNTHD=0,100 -LOOPCL=0,000 -LOOPST=0,000 -QGAP
-QGAPEXT=0,500 -XGAPOP=10,000 -XGAPET=0,500 -FGAPOP
-FGAPEXT=7,000 -YGAPOP=10,000 -YGAPET=0,500 -DELOP
-DELFXPT=7,000 -START=1 -MATRIX="diagram62" -TRANS=numLEN
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100
-MAXLEN=1000000 -MODE=LOCAL -OUTFILE=pis -NORM=ext -MINLEN
-MAXLEN=1000000 -USEPUSO3155076 @@CGN1_1-1327 -NCPU=1
-LOGLOG -NO_XLEXY -WAIT -THREADS=1

Search information block:
Query: US-09-155-076-2
Query length: 16
Database: EST:*
Database sequences: 5247842
Database length: ~2090053205
Search time (sec): 875.8900000

score_list:
Strd Orig ZScore Strd Orig ZScore Strd Orig ZScore Strd Orig ZScore
Seq6:AA385402 + 92.00 281.75 7.3e-07 24 + 92.00 280.72 8.3e-07 27 +
gb_est1:AW19017 - 92.00 280.68 8.3e-07 27 - 92.00 280.11 9.3e-07 29 +
gb..est2:AA319226 + 92.00 279.87 9.3e-07 30 + 92.00 279.85 1.0e-06 33 +
gb..est5:AA303751 + 92.00 279.87 9.3e-07 30 + 92.00 279.85 1.0e-06 33 +
gb..est7:RF0118 + 92.00 279.87 9.3e-07 30 + 92.00 279.85 1.0e-06 33 +
gb..est8:AW580695 - 92.00 279.85 1.0e-06 33 - 92.00 279.85 1.0e-06 33 +
gb..est26:AW1902528 + 92.00 278.98 1.0e-06 33 + 92.00 278.98 1.0e-06 33 +
gb..est5:AA310274 + 92.00 278.98 1.0e-06 33 + 92.00 278.98 1.0e-06 33 +
gb..est6:AI902529 + 92.00 278.97 1.1e-06 35 + 92.00 278.97 1.1e-06 35 +
gb..est5:AA304003 + 92.00 277.98 1.2e-06 38 + 92.00 277.95 1.3e-06 39 +
gb..est52:T49906 + 92.00 277.98 1.2e-06 38 + 92.00 277.95 1.3e-06 39 +
gb..est51:RI19709 + 92.00 277.95 1.3e-06 39 + 92.00 277.95 1.3e-06 39 +
gb..est2:AA134479 + 92.00 277.14 1.3e-06 41 + 92.00 276.26 1.5e-06 46 +
gb..est16:AI124771 - 92.00 277.14 1.3e-06 41 - 92.00 276.26 1.5e-06 46 +
gb..est4:AW601576 + 92.00 276.11 1.5e-06 46 + 92.00 276.11 1.5e-06 46 +
gb..est51:R25913 + 92.00 275.82 1.6e-06 48 + 92.00 275.82 1.6e-06 48 +
gb..est3:AA218652 + 92.00 275.16 1.6e-06 51.1 + 92.00 274.85 1.8e-06 50.6 +
gb..est44:AW60293 + 92.00 274.85 1.8e-06 50.6 + 92.00 273.80 2.0e-06 50.6 +
gb..est45:AW6734380 + 92.00 273.80 2.0e-06 50.6 + 92.00 273.66 2.1e-06 50.6 +
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gb..est18:AA181869 + 92.00 273.23 2.2e-06 50.2 + 92.00 272.73 2.3e-06 49.8 +
gb..est28:AI980795 + 92.00 272.73 2.3e-06 49.8 + 92.00 272.23 2.4e-06 49.4 +
gb..est3:AA218652 - 89.00 271.82 2.6e-06 52.4 + 89.00 271.33 2.6e-06 52.4 +
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gb..est44:AW608890 - 86.00 261.91 9.4e-06 48.6 + 86.00 261.91 9.4e-06 48.6 +
gb..est4:AW608448 + 86.00 254.14 2.5e-05 46.8 + 86.00 254.14 2.5e-05 46.8 +
gb..est28:AI980795 + 85.00 256.20 1.9e-05 48.8 + 85.00 256.20 1.9e-05 48.8 +
gb..est41:AW366795 + 84.00 252.72 3.0e-05 49.8 + 84.00 252.72 3.0e-05 49.8 +
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gb..est13:AA888590 + 73.00 220.93 6.0e-05 40.4 + 73.00 220.93 6.0e-05 40.4 +
gb..est53:W13895 + 73.00 218.77 0.0023 38.9 + 73.00 218.77 0.0023 38.9 +
gb..est2:AI0744807 + 73.00 218.31 0.0025 41.0 + 73.00 218.31 0.0025 41.0 +
gb..est13:AA911658 + 73.00 218.00 0.0026 42.5 + 73.00 218.00 0.0026 42.5 +
gb..est24:AI107076 + 73.00 217.62 0.0027 44.4 + 73.00 217.62 0.0027 44.4

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| -29082000_092504_15735/app_query.fasta_1.144 |                   |                                |  |  |  |  |
| -12.000                                      | -GPEXT4_000       |                                |  |  |  |  |
| 0.000  | -QGAOP_4_500      |                                |  |  |  |  |
| -0.500                                       | -FGAOP_6_000      |                                |  |  |  |  |
| -0.500                                       | -DELOP_6_000      |                                |  |  |  |  |
| 2  | -TRANS-human0.cdi |                                |  |  |  |  |
| -THR_MAX=100                                 | -THR_MIN=0        |                                |  |  |  |  |
| -ext-MINLEN=0                                |                   |                                |  |  |  |  |
| -1_1327                                      | -NCPU=6           | -ICPU=3                        |  |  |  |  |
|  |                   |                                |  |  |  |  |
| EScore                                       | Len               | Documentation                  |  |  |  |  |
| 7.3e-07                                      | 246               | Ak385402 EST90948 Thyroid Hc   |  |  |  |  |
| 8.3e-07                                      | 277               | AV379017 RC3-HT030-21099-0     |  |  |  |  |
| 8.3e-07                                      | 278               | Ak390276 QV-BT202-070599-188   |  |  |  |  |
| 9.3e-07                                      | 297               | Ak303751 EST16434 Aorta endod. |  |  |  |  |
| 9.3e-07                                      | 305               | F06018 HISCA0101 normalized    |  |  |  |  |
| 9.3e-07                                      | 306               | AV580695 RC4-LT001-010100-0    |  |  |  |  |
| 1.0e-06                                      | 335               | AV905258 QV-BT009-101198-075   |  |  |  |  |
| 1.0e-06                                      | 338               | AA322074 EST24653 Cerebellum   |  |  |  |  |
| 1.0e-06                                      | 338               | A1902529 QV-BT009-101198-074   |  |  |  |  |
| 1.1e-06                                      | 354               | AK304003 EST16883 Aorta endod. |  |  |  |  |
| 1.2e-06                                      | 383               | T499056 Y99b66.r1 Stratego     |  |  |  |  |
| 1.3e-06                                      | 399               | R19709 Yg3504.r1 Soares inf.   |  |  |  |  |
| 1.3e-06                                      | 417               | AA134475 zo1094.r1 Stratage    |  |  |  |  |
| 1.5e-06                                      | 461               | AI124771 am61h12.x1 Johnston   |  |  |  |  |
| 1.5e-06                                      | 469               | AW601576 QV3-BT0381-270100-0   |  |  |  |  |
| 1.6e-06                                      | 485               | R25913 yg56c07.r1 Soares inf.  |  |  |  |  |
| 1.6e-06                                      | 511               | AA218652 zg14d12.s1 stratage   |  |  |  |  |
| 1.6e-06                                      | 542               | AW602193 PM2-BT046-101000-0    |  |  |  |  |
| 2.0e-06                                      | 606               | AW673480 ba54e09.y NIH_MGC_    |  |  |  |  |
| 2.0e-06                                      | 611               | AA082558 zn25c07.r1 Stratage   |  |  |  |  |
| 2.2e-06                                      | 621               | AA091869 zn23g07.r1 Stratage   |  |  |  |  |
| 2.2e-06                                      | 652               | AI98095 pat-033.f.chn          |  |  |  |  |
| 2.6e-06                                      | 654               | AW362065 PM2-CT045-381099.y    |  |  |  |  |
| 2.6e-06                                      | 647               | AW581403 RCO-LT007-070100-0    |  |  |  |  |
| 2.7e-06                                      | 625               | AW607990 RCO-HT005-18100       |  |  |  |  |
| 2.8e-06                                      | 286               | AW608448 RCO-HT005-171000-0    |  |  |  |  |
| 2.5e-06                                      | 688               | AI299336 EST11904 Utensilium   |  |  |  |  |
| 2.5e-06                                      | 381               | AW364975 PM4-DT005.6-221299.y  |  |  |  |  |
| 1.9e-05                                      | 398               | AA297994 RC3-CN0013-030100-0   |  |  |  |  |
| 3.0e-05                                      | 530               | AL046001 DFKZP434016.r1 434    |  |  |  |  |
| 4.2e-05                                      | 289               | AA029792 zk07c09.r1 Soares_P   |  |  |  |  |
| 4.7e-05                                      | 440               | W13829 mb106.r1 Soares mou     |  |  |  |  |
| 5.8e-05                                      | 440               | AA034947 zk20a06.r1 Soares_P   |  |  |  |  |
| 6.0e-05                                      | 639               | AW608446 RCO-LT007-070100-0    |  |  |  |  |
| 2.2e-05                                      | 105               | AW577954                       |  |  |  |  |
| 0.0014                                       | 724               | W62339 y6b Human retina cDNA   |  |  |  |  |
| 0.0014                                       | 241               | AA869182 vq48e1.r1 Barstead    |  |  |  |  |
| 0.0018                                       | 304               | AA880590 yw92e08.r1 Stratego   |  |  |  |  |
| 0.003  | 389               | W13829 mb106.r1 Soares mou     |  |  |  |  |
| 0.0025                                       | 410               | AA074807 zm82c01.r1 Stratego   |  |  |  |  |
| 0.0026                                       | 425               | AA911456 yw96f07.r1 Soares_m   |  |  |  |  |
| 0.0026                                       | 425               | AI17077 D1r-f0 acu-f0.08.r1    |  |  |  |  |
| 0.0027                                       | 444               | AA462249 vf92c01.r1 Soares_m   |  |  |  |  |

|  |  |        |        |                            |          |                           |                       |
|--|--|--------|--------|----------------------------|----------|---------------------------|-----------------------|
| gb_est15:AA1045218   | -  | 73.00  | 217.33 | 0.0028                     | 459      | AI045218                  | UI-R-C1-Ju-g-11-0-U   |
| gb_est2:AA117593   | +  | 73.00  | 217.16 | 0.0029                     | 468      | AA137593                  | mq28e02.r1 Barstead   |
| gb_est3:AA121190   | +  | 73.00  | 216.97 | 0.0029                     | 478      | AW321190                  | uo22d05.y1 NCI CGAP   |
| gb_est3:AA174337   | +  | 73.00  | 216.51 | 0.0031                     | 504      | AA174337                  | m096511.r1 Stratagene |
| seq_name:  | gb_est6:AA385402   |        |        |                            |          |                           |                       |
| seq_documentation_block:   |  |        |        |                            |          |                           |                       |
| LOCUS  | AA385402   | 246 bp | mRNA   | CDNA 5'                    | EST      | 21-APR-1997               |                       |
| DEFINITION   | ESTR0408 Thyroid beta subunit, mRNA sequence.  |        |        | end similar to amyloid, A4 |          |                           |                       |
| ACCESSION  | AA385402   |        |        |                            |          |                           |                       |
| VERSION  | AA385402.1   |        |        |                            |          |                           |                       |
| KEYWORDS   | EST.   |        |        |                            |          |                           |                       |
| SOURCE   | human.   |        |        |                            |          |                           |                       |
| ORGANISM   | Homo sapiens   |        |        |                            |          |                           |                       |
| Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  |  |        |        |                            |          |                           |                       |
| Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.   |  |        |        |                            |          |                           |                       |
| REFERENCE  | 1 (bases 1 to 246)   |        |        |                            |          |                           |                       |
| AUTHORS  | Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blakie,J.A., Brandon,R.C., Man-Rai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghegan,N.S., Gloeck,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palangues,R.F., McDonald,I.A., Nguyen,D.T., Pelliottino,S.M., Phillips,C.A., Ryer,S.E., Scott,J.L., Sauder,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M., Coleman,T.A., Collins,E.J., Dinkin,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hui,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hung-jun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wang,J., Xu,G.L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C. |        |        |                            |          |                           |                       |
| TITLE  | Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence  |        |        |                            |          |                           |                       |
| JOURNAL  | Nature 377 (6547 suppl.), 3-174 (1995)   |        |        |                            |          |                           |                       |
| MEDIUM   | 12140200   |        |        |                            |          |                           |                       |
| COMMENT  | Other ESTs: THC172078<br>Contact: kerlavage, AR  |        |        |                            |          |                           |                       |
| Bioinformatics   | The Institute for Genomic Research<br>9712 Medical Center Drive, Rockville, MD 20850 USA   |        |        |                            |          |                           |                       |
| TELEPHONE  | 3018699056   |        |        |                            |          |                           |                       |
| FAX  | 3018699423   |        |        |                            |          |                           |                       |
| EMAIL  | arkerav@tigr.org   |        |        |                            |          |                           |                       |
| For clone availability, additional sequence and expression information related to this EST, Please check the TIGR Human Gene Index ( <a href="http://www.tigr.org/tdb/hg1/hgi.html">http://www.tigr.org/tdb/hg1/hgi.html</a> ) |  |        |        |                            |          |                           |                       |
| Seq primer: M13 Reverse  |  |        |        |                            |          |                           |                       |
| FEATURES   | Location/Qualifiers  |        |        |                            |          |                           |                       |
| Source   | 1. .246<br>/organism="Homo sapiens"<br>/db_xref="ArICC (inhost):189572"<br>/db_xref="taxon:9606"<br>/clone.lib="Thyroid"<br>/dev_stage="adult"<br>/note="Organ: thyroid gland; Vector: pBluescript SK-";<br>Site_1:EcorI; Site_2:XbaI"   |        |        |                            |          |                           |                       |
| BASE COUNT   | 70 a   | 48 c   | 68 g   | 58 t                       | 2 others |                           |                       |
| ORIGIN   |  |        |        |                            |          |                           |                       |
| alignment_scores:  | Quality: 92.00   |        |        |                            |          | Length: 16                |                       |
| ..   | Ratio: 5.750   |        |        |                            |          | Gaps: 0                   |                       |
| Percent Similarity: 100.000  |  |        |        |                            |          | Percent Identity: 100.000 |                       |
| alignment_block:   | AA385402   |        |        |                            |          |                           |                       |
| ..   | AA385402   |        |        |                            |          |                           |                       |

Align seg 1/1 to: AA385402 from: 1 to: 246  
 1 AspalaGlupheAegHISaspSerGlyTyrGluvalHisGlnLys 16  
 116 GATCGAAATTCCACATGACTAGGATGAGTCATCAAAA 163

seq\_name: qb\_est41:AW379017  
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 LOCUS AW379017 277 bp mRNA EST 04-FEB-2000  
 DEFINITION Homo sapiens cDNA, mRNA sequence.  
 ACCESSION AW379017  
 VERSION 1  
 KEYWORDS EST.  
 SOURCE Human.  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 278)  
 AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F. F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Sores, P., Brentani, R.R., Reis, I.F., de Souza, S.J. and Simpson, A.J.  
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7); 3491-3496 (2000).  
 COMMENT On Jan 19, 1998 this sequence version replaced gi:2284565.  
 CONTACT: Simpson A.J.G.  
 LABORATORY: Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, São Paulo-SP, Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
 (<http://www.ludwig.org.br/seq/gethtml.pl?ti=QV&t1=QV-BT202-188.html&t3=070599&st=1>)  
 Seq primer: puc 18 forward.

FEATURES source  
 1. .278  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="Br202"  
 /sex="female"  
 /dev\_stage="Adult"  
 /note="organ: breast; Vector: puc18; Site\_1: SmaI; Site\_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."  
 BASE COUNT 71 a 79 c 54 g 74 t  
 ORIGIN alignment\_scores:  
 Quality: 92.00 Length: 16  
 Ratio: 5.750 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000  
 alignment\_block:  
 US-09-155-076-2 x AW909276/rev ..  
 Align seg 1/1 to reverse of: AW909276 from: 1 to: 278  
 seq\_documentation\_block:  
 LOCUS AA303751 297 bp mRNA EST 18-APR-1997  
 DEFINITION EST 16434 Aorta endothelial cells, TNF alpha-treated Homo sapiens CDNA 5', end similar to amyloid, A4 beta subunit, mRNA sequence.  
 ACCESSION AA303751  
 VERSION 1  
 KEYWORDS EST.  
 SOURCE human.

Align seg 1/1 to reverse of: AW379017 from: 1 to: 277  
 1 AspalaGlupheAegHISaspSerGlyTyrGluvalHisGlnLys 16  
 220 GATGCCGAAATTCCACATGACTAGGATATAAGTTCATCATCAAAA 173

seq\_name: qb\_est27:AW379017  
 seq\_documentation\_block:  
 LOCUS AI909276 278 bp mRNA sapiens cDNA, mRNA sequence.  
 DEFINITION QV-BT202-070599-188 BT202 Homo sapiens cDNA, mRNA sequence.





Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A., Reseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

Nature 377 (6547 Suppl.), 3-174 (1995)

COMMENT MEDLINE

Contact: Kerlavage, AR Bioinformatics

The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850 USA

FAX: 3018690566  
Email: arkerlavatigr.org

For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)

seq primer: M13 Reverse.

FEATURES source

1. .338 /organism="Homo sapiens"  
/db\_xref="ANTCC (inhost):122569"  
/clone\_lib="taxon:9606"  
/db\_xref="taxon:9606"  
/clone.lib="Cerebellum II"  
/tissue\_type="cerebellum"  
/dev\_stage="adult"  
/note="Organ: brain; Vector: pBluescript SK-; Site\_1:  
EcoRI; Site\_2: XbaI"  
BASE COUNT 86 a 78 c 95 g 79 t  
ORIGIN

alignment\_scores:

|                     |         |           |         |
|---------------------|---------|-----------|---------|
| Quality:            | 92.00   | Length:   | 16      |
| Ratio:              | 5.750   | Gaps:     | 0       |
| Percent Similarity: | 100.000 | Identity: | 100.000 |

alignment\_block:  
US-09-155-076-2 x AA322074 ..

Align seg 1/1 to: AA322074 from: 1 to: 338

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisHisGlnLys 16  
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
21.0 GATCGAGATTCCACAGTCACTAGGATACTCATCAAAAAA 257

seq\_name: gb\_est26:AI902529

seq\_documentation\_block:  
LOCUS AI902529 338 bp mRNA EST 30-MAR-2000  
DEFINITION Homo sapiens cDNA, mRNA sequence.  
VERSION AI902529.1 GI:6492916  
KEYWORDS human, Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 338)  
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., de Oliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J., Simpson,A.J.

TITLE shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (?) 3491-3496 (2000)  
COMMENT On Oct 30, 1998 this sequence version replaced gi:3814489.  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, São Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2701001  
Email: [bsimpson@ludwig.org.br](mailto:bsimpson@ludwig.org.br)

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/seq/gethtml.pl?it1=QV&it2=QV-BT009-074.htm1&t3=10.119864=1>)

FEATURES source

1. .338 /organism="Homo sapiens"  
/clone.lib="Bro006"  
/db\_xref="taxon:9606"  
/sex="female"  
/dev\_stage="Adult"  
/note="Organ: breast; Vector: puc18; Site\_1: SmaI; Site\_2: SmaI; A mini-library was made by cloning products derived from GRESPES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the PUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 78 a 89 c 76 g  
ORIGIN

alignment\_scores:

|                     |         |                   |         |
|---------------------|---------|-------------------|---------|
| Quality:            | 92.00   | Length:           | 16      |
| Ratio:              | 5.750   | Gaps:             | 0       |
| Percent Similarity: | 100.000 | Percent Identity: | 100.000 |

alignment\_block:  
US-09-155-076-2 x AI902529/rev ..

Align seg 1/1 to reverse cf: AI902529 from: 1 to: 338

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisHisGlnLys 16  
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
315 GATCGAGATTCCACAGTCACTAGGATACTCATCAAAAAA 268

seq\_name: gb\_est5:AA304003

seq\_documentation\_block:  
LOCUS AA304003 354 bp mRNA EST 18-APR-1997  
DEFINITION EST16983 Aorta endothelial cells, TNF alpha-treated Homo sapiens cDNA 5' end similar to amyloid, A4 beta subunit, mRNA sequence.

ACCESSION AA304003  
VERSION AA304003.1 GI:1956491  
KEYWORDS EST  
ORGANISM Homo sapiens  
SOURCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 354)  
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fulndner,R.A., Bult,C.J., Lee,N.H., Kirane,K.G., Gooley,J.D., White,O., Sutten,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Barile,Hughes,J., Fine,L.D., Fitzgerald,L.M., FitzHugh,W.M., McDonald,L.A., Geoghegan,N.S., Glodek,A., Gnehm,C.I., Hana,M.C., Hechblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.J.C., Liu,J.-I., Marmaros,S.M., Merrick,J.W., Moreno-Palangues,R.F., Peilligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,T., Hudson,P., Kim,A.K., Razook,D.L., Kunsch,C., Hungjung,L.H., Melssen,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wang,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,N.A., Haseltine,W.A., Fields,C.,

**TITLE** Fraser, C.M. and Venter, J.C.  
**JOURNAL** Initial assessment of human gene diversity and expression patterns  
**MEDLINE** based upon 83 million nucleotides of cDNA sequence  
**COMMENT** Nature 377 (654 Suppl.), 3-174 (1995)  
**BASE COUNT** On Jan 17, 1998 this sequence version replaced g1:1900069.  
**ORGANISM** Other ESTs: THC172078  
**ORIGIN** Contact: Kerlavage, AR  
**FEATURES** Bioinformatics  
**SOURCE** The Institute for Genomic Research  
 9712 Medical Center Drive, Rockville, MD 20850 USA  
**SEQUENCE**  
 tel: 3018659056  
 fax: 3018659423  
 Email: arkerlavage@tigr.org  
 For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)  
**SEQ PRIMER:** M13 Reverse  
**LOCATION/QUALIFIERS**  
 1 - 354  
 /organism="Homo sapiens"  
 /db\_xref="AffCC (Inhost):115766"  
 /db\_xref="Taxon:1606"  
 /clone\_lib="Aorta endothelial cells, TNF alpha-treated"  
 /cell\_type="endothelial cell"  
 /dev\_stage="adult"  
 /note="Organ: aorta; Vector: pBluescript SK-; Site\_1:  
 ECORI; Site\_2: XbaI"  
 102 a 80 c 92 g 78 t 2 others  
**ALIGNMENT\_SCORES:**  
 Quality: 92.00 Length: 16  
 Ratio: 5.750 Gaps: 0  
 Percent Similarity: 100.000 Identity: 100.000  
**ALIGNMENT\_BLOCK:**  
 US-09-155-076-2 x AA304003 ..  
 Align seg 1/1 to: AA304003 from: 1 to: 354  
 1 AspAlaGluPheArgHisAspSerGlyTrpGluValHisHisGlnLys 16  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 10 GATGAGAAATTCCGACATGACTCGAGATTGAAGTTCATCATCAAAA 57  
**SEQ\_NAME:** gb\_est52:T49906  
**SEQ DOCUMENTATION\_BLOCK:**  
**LOCUS** T49906 mRNA EST 06-FEB-1995  
**DEFINITION** YN99b06.r1 Striatine Placenta (#9377225) Homo sapiens cDNA clone IMAGE:977975, similar to gb:X06989\_r1nai ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN PRECURSOR (HUMAN), mRNA sequence.  
**ACCESSION** T49906  
**VERSION** 1 GI:651766  
**EST.**  
**HUMAN.**  
**ORGANISM** Homo sapiens  
**EUKARYOTA;** Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
**MAMMALIA;** Eutheria; Primates; Catarrhini; Hominidae; Homo.  
**REFERENCE** 1 (bases 1 to 363)  
**AUTHORS** Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., Dubuque,T., Favell,M., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schallenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,M., and Marr,A.M.  
**TITLE** Generation and analysis of 280,000 human expressed sequence tags  
**JOURNAL** Genome Res. 6 (9), 807-828 (1996)  
**MEDLINE** 97044478  
**COMMENT** On Nov 2, 1998 this sequence version replaced g1:3828645.  
**CONTACT** Wilson RK

Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: estewatson.wustl.edu  
 Source: IMAGE Consortium, LInL  
 This clone is available royalty-free through LInL; contact  
 IMAGE Consortium (info@image.llnl.gov) for further info  
 Seq. Primer: M3RP1  
 High quality sequence stop: 384.  
**FEATURES**  
 Source  
 Location/qualifiers  
 1. .333  
 /organism="Homo sapiens"  
 /db\_xref="GDB:90676"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:69779"  
 /clone\_libr="Stratagene Placenta (#937225)"  
 /sex="male"  
 /lab\_host="SOIL cells (kanamycin resistant)"  
 /note="Organ: placenta; Vector: pBluecript SK  
 ECORI; Site 2: XbaI; Cloned unidirectionally."  
 Oligo dT. Caucasian. Average insert size: 1.2  
 XR Vector; -5' adaptor sequence: 5'- GATTCGGCA  
 adaptor sequence: 5' CTCGAATCTTTTTTTTTTTTTTTTT  
 BASE COUNT 113 a 81 c 103 g 86 t  
 ORIGIN  
 alignment\_scores:  
 Quality: 92.00 Length: 16  
 Ratio: 5.750 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000  
 alignment\_block:  
 US-09-155-076-2 x T49906 ..  
 Align seg 1/1 to: T49906 from: 1 to: 383  
 1 AspAlaGluPheArgHisAspSerGlyTrpGluValIleHisGlnLys 16  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 61 GATGCAGAAATTCCGACANGACTCAGGATAATGAGTTCAATCAAAA 108  
 seq\_name: gb\_est5i:R19709  
 seq\_documentation\_block:  
 LOCUS R19709 399 bp mRNA EST 17-AP-  
 DEFINITION Y93504.1 soares infant brain 1NIB Homo sapiens CDNA C  
 IMAGE:34389 5' similar to gb:X06999 final ALZHEIMER'S D1  
 AMYLOID A4 PROTEIN PRECURSOR (HUMAN); mRNA sequence.  
 ACCESSION R19709  
 VERSION R19709\_1 GI:774343  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute  
 Mammalia; Butherida; Primates; Catarrhini; Hominidae; Ho  
 REFERENCE 1 (bases 1 to 399)  
 AUTHORS Hillier,L., Clark,N., Dubouque,T., Elliston,K., Hawkins  
 Holman,M., Hultman,M., Kucabla,T., Le,M., Lennon,G., Mar  
 Parsons,J., Riftkin,L., Roblin,F., Soresi,M., Tan,F.,  
 Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P.,  
 Wilson,R.  
 TITLE The WashU-Merck EST Project  
 JOURNAL Unpublished (1995)  
 COMMENT On Jan 19, 1998 this sequence version replaced gi:22846  
 Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: estewatson.wustl.edu  
 Insert Size: 1369  
 High quality sequence stops: 214 Source: IMAGE Consortium

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 1369 Std Error: 0.00

Seq Primer: M13Rp1

Location/Qualifiers

1. .399

/organism="Homo sapiens"

/db\_xref="GDB:406736"

/db\_xref="taxon:19606"

/clone IMAGE:34389

/sex="Female"

/dev\_stage="73 days Post natal"

/lab\_host="DH10B (ampicillin resistant)"

/note="Organ: whole brain; Vector: Lamid BA; Site\_1: Not

I; Site\_2: Hind III; 1st strand cDNA was primed with a Not

I - Oligo(dT) Primer [5'

AACTGGAGAATTCGGCCAGAAATTCTTTTTTTTTTTTTTTT 3'];

double-stranded cDNA was ligated to Hind III adaptors

(Pharmacia), digested with Not I and directionally cloned

into the Not I and Hind III sites of the Lamid BA vector.

Library went through one round of normalization. Library

constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 104 a 85 C 106 g 94 t 10 Others

ORIGIN

alignment\_scores:

Quality: 92.00

Length: 16

Ratio: 5.750

Gaps: 0

Percent Identity: 100.000

alignment\_block:

US-09-155-076-2 x R19709 ..

Align seg 1/1 to: R19709 from: 1 to: 399

1 AspAlaGluPheArgHisAspSerGlyTyroGluValHisHisGlnLys 16

||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

219 GATGCCAGAAATTCCGACATGACTCAAGGTATGAAGTTCATCATCAAAA 266

seq\_name: qb\_est2:AA134479

seq\_documentation\_block:

LOCUS AA134479 417 bp mRNA EST

DEFINITION z010904.r1 Stratagene neuroepithelium NT2RMI 937234 Homo sapiens

cDNA clone IMAGE:567318 5' similar to 9b:x06983\_rna1 ALZHEIMER S DISEASE

ACCESSION AA134479

VERSION AA134479.1 GI:1692245

EST.

SOURCE human

ORGANISM Homo sapiens

Mammalia: Eutheria: Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 417)

REFERENCE AUTHORS

Chissoe, S., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,

Hawkins, M., Dietrich, N., Dubuque, T., Favell, A., Gish, W.,

Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,

Morris, B., Morris, J., Parsons, J., Prange, C., Rifkin, L.,

Rohlfing, T., Scheellenberg, K., Soares, M.B., Tan, F., Thierry-Deg, J.,

Trevisakis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.,

and Marra, M.

Title

JOURNAL Genome Res.

COMMENT MEDLINE

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

WARNING: There is evidence that suggests that the 384-well parent plate of this clone contains both human and mouse derived clones. Thus, the origin of this clone is uncertain. This caution should be kept in mind should you use this clone.

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES source /clone IMAGE:34389

/clone lib="Soares Infant brain INIB"

/sex="Female"

/dev\_stage="73 days Post natal"

/lab\_host="DH10B (ampicillin resistant)"

/note="Organ: whole brain; Vector: Lamid BA; Site\_1: Not

I; Site\_2: Hind III; 1st strand cDNA was primed with a Not

I - Oligo(dT) Primer [5'

AACTGGAGAATTCGGCCAGAAATTCTTTTTTTTTTTTTTTT 3'];

double-stranded cDNA was ligated to Hind III adaptors

(Pharmacia), digested with Not I and directionally cloned

into the Not I and Hind III sites of the Lamid BA vector.

Library went through one round of normalization. Library

constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 110 a 93 C 117 g 95 t 2 Others

ORIGIN

alignment\_scores:

Quality: 92.00

Length: 16

Ratio: 5.750

Gaps: 0

Percent Identity: 100.000

alignment\_block:

US-09-155-076-2 x AA134479 ..

Align seg 1/1 to: AA134479 from: 1 to: 417

1 AspAlaGluPheArgHisAspSerGlyTyroGluValHisHisGlnLys 16

||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

159 GATCCAGAAATTCCGACATGACTCAAGGTATGAAGTTCATCATCAAAA 206

seq\_name: qb\_est1:AA124771

seq\_documentation\_block:

LOCUS AA124771 461 bp mRNA EST

DEFINITION am61h12.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:154013 3' similar to gb:X06989\_rna1 ALZHEIMER S DISEASE

AMYLOID A4 PROTEIN PRECURSOR (HUMAN); mRNA sequence,

ACCESSION AA124771

VERSION AA124771/1 GI:3593285

KEYWORDS EST.

SOURCE human

ORGANISM Homo sapiens

Mammalia: Eutheria: Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 461)

REFERENCE AUTHORS

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,

Krizzman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,

Martin, J., Moore, B., Scheellenberg, K., Steptoe, M., Tan, F.,

Theising, B., White, Y., Wylie, T., Waterston, R., and Wilson, R.

Title

JOURNAL Unpublished (1997)

COMMENT Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -40m13 fwd. ET from Amersham  
 High quality sequence stop: 423.

|            |   |
|------------|---|
| FEATURES   | Location/Qualifiers   |
| source     | 1..461  |
|            | /organism="Homo sapiens"  |
|            | /db_xref="Taxon:9606"   |
|            | /clone="IMAGE:1540105"  |
|            | /clone_lib="Johnston frontal cortex"  |
|            | /sex="male"   |
|            | /tissue_type="pooled frontal lobe"  |
|            | /dev_stage="adult"  |
|            | /lab_host="SOLR (kanamycin resistant)"  |
|            | /note="Organ: brain; Vector: Bluescript SK-; site_1:<br>ECORI; Stanley Neuropathology Consortium<br>(www.stanleylab.org) brains S-58, S-65, S-67, S-78.<br>Random + oligo-dT primed into EcoRI site of ZAP II Vector.<br>Mass excised. Avg insert length 1.9kb. Cuscom library<br>provided by Dr. Nancy Johnston [(410) 614-3918,<br>njl@weichlink.welch.jhu.edu]." |
| BASE COUNT | 101 a 123 c 110 g 126 t   |
| ORIGIN     | 1 others  |

alignment\_scores:

|                             |                           |
|-----------------------------|---------------------------|
| Quality: 92.00              | Length: 16                |
| Ratio: 5.750                | Gaps: 0                   |
| Percent Similarity: 100.000 | Percent Identity: 100.000 |

align seg 1/1 to reverse of: AII24771 from: 1 to: 461

alignment\_scores:

|                             |                           |
|-----------------------------|---------------------------|
| Quality: 92.00              | Length: 16                |
| Ratio: 5.750                | Gaps: 0                   |
| Percent Similarity: 100.000 | Percent Identity: 100.000 |

align seg 1/1 to reverse of: AII24771/rev ..

Align seg 1/1 to reverse of: AII24771 from: 1 to: 461

1 ASPAlaGluPheArgHisASPSerGlyTyrGluValHisGlnLys 16  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 314 GATGCGAAATTCCGACATGACTCAGGATAATGAAGTTCATCATCAAAA 267

seq\_name: gb\_est44:AW601576

seq.documentation\_block:

|            |   |        |              |       |                |
|------------|---|--------|--------------|-------|----------------|
| LOCUS      | AW601576  | 469 bp | mRNA         | EST   | 23-NAR-2000    |
| DEFINITION | QV3-BT0381-270100-073-f06   | BT0381 | Homo sapiens | cDNA, | mRNA sequence. |
| ACCESSION  | AW601576  |        |              |       |                |
| VERSION    | AW601576.1  |        |              |       |                |
| KEYWORDS   | EST.  |        |              |       |                |
| SOURCE     | human.  |        |              |       |                |
| ORGANISM   | Homo sapiens  |        |              |       |                |
|            | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |        |              |       |                |
|            | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.        |        |              |       |                |

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

seq.documentation\_block:

|            |   |        |              |       |                |
|------------|---|--------|--------------|-------|----------------|
| LOCUS      | AW601576  | 469 bp | mRNA         | EST   | 23-NAR-2000    |
| DEFINITION | QV3-BT0381-270100-073-f06   | BT0381 | Homo sapiens | cDNA, | mRNA sequence. |
| ACCESSION  | AW601576  |        |              |       |                |
| VERSION    | AW601576.1  |        |              |       |                |
| KEYWORDS   | EST.  |        |              |       |                |
| SOURCE     | human.  |        |              |       |                |
| ORGANISM   | Homo sapiens  |        |              |       |                |
|            | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |        |              |       |                |
|            | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.        |        |              |       |                |

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil

Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
 (<http://www.ludwig.org.br/scripts/gethtm12.pl?tl=QV3&t2=QV3-BT0381-270100-073-f06&t4=1>)

Seq primer: Puc 18 forward

High quality sequence start: 111  
 High quality sequence stop: 469.

FEATURES

source

/organism="Homo sapiens"  
 /db\_xref="taxon:9606"



(ISIS-) ISIS INNOVATION LTD.  
 PI Greenfield SA, Vaux DJ;  
 DR WPI: 97-189626/45;  
 PT Peptide(s) from acetylcholine esterase which open calcium channels - used for treating disorders of the central nervous system, cancer and stroke.  
 PT and stroke.  
 PT  
 PS Claim 3; Page 20; 27pp; English.  
 CC This 16mer Peptide is present in a region of the beta-amyloid precursor polypeptide. This region lies at the amino acid terminus of the 42 residue Peptide which accumulates in Alzheimer's disease. The 16-mer has at least 70% homology with the beta-amyloid precursor. This peptide is known to act alone or in synergism with a fragment of acetylcholinesterase (W35340-W35443) to contribute to neuronal degeneration. Compounds that inhibit the biological activity of the novel peptides, and antibodies, can be used to control cytoplasmic calcium ion currents *in vivo*, and are useful for treating disorders of the central nervous system (e.g. Parkinson's and Alzheimer's diseases), stroke and cancer.  
 Sequence 16 AA;

Query Match 100.0%; Score 16; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 5.6e-12; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQK 16  
 Db 1 DAEFRHDSGYEVHHQK 16

RESULT 3  
 W08361 standard; peptide; 21 AA.  
 AC W08361;  
 DT 05-SEP-1997 (first entry)  
 DE Beta-secretase substrate #3.  
 KW Beta-secretase site; beta amyloid precursor protein; APP; beta-secretase; inhibitor; Alzheimer's disease.  
 PR alpha-secretase; proteolytic cleavage; inhibitor; Alzheimer's disease.  
 OS Synthetic.  
 PN W0964085-A2.  
 PD 19-DEC-1996.  
 PF 07-JUN-1995; U09985  
 PR 07-JUN-1995; US 4 98152.  
 PR 07-JUN-1995; US 4 90198.

(ATHE-) ATHERNA NEUROSCIENCES INC. Anderson JE, Chrysler SNS, Jacobson-croak KL, Keim PS;  
 PI McCortney LC, Sinha S, Tan H;  
 DR WPI: 97-052304/05;  
 PT Beta-secretase which specifically cleaves beta-amyloid precursor protein - useful to screen for inhibitors useful in treatment of Alzheimer's disease.  
 PS Disclosure; Page 45; 92pp; English.  
 CC W08359 W08362 represent substrates for the enzyme of the invention. The enzyme of the invention is beta-secretase, and specifically cleaves beta-APP beta-amyloid precursor protein (beta-APP). Normal Processing of beta-APP is thought to occur via cleavage between residues 16 and 17 of the beta-amyloid peptide region by an alpha-secretase. Pathogenic processing is thought to occur by beta-secretase cleavage of beta-APP.  
 CC Beta-secretase activity can be detected and measured using a method of the invention, which detects at least one of the beta-secretase cleavage products formed on cleavage. The method can be used to determine whether a test substance inhibits proteolytic cleavage, by beta-secretase, of beta-APP. Compounds effective to at least partially inhibit beta-secretase activity can be used to inhibit cleavage of beta-APP in cells or mammalian hosts. Isolation and purification of beta-secretase will permit chemical modelling of a critical event in the pathology of Alzheimer's disease.  
 Sequence 21 AA;

Query Match 100.0%; Score 16; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 7.1e-12; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQK 16  
 Db 1 DAEFRHDSGYEVHHQK 16

RESULT 5  
 P90381 standard; protein; 28 AA.  
 AC P90381;  
 DT 1-NOV-1989 (first entry)  
 DE Synthetic; A4 amyloid polypeptide; Alzheimer's disease;  
 KW Immunassays; antibodies.  
 OS W08906242-A.  
 PD 13-JUL-1989.  
 PF 08-OCT-1987; US-105751.  
 PR (MCLE) McLean Hospital Corp; (UYRO) University of Rochester.  
 PA Majocha R, Marotta CA, Zain S;  
 PI DR WPI; 89-22051/30.  
 PT Antibodies to A4 amyloid polypeptide used in immunoassays and for imaging of A4 amyloid.  
 PT in Alzheimer's disease patients.  
 PS Claim 1; page 27; 30pp; English.  
 CC Synthetic A4 amyloid polypeptide (see also P90382, P90383). Used as immunogen, (un)coupled, or to produce antibodies. Used in immunoassays and for imaging of A4 amyloid in Alzheimer's disease.  
 CC Sequence 28 AA;

Query Match 100.0%; Score 16; DB 1; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 7.1e-12; Indels 0; Gaps 0;

Query Match 100.0%; Score 16; DB 1; Length 28;

Qy 1 DAEFRHDSGYEVHHQK 16  
 Db 6 DAEFRHDSGYEVHHQK 21

RESULT 4  
 R07753 standard; protein; 22 AA.  
 ID R07753; AC R07753;  
 DT 22-FEB-1991 (first entry)  
 DE Bta-amyloid protein, SCYAP2.  
 KW Monoclonal antibody SV17-6E10; Down's syndrome; Alzheimer's disease; beta amyloid precursor; amyloid plaques.  
 OS Synthetic.  
 PN W0902871-A.  
 PD 13-APR-1980; U02003.  
 PR 14-APR-1989; US-333983.  
 PA (REME) Rus Found MENTAL HY.  
 PI Kim RS, Wisniewski HM, Wen GY, Chen CMJ, Sapienza VJ;  
 DR WPI; 90-348474/46.  
 PT Cerebrovascular amyloid protein-specific monoclonal antibody SV17-6E10 - for immunoassay of peptide whose levels are raised in Down's syndrome or Alzheimer's disease patients.  
 Example 4; page 11; 24pp; English.  
 This Peptide is used in a "Double Ab Sandwich Immunoassay" to detect beta-amyloid protein. SV17-6E10 MAb (capture Ab) is used to coat microtitre plate wells. The plate is then washed (distilled water), coated with PBS(TGB) and this (SCYAP2) protein is added. The plate is washed and a 2nd Ab (detection Ab), Mab 4G8-CC This double Ab sandwich ELISA test is a highly sensitive and accurate detection system for the beta-amyloid protein.  
 CC See also R07752.  
 SQ Sequence 22 AA;

Query Match 100.0%; Score 16; DB 1; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-12; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQK 16  
 Db 1 DAEFRHDSGYEVHHQK 16

RESULT 5  
 P90381 standard; protein; 28 AA.  
 AC P90381;  
 DT 1-NOV-1989 (first entry)  
 DE Synthetic; A4 amyloid polypeptide; Alzheimer's disease;  
 KW Immunassays; antibodies.  
 OS W08906242-A.  
 PD 13-JUL-1989.  
 PF 08-OCT-1987; US-105751.  
 PR (MCLE) McLean Hospital Corp; (UYRO) University of Rochester.  
 PA Majocha R, Marotta CA, Zain S;  
 PI DR WPI; 89-22051/30.  
 PT Antibodies to A4 amyloid polypeptide used in immunoassays and for imaging of A4 amyloid.  
 PT in Alzheimer's disease patients.  
 PS Claim 1; page 27; 30pp; English.  
 CC Synthetic A4 amyloid polypeptide (see also P90382, P90383). Used as immunogen, (un)coupled, or to produce antibodies. Used in immunoassays and for imaging of A4 amyloid in Alzheimer's disease.  
 CC Sequence 28 AA;

CC beta-amyloid and its derivatives for diagnosis of Alzheimer's  
 CC disease.  
 SQ sequence 28 AA;

|                       |        |            |       |            |
|-----------------------|--------|------------|-------|------------|
| Query Match           | 100.0% | Score 16;  | DB 1; | Length 28; |
| Best Local Similarity | 100.0% | Pred. No.  | 9     | $2e-12$    |
| Matches               | 16;    | Mismatches | 0;    | Indels 0;  |
| Conservative          |        |            |       |            |

Qy    1 DAEFRHDSGYEVHKQ 16  
       | | | | | | | | | | | | | | | | | |  
       1 DAEFRHDSGYEVHKQ 16

Db    1 DAEFRHDSGYEVHKQ 16

RESULT 8  
 W01413  
 ID W0113 standard; protein; 28 AA.  
 AC W0113;  
 DT 20-TAN-1997 (first entry)  
 DE Beta/A4 -amyloid peptide; residues 1-28.  
 KW Beta/A4 -amyloid peptide; tissue plasminogen activator;  
 Alzheimer's disease; stimulation; investigation; pathogenesis;  
 hereditary cerebral haemorrhage with amyloidosis-Dutch type;  
 control; cerebral amyloid angiopathy; cerebral; haemorrhage;  
 KW hemorrhage.  
 OS Homo sapiens.  
 PN WO9515793-A1.  
 PD 30-MAY-1996.  
 PF 22-NOV-1995; U15007.  
 PR 22-NOV-1994; US-3-47144.  
 PA (CRUFT ) UNIV RUTGERS STATE NEW JERSEY.  
 PI Anderson S;  
 PI WPI; 96-268332/27.  
 DR

| RESULT |                    |                       |       |              |            |        |
|--------|--------------------|-----------------------|-------|--------------|------------|--------|
| Query  | Match              | Best Local Similarity | Score | DB           | Length     | Gaps   |
| QY     | 1 DAEFRHDSGYEVHHQK | 100.0%                | 16    | 1            | 28         |        |
| Ddb    | 1 DAEFRHDSGYEVHHQK | 100.0%                | 16    | 0            | 28         | 0;     |
|        |                    | Matches               | 16;   | Conservative | Mismatches | Indels |
|        |                    |                       |       |              | 0;         |        |
|        |                    |                       |       |              |            | Gaps   |

prevention and treatment of vascular damage caused by amyloid deposits, partic. in haemorrhaging and Alzheimer's disease Example 1; Fig 1; 5pp; English.

To investigate the effects of beta-amyloid peptide (BAP) on tissue plasminogen activator (t-PA) 3 synthetic peptides were made. One peptide contained 42 amino acids and correspond. to the full length BAP (R95248). The other 2 peptides (R95249 and 50) contained the 28 N-terminal residues of the BAP found in Alzheimer's disease and hereditary cerebral haemorrhage with amyloidosis-Dutch type (HCHWA-D), respectively. In an assay to determine the effect of the peptides on t-PA activation, each peptide (R95248, 49 and 50) gave 1st order rate constant of activation ( $k_{app}$ ) values of 13.4, 13.9 and 14.5, respectively, compared to 1.7 and 7.8 for fibrinogen controls. The results demonstrate that the BAP is able to stimulate t-PA activity *in vitro*, which is significant in that it provides a means for investigating and controlling the pathogenesis of Alzheimer's disease, HCHWA-D and cerebral angiopathy related cerebral haemorrhage.

PD 04-AUG-1994.  
 PF 24-JAN-1994; J00089.  
 PF 25-JAN-1993; JP-010132.  
 PR 05-FEB-1993; JP-019035.  
 PR 16-NOV-1993; JP-286985.  
 PR 28-DEC-1993; JP-334773.

(TAKE ) TAKEDA CHEM IND LTD.  
 PA Kitada C., Odaka A., Suzuki N;  
 PA WPI; 94-264110/32.  
 PT Antibodies recognising specific parts of beta-amyloid - can be  
 used for diagnosis of diseases implicating beta-amyloid, such as,  
 Alzheimer's disease  
 Claim 7; Page 84; 116pp; Japanese.  
 Antibodies which recognise specifically subfragments of the beta-amyloid  
 protein are claimed. Specifically, the antibodies (which are pref.  
 monoclonal) recognise residues 1-16 and/or 1-28 from the N-terminal  
 portion of beta-amyloid or they recognise residues 25-35 or 35-43  
 from the C-terminal portion. The antibodies are monoclonal.

| Query Match              |   |                              |        |                   |  |  |
|--------------------------|---|------------------------------|--------|-------------------|--|--|
| Best Local Similarity    |   | Score 16; Pred. No. 9.2e-12; |        | DB 1; Length 28;  |  |  |
| Matches 16; Conservative |   | 0; Mismatches 0;             |        | Indels 0; Gaps 0; |  |  |
| Qy                       | 1   | DAEFRHDSGYEVHHQK             | 16     |                   |  |  |
|                          |   |                              |        |                   |  |  |
| Db                       | 1   | DAEFRHDSGYEVHHQK             | 16     |                   |  |  |
| RESULT 9                 |   |                              |        |                   |  |  |
| W01414                   |   |                              |        |                   |  |  |
| ID                       | W01414 standard;  | Protein:                     | 28 AA. |                   |  |  |
| AC                       | W01414;   |                              |        |                   |  |  |
| DT                       | 20-JAN-1997   | (first entry)                |        |                   |  |  |
| DE                       | Beta/A4-an Amyloid Peptide  | residues 1-28                | Dutch. |                   |  |  |
| KW                       | Beta/A4-an Amyloid Peptide; tissue plasminogen activator; Dutch; Alzheimer's disease; stimulation; investigation; pathogenesis; |                              |        |                   |  |  |
| KW                       |   |                              |        |                   |  |  |

KW control; cerebral amyloid angiopathy; cerebral; haemorrhage;  
 KW hemorrhage.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT misc\_difference 22  
 /note= "wild type Glu subst. with Gln"  
 FT  
 PN W09615799-A1.  
 PD 30-MAY-1996.  
 PR 22-NOV-1995; US-15007.  
 PR (RUTF) UNIV RUTGERS STATE NEW JERSEY.  
 PA  
 PI Anderson S.  
 PR  
 WP: 96-268332/27.  
 PR use of agents which bind beta-amyloid peptide - for diagnosis,  
 PT prevention and treatment of vascular damage caused by amyloid  
 PT deposits, partic. in haemorrhaging and Alzheimer's disease  
 PS Example 1; Fig 1; 52pp; English.  
 CC To investigate the effects of beta-amyloid peptide (BAP) on  
 CC tissue plasminogen activator (t-PA) 3 synthetic peptides were used.  
 CC One peptide contained 42 amino acids and corresp. to the full  
 CC length BAP (R95249). The other 2 peptides (R95249 and 50) contained  
 CC the 28 N-terminal residues of the BAP found in Alzheimer's disease  
 CC and hereditary cerebral haemorrhage with amyloidosis-Dutch type  
 CC (HCHWA-D), respectively. In an assay to determine the effect of  
 CC the peptides on t-PA activation each peptide (R95248, 49 and 50)  
 CC gave 1st order rate constant of activation (k<sub>app</sub>) values of  
 CC 13.4, 13.9 and 14.5, respectively, compared to 1.7 and 7.8 for nill  
 CC and fibrinogen controls. The results demonstrate that the BAP are  
 CC able to stimulate t-PA activity in vitro, which is significant in  
 CC that it provides a means for investigating and controlling the  
 CC pathogenesis of Alzheimer's disease, HCHWA-D and cerebral amyloid  
 CC angiopathy related cerebral haemorrhage.  
 SQ Sequence 28 AA;

Query Match 100.0%; Score 16; DB 1; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-12;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DAEFRHDSGYEVHKQ 16  
 ||||||| ||||| |||||  
 Db 1 DAEFRHDSGYEVHKQ 16

RESULT 10  
 R64170 standard; peptide; 28 AA.  
 ID R64170  
 AC R64170;  
 DT 03-AUG-1995 (first entry)  
 DE A4-O(1-28) a partial beta amyloid peptide.  
 KW beta amyloid protein; mutant; variant; detection; amyloid deposition;  
 KW diagnosis; amyloidosis associated disease; Alzheimer's disease;  
 KW Down's syndrome; A4-O(1-28).  
 OS Synthetic  
 PR  
 PN W0928412-A.  
 PD 08-DEC-1994.  
 PR 27-MAY-1993; US-150809.  
 PR (MIRI-) MIRIAM HOSPITAL.  
 PI Majocha RE, Marotta CA;  
 DR WPI:95-023013/03.  
 PT Amyloid binding composition comprising labelled amyloid protein  
 PT and carrier - useful for *in vivo* imaging of amyloid deposits, for  
 PT diagnosing Alzheimer's disease and Down's Syndrome.  
 PS Example 1; Page 23; 52pp; English.

CC R64172, the A4-B(1-28) polypeptide is deriv. from vascular amyloid of the  
 CC brain and a Down Syndrome brain. Three of the  
 CC amino acids are different from the A4-O(1-28) peptide shown in R64170.  
 CC A4-O has strong aggregation properties, and binds to itself strongly. It  
 CC is used to obtain and select beta amyloid proteins that can be used for  
 CC *in vivo* imaging of amyloid deposits and hence diagnosis of an  
 CC amyloidosis-associated disease, such as AD or Down's syndrome. R64165  
 CC shows the generic sequence of the amyloid protein for generation of  
 CC variants.  
 SQ Sequence 28 AA;

Query Match 100.0%; Score 16; DB 1; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-12;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DAEFRHDSGYEVHKQ 16  
 ||||||| ||||| |||||  
 Db 1 DAEFRHDSGYEVHKQ 16

RESULT 12  
 W81467 standard; peptide; 28 AA.  
 ID W81467  
 AC W81467;  
 DT 28-JUN-1999 (first entry)  
 DE Synthetic amyloid beta (Abeta) peptide 2 (residues 1-28).  
 MAJOCHA RE; Marotta CA;  
 DR WPI:95-023013/03.  
 PT Amyloid binding composition comprising labelled amyloid protein  
 PT and carrier - useful for *in vivo* imaging of amyloid deposits, for  
 PT diagnosing Alzheimer's disease and Down's Syndrome.  
 PS Example 1; Page 23; 52pp; English.  
 CC R64170, the A4-O(1-28) polypeptide is the first 28 amino acids of the  
 CC 42 kd peptide deriv. from senile plaque cores of an AD Alzheimer's  
 CC disease brain, known as amyloid. A4-O has strong aggregation  
 CC properties, and binds to itself strongly. This peptide is used to obtain  
 CC and select beta amyloid proteins that can be used for *in vivo* imaging  
 CC of amyloid deposits and hence diagnosis of an amyloidosis associated  
 CC disease, such as AD or Down's syndrome. R64165 shows the generic sequence  
 CC of the amyloid protein for generation of variants.

Claim 5; Columns 9-10; 14pp; English.

CC Sequences W81466 to W81476 represent synthetic amyloid beta (Abeta) peptides. The invention provides a process for treating a synthetic Abeta peptide that comprises dissolving the peptide in a deoxygenated solvent selected from trifluoroethanol, hexafluorocyclohexane, dimethylsulphoxide, morpholinopropenesulphonic acid, dimethylformamide and acetonitrile to a concentration of 0.01-10 mg/ml, incubating the solution at 20-65 deg. C for 0.5-4 hour, and removing the solvent by evaporative deposition, in 5-10 minutes. Synthetic amyloid beta peptides are useful as research tools for studying neurotoxicity resulting from Abeta peptide-enhanced free-radical production. The treatment increases the activity of the synthetic Abeta peptides in tests to determine free-radical generating capacity and glutamine synthetase inactivation. Sequence 28 AA;

Query Match 100.0%; Score 16; DB 1; Length 28;  
Best Local Similarity 100.0%; Pred. No. 9.2e-12; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Matches 16; OS

Qy 1 DAEFRHDSGYEVHHQK 16  
Db 1 DAEFRHDSGYEVHHQK 16

RESULT 13  
ID W81468 standard; peptide; 30 AA.  
W81468  
AC W81468;  
DT 28-JAN-1999 (first entry)  
DE Synthetic amyloid beta (Abeta) Peptide 3 (residues 1-30).  
Anyloid beta; Abeta; deoxygenated solvent; evaporative deposition;  
KW research; neurotoxicity; free-radical; glutamine synthetase.  
OS Synthetic.

PN US5840838-A.  
PD 24-NOV-1998.  
PF 29-FEB-1996; 609090.  
PR 29-FEB-1996; US-609090.  
(KENT ) UNIV KENTUCKY RES FOUND.  
PI Aksenenov M, Butterfield DA, Carney JM, Hensley K;  
DR WPI; 99-034120/03.  
PT Process for treating synthetic amyloid beta peptides - by organic solvent treatment, useful for studying neurotoxicity

PS Claim 5: Columns 9-10: 14pp; English.  
Claim 5: Columns 9-10: 14pp; English.  
Sequences W81466 to W81476 represent synthetic amyloid beta (Abeta) peptides. The invention provides a process for treating a synthetic Abeta peptide that comprises dissolving the peptide in a deoxygenated solvent selected from trifluoroethanol, hexafluorocyclohexane, dimethylsulphoxide, morpholinopropenesulphonic acid, dimethylformamide and acetonitrile to a concentration of 0.01-10 mg/ml, incubating the solution at 20-65 deg. C for 0.5-4 hour, and removing the solvent by evaporative deposition, in 5-10 minutes. Synthetic amyloid beta peptides are useful as research tools for studying neurotoxicity resulting from Abeta peptide-enhanced free-radical production. The treatment increases the activity of the synthetic Abeta peptides in tests to determine free-radical generating capacity and glutamine synthetase inactivation. Sequence 30 AA;

Query Match 100.0%; Score 16; DB 1; Length 30;  
Best Local Similarity 100.0%; Pred. No. 9.8e-12; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Matches 16; OS

Qy 1 DAEFRHDSGYEVHHQK 16  
Db 1 DAEFRHDSGYEVHHQK 16

RESULT 14  
ID W08359 standard; peptide; 33 AA.  
W08359  
AC W08359;  
DT 05-SEP-1997 (first entry)  
DE Beta-secretase substrate #1.

Beta-cleavage site; beta amyloid precursor protein; APP; beta-secretase; alpha-secretase; proteolytic cleavage; inhibitor; Alzheimer's disease.  
KW KW  
CC OS  
CC Synthetic.  
CC PN W09640885-A2.  
CC PD 19-DEC-1996  
CC PP 07-JUN-1996; U09985.  
CC PR 07-JUN-1995; US-485152.  
CC PR 07-JUN-1995; US-480498.  
(ATHE ) ATHENA NEUROSCIENCES INC  
PA Anderson JP, Chrysler SMS, Jacobson croak KL, Keim PS;  
PI McConlogue LC, Sinha S, Tan H;  
WP; 97-052304/05.  
PT Beta-secretase which specifically cleaves beta-amyloid precursor protein - useful to screen for inhibitors useful in treatment of PT Alzheimer's disease.  
PT Disclosure; Page 44; 92pp; English.  
PS W08359-W08362 represent substrates for the enzyme of the invention. The CC enzyme of the invention is beta-secretase, and specifically cleaves beta-amyloid precursor protein (beta-APP). Normal processing of beta-APP CC is thought to occur via cleavage between residues 16 and 17 of the beta-amyloid peptide region by an alpha-secretase. Pathogenic processing CC is thought to occur by beta-secretase cleavage of beta-APP. Beta-secretase activity can be detected and measured using a method of CC products formed on cleavage. The method can be used to determine whether CC a test substance inhibits proteolytic cleavage, by beta-secretase, of beta-APP. Compounds effective to at least partially inhibit CC beta-secretase activity can be used to inhibit cleavage of beta-APP in CC cells or mammalian hosts. Isolation and purification of beta-secretase CC will permit chemical modelling of a critical event in the pathology of CC Alzheimer's disease.  
SQ Sequence 33 AA;

Query Match 100.0%; Score 16; DB 1; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.1e-11;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
PS 1 DAEFRHDSGYEVHHQK 16  
Db 18 DAEFRHDSGYEVHHQK 33

RESULT 15  
W81469  
ID W81469 standard; peptide; 33 AA.  
AC W81469;  
DT 28-JAN-1999 (first entry)  
DE Synthetic amyloid beta (Abeta) peptide 4 (residues 1-33).  
Anyloid beta; Abeta; deoxygenated solvent; evaporative deposition;  
KW research; neurotoxicity; free-radical; glutamine synthetase.  
OS Synthetic.

PN US5840838-A.  
PD 24-NOV-1998.  
DR WPI; 99-034120/03.  
PT Process for treating synthetic amyloid beta peptides - by organic solvent treatment, useful for studying neurotoxicity

PS Claim 5; Columns 9-10: 14pp; English.  
Sequences W81466 to W81476 represent synthetic amyloid beta (Abeta) peptides. The invention provides a process for treating a synthetic Abeta peptide that comprises dissolving the peptide in a deoxygenated solvent selected from trifluoroethanol, hexafluorocyclohexane, dimethylsulphoxide, morpholinopropenesulphonic acid, dimethylformamide and acetonitrile to a concentration of 0.01-10 mg/ml, incubating the solution at 20-65 deg. C for 0.5-4 hour, and removing the solvent by evaporative deposition, in 5-10 minutes. Synthetic amyloid beta peptides are useful as research tools for studying neurotoxicity resulting from Abeta peptide-enhanced free-radical production. The treatment increases the activity of the synthetic Abeta peptides in tests to determine free-radical generating capacity and glutamine synthetase inactivation. Sequence 30 AA;

Query Match 100.0%; Score 16; DB 1; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.1e-11;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
PS 1 DAEFRHDSGYEVHHQK 16  
Db 18 DAEFRHDSGYEVHHQK 33

RESULT 15  
W81466 to W81476; English.  
(KENT ) UNIV KENTUCKY RES FOUND.  
ID W81469 standard; peptide; 33 AA.  
AC W81469;  
DT 28-FEB-1996; 609090.  
PR 29-FEB-1996; 609090.  
PA (KENT ) UNIV KENTUCKY RES FOUND.  
PI Aksenenov M, Butterfield DA, Carney JM, Hensley K;  
DR WPI; 99-034120/03.  
PT Process for treating synthetic amyloid beta peptides - by organic solvent treatment, useful for studying neurotoxicity

PS Claim 5; Columns 9-10: 14pp; English.  
Sequences W81466 to W81476 represent synthetic amyloid beta (Abeta) peptides. The invention provides a process for treating a synthetic Abeta peptide that comprises dissolving the peptide in a deoxygenated solvent selected from trifluoroethanol, hexafluorocyclohexane, dimethylsulphoxide, morpholinopropenesulphonic acid, dimethylformamide and acetonitrile to a concentration of 0.01-10 mg/ml, incubating the solution at 20-65 deg. C for 0.5-4 hour, and removing the solvent by evaporative deposition, in 5-10 minutes. Synthetic amyloid beta peptides are useful as research tools for studying neurotoxicity resulting from Abeta peptide-enhanced free-radical production. The treatment increases the activity of the synthetic Abeta peptides in tests to determine free-radical

CC generating capacity and glutamine synthetase inactivation.  
SQ Sequence 33 AA;

Query Match 100.0%; Score 16; DB 1; Length 33;  
Best Local Similarity 100.0%; Pred. Nc. 1.1e-11;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 DAEFRHDSGYEVHK 16  
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Db 1 DAEFRHDSGYEVHK 16

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